

RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals.";  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 DR InterPro: IPR002181; Fibrinogen C.  
 DR PROSITE: PSC0514; FIBRIN AG C DOMAIN, PARTIAL.  
 KW Blood coagulation; Plasma; Sulfation.  
 FT PEPTIDE 1 20  
 FT MOD RES 5 5  
 FT NON TER 20 20  
 FT SEQUENCE 20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;  
 SQ  
 Query Match 27.3%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLP 9  
 DB 14 KLP 16  
 RESULT 11  
 ID M117 BOVIN STANDARD; PRT; 20 AA.  
 AC P3545;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE 17 kDa milk glycoprotein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Milk;  
 RX MEDLINE=93308294; PubMed=8320368;  
 RA Soerensen E.S., Petersen T.E.;  
 RT "Purification and characterization of three proteins isolated from  
 RT the porcine peptone fraction of bovine milk.";  
 RL J. Dairy Res. 60:189-197(1993).  
 CC -!- FTM: N-GLYCOSYLATED.  
 CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.  
 KW Glycoprotein; Milk.  
 FT NON TER 1 1  
 FT NON TER 20 20  
 FT SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;  
 SQ  
 Query Match 27.3%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLP 9  
 DB 11 KLP 13  
 RESULT 12  
 ID FYRI ANTEL STANDARD; PRT; 4 AA.  
 AC P59706;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Antho-Riamide I [Contains: Antho-Riamide II].  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 CC Nymantidae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92270459; PubMed=1821096;  
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
 RA Gimmelikhuijzen C.J.P.;  
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
 RT biologically active L-3-phenylacetyl-Tyr-Arg-Ile-NH2 and its  
 RT des-phenylacetyl fragment Tyr-Arg-Ile-NH2.";  
 RL Peptides 12:1165-1173(1991).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=93391436; PubMed=8397415;  
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Gimmelikhuijzen C.J.P.;  
 RT "The expansion behaviour of sea anemones may be coordinated by two  
 RT inhibitory neuropeptides, Antho-Kaamide and Antho-Riamide.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993)  
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
 CC groups. May be involved in the expansion phase of feeding  
 CC behaviour in sea anemones.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron-specific.  
 KW Neuropeptide; Amidation.  
 FT CHAIN 1 4  
 FT CHAIN 2 4  
 FT MOD RES 1 1  
 FT MOD RES 4 4  
 FT SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;  
 SQ  
 Query Match 18.2%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FY 6  
 DB 1 FY 2  
 RESULT 13  
 ID PRCT PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Proctolin.  
 OS Periplaneta americana (American cockroach),  
 OS Limulus polyphemus (Atlantic horseshoe crab), and  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 6850, 6759;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Starratt A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 RT in insects.";  
 RL Life Sci. 17:1253-1256(1975).  
 RN [2]  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=81225865; PubMed=6113690;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron.";  
 RL Science 213:567-569(1981).  
 RN [3]

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RP SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RL horseshoe crab, Limulus polyphemus.";
RN Peptides 11:205-211(1990).
RP [4]
RP SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangler J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RL pericardial organs of the shore crab, Carcinus maenas.";
RN Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
DB 3 LP 4

RESULT 14
FARP MONEX
ID FARP MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FMRPamide-like neuropeptide GNFRP-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28641;
RN [1]
RP SPECIES=
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRPamide: a novel FMRPamide-immunoreactive peptide isolated from
RT the sheep tapeworm, Moniezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A43129; A43129.
KW Neuropeptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 2 NF 3

RESULT 15
OVM LEPE
ID OVM LEPE STANDARD; PRT; 6 AA.

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AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (Lep-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OX Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SPECIES=
RX MEDLINE=91271080; PubMed=2052497;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
RL decemlineata";
RN Peptides 12:31-36(1991).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YK 7
DB 3 YK 4

RESULT 16
TRPI PSEPU
ID TRPI PSEPU STANDARD; PRT; 6 AA.
AC P36474;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TRPA operon transcriptional activator (fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SPECIES=
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RL putida";
RN Biochimie 71:521-531(1989).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
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EMBL; X13299; CAA31660.1; -.

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DR InterPro: IPR000847; HTH_LYSR.
DR PROSITE: PS00044; HTH_LYSR FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
Db 5 LP 6

RESULT 17
CARP_MYTED
ID FARI_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka I.;
RL "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
DR PIR; A29342; BCMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 67340726876659DB0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
Db 2 MP 3

RESULT 18
FARI_MACRS
ID FARI_MACRS STANDARD; PRT; 7 AA.
AC P83274;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLPL (DNPFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).

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CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO: GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540A0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
Db 3 NF 4

RESULT 19
FARI_PROCL
ID FARI_PROCL STANDARD; PRT; 7 AA.
AC P38499;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cardiac excitatory FMRFamide homolog NPL.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;
RA Mercier A.J., Orchard I., Tebruggge V., Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish
RT pericardial organs.";
RL Peptides 14:137-143(1993).
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540A20 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
Db 3 NF 4

RESULT 20
FARI_PROCL
ID FARI_PROCL STANDARD; PRT; 7 AA.
AC P38498;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cardiac excitatory FMRFamide homolog DP2.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;

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RA Merrier A.J., Orchard I., Tebrugge V., Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish
RL pericardial organs.";
CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 21
FAR4_PANRE STANDARD; PRT; 7 AA.
AC P41675;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuroptide PP4 (KPNFIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OC NCBI_TaxID=6233;
[1]
SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
RA Tim L., Kubiak T.M., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of
RT KPNFIRFamide, a novel FMRFamide-related peptide from the free-living
RT nematode, Panagrellus redivivus.";
RL Peptides 16:87-93(1995).
CC -1- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
CC MUSCLE TENSION INCREASE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 22
FARB_CALVO STANDARD; PRT; 7 AA.
AC F41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OC NCBI_TaxID=27454;

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RN SEQUENCE.
RP TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.P., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B44787;
DR Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 23
HY7_PIG STANDARD; PRT; 7 AA.
ID HY7_PIG
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
[1]
SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saffran K., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981).
DR PIR; A01417; NYPG7.
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YK 7
Db 6 YK 7

RESULT 24
IGAO_DACDE STANDARD; PRT; 7 AA.
ID IGAO_DACDE
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OC NCBI_TaxID=5132;
[1]
SEQUENCE.
RN Avigad G., Markus Z.;

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RT      "Identification of a peptide inhibitor of galactose oxidase from
RL      Dactylium dendroides."
CC      -1- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
CC      GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC      BINDING TO ITS PROSTHETIC COPPER GROUP.
DR      PIR; A01341; KEYDGD.
KW      Copper; Metalloenzyme inhibitor.
SQ      SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QN 4
DB      3 QN 4

RESULT 25
UN06 PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LP 9
DB      5 LP 6

RESULT 26
WWA2 ACHFU
ID WWA2_ACHFU STANDARD; PRT; 7 AA.
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-2
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RA "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from

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RT      ganglia of the African giant snail, Achatina fulica."
RL      FEBS Lett. 323:104-108(1993).
DR      PIR; S33246; S33246.
KW      Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362DSB686D32310 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 QM 11
DB      3 QM 4

RESULT 27
AKHG GRYBI
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88108553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus."
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera."
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 NF 5
DB      3 NF 4

RESULT 28
AKH LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;

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RESULT 30
ALL6_CVDPO          STANDARD;          PRT;          8 AA.
ID AC 82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
DE Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyosia;
OC Tortricodea; Tortricidae; Olethreutinae; Cydia.
OC NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX TISSUE=Larva;
RC MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Minstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
RW -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
FT MDL RES 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB ||
5 NF 6

RESULT 31
COM2_CONPU          STANDARD;          PRT;          8 AA.
ID AC P88785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OC Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clyborton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99 (1999).
RW -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4
FT MDL RES 4 4
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No.1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
DB ||

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Db 5 LP 6

RESULT 32  
COXG RAT  
ID COXG RAT STANDARD; PRT; 8 AA.  
AC P80430;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIB (EC 1.9.3.1) (AED) (Fragment).  
GN COX6B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RN SEQUENCE.  
RP STRAIN=Wistar; TISSUE=Liver;  
RX MEDLINE=95324529; PubMed=7601105;  
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
amino-terminal sequences suggest identity of the fetal heart and the  
adult liver isoform";  
RL Bur. J. Biochem. 230:235-241(1995).  
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN  
MITOCHONDRIAL ELECTRON TRANSPORT. THIS PROTEIN MAY BE ONE OF THE  
HEME-BINDING SUBUNITS OF THE OXIDASE.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
c + 2 H(2)O.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIB FAMILY.  
DR PIR; S65381; S65391.  
KW Oxidoreductase; Mitochondrion.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4  
1 QN 2

Db

RESULT 33  
FAR1 PANRE  
ID FAR1 PANRE STANDARD; PRT; 8 AA.  
AC P41872;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide PF1 (SDPNFLRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RN SEQUENCE.  
RX MEDLINE=93027659; PubMed=1408999;  
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
RA Garrison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRFamide-like peptides from the free-living nematode  
Panagrellus redivivus";  
RL Peptides 13:209-214(1992).  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CAUDALLY TO THE BASE OF THE PHARYNX.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY  
KW Neuropeptide; Amidation.

FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5  
4 NF 5

Db

RESULT 34  
FAR1 PENWO  
ID FAR1 PENWO STANDARD; PRT; 8 AA.  
AC P83316;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP1 (GDRNFLRF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RP TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupoen J., Krungkeasem C., Longyant S.,  
RA Chaivachangkur P.;  
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
of the giant tiger prawn Penaeus monodon";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5  
4 NF 5

Db

RESULT 35  
FAR2 MACRS  
ID FAR2 MACRS STANDARD; PRT; 8 AA.  
AC P83275;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP2 (ADKNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RP TISSUE=Eyestalk;  
RX Sithigorngul P., Saraihongkum W., Jaidechoy S., Longyant S.,  
RA Sithigorngul W.;  
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
freshwater prawn Macrobrachium rosenbergii";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NF 5  
 DB 4 NF 5  
 RESULT 36  
 FAR3\_HOMAM ID FAR3\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).  
 OS Homarus americanus (American lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 CC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=86116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamidlike immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -1- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM  
 CC POTASSIUM IN THE PRESENCE OF CALCIUM.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8 AMIDATION  
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NF 5  
 DB 4 NF 5  
 RESULT 37  
 FAR4\_HOMAM ID FAR4\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41487;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).  
 OS Homarus americanus (American lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 CC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;

RT "Purification and characterization of FMRFamidlike immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC  
 CC NEUROMUSCULAR JUNCTIONS.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8 AMIDATION  
 SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NF 5  
 DB 4 NF 5  
 RESULT 38  
 HTF1\_PERAM ID HTF1\_PERAM STANDARD; PRT; 8 AA.  
 AC P04578;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertrihaloaemic factor 1 (Neuropeptide M-I) (Periplanetin CC-I)  
 DE (Pea-CAH-1) (Ied-CC-1) (Hypertrihaloaemic neuropeptide 1).  
 OS Periplaneta americana (American cockroach).  
 OS Blattella germanica (German cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 7539, 6976;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=85046530; PubMed=6548628;  
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
 RA Rinehart K.L. Jr.;  
 FT "Structures of two cockroach neuropeptides assigned by fast atom  
 FT bombardment mass spectrometry.";  
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=84298179; PubMed=6591205;  
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
 RA Miller C.A., Schooley D.A.;  
 RT "Isolation and primary structure of two peptides with  
 RT cardioacceleratory and hyperglycemic activity from the corpora  
 RT cardiaca of Periplaneta americana.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=L.deceimlineata; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90160053; PubMed=2576128;  
 RA Gaede G., Kellner R.;  
 FT "The metabolic neuropeptides of the corpus cardiaca from the potato  
 FT beetle and the American cockroach are identical.";  
 RL Peptides 10:1287-1289(1989).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrihaloaemic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast

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RT atom bombardment mass spectrometry.
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A44960; A44960.
DR PIR; A49823; A49823.
DR PIR; S08995; S08995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 3 NF 4

RESULT 39
HTF TENMO
ID HTF TENMO STANDARD; PRT; 8 AA.
AC P25719;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypertrichalosemic factor (HOTH) (Hypertrichalosemic neuropeptide).
OS Tenebrio molitor (Yellow mealworm), and
OS Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067, 7075;
[1] SEQUENCE.
RP SPECIES=T.molitor, and Z.rugipes;
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90341091; PubMed=2381871;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrichalosemic neuropeptide from
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL Peptides 11:453-459(1990).
CC -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A43976; A43976.
DR PIR; B43976; B43976.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 3 NF 4

RESULT 40
LCK8 LEUNA
ID LCK8 LEUNA STANDARD; PRT; 8 AA.

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AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
[1] SEQUENCE.
RP TISSUE=Head;
RC Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
DB 4 FY 5

RESULT 41
NPB BOVIN
ID NPB BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1] SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3
DB 5 PQ 6

RESULT 42

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RPCH\_PANBO  
ID \_RPCH\_PANBO STANDARD; PRT; 8 AA.  
AC P08939;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Red pigment concentrating hormone (RPCH)  
OS Pandanus borealis (Northern red shrimp)  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Pandaloidae;  
OC Pandalidae; Pandalus.  
OX NCBI\_TaxID=6703;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75054965; PubMed=4433569;  
RA Fernlund P.;  
RT "Structure of the red-pigment-concentrating hormone of the shrimp,  
RT Pandanus borealis.";  
RL Biochim. Biophys. Acta 371:304-311(1974).  
CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY  
CC -1- STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-  
CC CHROMATOPHORES.  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A61348; A61348.  
DR InterPro: IPR002047; AKH.  
DR PROSITE; PS00256; AKH.1.  
KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 8 8  
FT MOD\_RES 8 AA; 948 MW; 86786775B9C44736 CRC64;  
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4 NF 5  
DB 3 NF 4  
RESULT 43  
UPAA\_HUMAN  
ID \_UPAA\_HUMAN STANDARD; PRT; 8 AA.  
AC P30096;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.  
DR SWISS-2DPAGE; P30096; HUMAN.  
FT NON\_TER 1 1  
FT VARIANT 5 5 F -> P.  
FT NON\_TER 8 8 /FTID=VAR\_000004.  
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FY 6  
DB 5 FY 6  
RESULT 44  
ALLO\_CARMA  
ID \_ALLO\_CARMA STANDARD; PRT; 9 AA.  
AC P81813;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 10.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD\_RES 9 9  
FT MOD\_RES 9 AMIDATION.  
FT SEQUENCE 9 AA; 963 MW; 372D79CDBA776C7 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 PQ 3  
DB 2 PQ 3  
RESULT 45  
FARI\_CALVO  
ID \_FARI\_CALVO STANDARD; PRT; 9 AA.  
AC P41856;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Calliphramide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Renfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliphramides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
CC SALIVARY GLAND OF CALLIPHORA.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A41978; A41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 AMIDATION.  
FT MOD\_RES 9



SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQ 3  
 ||  
 Db 2 PQ 3

RESULT 46  
 FAR2 PANRE  
 ID FAR2 PANRE STANDARD; PRT; 9 AA.  
 AC P41873;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRamide-like neuropeptide PF2 (SADPNFLRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OC NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RA Garrison R.D., Williams J.F., Friedman A.R.;  
 RT "Two FMRamide-like peptides from the free-living nematode  
 Panagrellus redivivus";  
 RL Peptides 13:209-214(1992).  
 CC -!- FUNCTION: WTCACTIVE.  
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
 CC -!- CAUDALLY TO THE BASE OF THE PHARYNX.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5  
 ||  
 Db 5 NF 6

RESULT 47  
 FAR3 MACRS  
 ID FAR3 MACRS STANDARD; PRT; 9 AA.  
 AC P83276;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLP3 (NYDKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OC NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P.; Saraithongkum W., Jaidechoey S., Longyant S.,  
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
 freshwater prawn Macrobrachium rosenbergii";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.

DR GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5  
 ||  
 Db 5 NF 6

RESULT 48  
 FAR5 PENMO  
 ID FAR5 PENMO STANDARD; PRT; 9 AA.  
 AC P83320;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLP5 (SMPSLRFLRF-amide).  
 OS Penaeus monodon (Pencoid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OC NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P.; Pupiem J.; Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk  
 of the giant tiger prawn Penaeus monodon";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MP 2  
 ||  
 Db 2 MP 3

RESULT 49  
 FAR6 MACRS  
 ID FAR6 MACRS STANDARD; PRT; 9 AA.  
 AC P83279;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLP6 (DGGNFELRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OC NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P.; Saraithongkum W., Longyant S., Panchan N.,  
 RA Sithigorngul W., Petsom A.;  
 RT "Three more novel FMRamide-like neuropeptide sequences from the

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RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 50
FARP MACRS STANDARD; PRT; 9 AA.
AC P83281;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRFamide-like neuropeptide FL98 (VSHNNFLSF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraihongkul W., Longyant S., Panchan N.,
RA Sithigorngul W., Petson A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C4441F5 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 51
OXYT CVPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE Vasotocin.
OS Cyprinus carpio (Common carp), and
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962, 7757;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Isolation of finback whale oxytocin and vasopressin.";

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RP SEQUENCE.
RC SPECIES=C. carpio; TISSUE=Pituitary;
RX MEDLINE=88225976; PubMed=3371648;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. marinus; TISSUE=Pituitary;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawachi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4
DB 4 QN 5

RESULT 52
OXYT RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus), (Common torquall),
OS Balaeoptera physalus (Finback whale),
OS Tachygllossus aculeatus aculeatus (Austrian echidna), and
OS Hydroclaus collieri (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Isolation of finback whale oxytocin and vasopressin.";

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Query Match      18.2%, Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PQ 3
      ||
DB      7 PQ 8

RESULT 54
OXYV_SQUAC
ID OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
OC NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=71218038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT FT 9 ANIDATION.
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match      18.2%, Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QN 4
      ||
DB      4 QN 5

RESULT 55
RS10_SERMA
ID RS10_SERMA STANDARD; PRT; 9 AA.
AC O68936;
30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment).
GN RPSU.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OC NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA Noorani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBS databases.
CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By

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CC      similarity).
CC      -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AF058451; AAC14294.1; -.
CC      HMAP; MF_00508; -. 1. Ribosomal S10.
CC      InterPro; IPR001848; Ribosomal_S10.
CC      PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
CC      KW Ribosomal protein.
CC      FT NON TER 9
CC      SQ SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;
CC
CC      Query Match 18.2%; Score 2; DB 1; Length 9;
CC      Best Local Similarity 100.0%; Pred. No. 1.3e+05;
CC      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 3 QN 4
CC      ||
CC      Db 2 QN 3
CC
CC      RESULT 56
CC      TKCL CALVO
CC      ID TKCL_CALVO STANDARD; PRT; 9 AA.
CC      AC P41517;
CC      DT 01-NOV-1995 (Rel. 32, Created)
CC      DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC      DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC      DE Callitachykinin I.
CC      OS Calliphora vomitoria (Blue blowfly).
CC      OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC      OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC      OC Calliphoridae; Calliphora.
CC      OX NCBI_TaxID=27454;
CC      RN [1]
CC      RP SEQUENCE, AND SYNTHESIS.
CC      RX MEDLINE=95075727; PubMed=7984492;
CC      RA Lundquist C.F., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
CC      Maessel D.R.;
CC      RT "Callitachykinin I and II, two novel myotropic peptides isolated from
CC      the blowfly, Calliphora vomitoria, that have resemblances to
CC      tachykinins."
CC      RL Peptides 15:761-768(1994).
CC      CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC      CC -!- SUBCELLULAR LOCATION: Secreted.
CC      CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
CC      KW Tachykinin; Neuropeptide; Amidation.
CC      FT MOD RES 9
CC      SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;
CC
CC      Query Match 18.2%; Score 2; DB 1; Length 9;
CC      Best Local Similarity 100.0%; Pred. No. 1.3e+05;
CC      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 5 FY 6
CC      ||
CC      Db 5 FY 6
CC
CC      RESULT 57
CC      TKLI LOCOMI
CC      ID TKLI_LOCOMI STANDARD; PRT; 9 AA.
CC      AC P16223;
CC      DT 01-APR-1990 (Rel. 14, Created)
CC      DT 01-APR-1990 (Rel. 14, Last sequence update)
CC      DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE      Locustatachykinin I (TK-I).
OS      Locusta migratoria (Migratory locust).
OC      Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC      Acridoidea; Acrididae; Oedipodinae; Locusta.
OX      NCBI_TaxID=7004;
RN      [1]
RP SEQUENCE.
RX MEDLINE=90194489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family."
RL FBBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;
CC
CC      Query Match 18.2%; Score 2; DB 1; Length 9;
CC      Best Local Similarity 100.0%; Pred. No. 1.3e+05;
CC      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 5 FY 6
CC      ||
CC      Db 5 FY 6
CC
CC      RESULT 58
CC      ANGI BOTJA
CC      ID ANGI_BOTJA STANDARD; PRT; 10 AA.
CC      AC Q10581;
CC      DT 01-OCT-1996 (Rel. 34, Created)
CC      DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC      DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC      DE Angiotensin-like peptide I (Fragment).
CC      OS Bothrops jararaca (Jararaca).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
CC      OC Viperidae; Crotalinae; Bothrops.
CC      OX NCBI_TaxID=8724;
CC      RN [1]
CC      RP SEQUENCE.
CC      RX MEDLINE=96208932; PubMed=8829801;
CC      RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
CC      RT "Isolation and identification of angiotensin-like peptides from the
CC      plasma of the snake Bothrops jararaca."
CC      RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC      CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC      KW InterPro; IPR000215; Serpin.
CC      DR PROSITE; PS00284; SERPIN; PARTIAL.
CC      KW Vasoconstrictor; Plasma; Serpin.
CC      FT NON TER 10
CC      SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;
CC
CC      Query Match 18.2%; Score 2; DB 1; Length 10;
CC      Best Local Similarity 100.0%; Pred. No. 8.3e+03;
CC      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY 5 FY 6
CC      ||
CC      Db 8 FY 9
CC
CC      RESULT 59
CC      BPP2 BOTIN
CC      ID BPP2_BOTIN STANDARD; PRT; 10 AA.
CC      AC P30422;
CC      DT 01-APR-1993 (Rel. 25, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QN 4  
 DB 1 QN 2  
 RESULT 60  
 ID BPP2 BOTJA STANDARD; PRT; 10 AA.  
 AC P01022;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme  
 DE inhibitor V-6-II). (Jararaca).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,  
 RA Kocy O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
 RT jararaca. Isolation, elucidation of structure, and synthesis.";  
 RL Biochemistry 10:4033-4039(1971).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01255; XAV16B.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QN 4  
 DB 1 QN 2

Db 1 QN 2  
 RESULT 61  
 ID CATB SHEEP STANDARD; PRT; 10 AA.  
 AC P83205;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
 GN CTSB  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Placenta;  
 RX MEDLINE=23394055; PubMed=12506352;  
 RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,  
 RA Mooko H.B., Beckers J.-F.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated  
 RT glycoproteins from the ewe placenta.";  
 RL Mol. Reprod. Dev. 64:199-206(2003).  
 CC -!- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins. Has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves Arg-Arg-|-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin L). In  
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
 CC by a disulfide bond (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro; IPR000169; SHP01 acsite.  
 DR PROSITE; PS00640; THIOI\_PROTEASE ASN; PARTIAL.  
 DR PROSITE; PS00139; THIOI\_PROTEASE CYS; PARTIAL.  
 DR PROSITE; PS00639; THIOI\_PROTEASE HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9DSBA CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LP 9  
 DB 1 LP 2  
 RESULT 62  
 ID COXK ONCMY STANDARD; PRT; 10 AA.  
 AC P80332;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).  
 OS Oncomorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=94237150; PubMed=8181469;  
 RA Freund R., Kadenbach B.;

RT "Identification of tissue-specific isoforms for subunits Vb and VIa  
 of cytochrome c oxidase isolated from rainbow trout."  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferrocyclochrome  
 c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIaA FAMILY.  
 DR PIR: S43631; 943631  
 KW Oxidoreductase; inner membrane; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KL 8  
 ||  
 Db 9 KL 10

RESULT 63  
 FAR6 PANRE  
 ID FAR6 PANRE STANDARD; PRT; 10 AA.  
 AC P82660;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRPamide-like neuropeptide PF6 (NGAPQFVRP-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OC NCBI\_TaxID=6233;  
 [1]  
 RN SEQUENCE, FUNCTION, AND AMIDATION.  
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 Maule A.G.;  
 RA "Isolation, characterization and pharmacology of FMRPamide-related  
 peptides (FARPs) from free-living nematode, Panagrellus redivivus."  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1132 MW; C813E4C9D776C76D CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PQ 3  
 ||  
 Db 4 PQ 5

RESULT 64  
 FAR7 MACRS  
 ID FAR7 MACRS STANDARD; PRT; 10 AA.  
 AC P83280;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRPamide-like neuropeptide Flp7 (GIGRNRFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OC NCBI\_TaxID=79674;  
 [1]  
 RN

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=eyestalk;  
 RX MEDLINE=21107394; PubMed=11179812;  
 RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,  
 Sithigorngul W., Petson A.;  
 RT "Three more novel FMRPamide-like neuropeptide sequences from the  
 eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."  
 RT Peptides 22:191-197(2001).  
 RL CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC GO: GO:0007218; P-neuropeptide signaling pathway; IDA.  
 DR Neuropeptide; Amidation.  
 KW MOD\_RES 10 10  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1244 MW; 3CF9C29C4540A8 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NF 5  
 ||  
 Db 6 NF 7

RESULT 65  
 FAR6 CALVO  
 ID FAR6 CALVO STANDARD; PRT; 10 AA.  
 AC P41867;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE CalliFMRPamide 12.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OC NCBI\_TaxID=27454;  
 [1]  
 RN SEQUENCE.  
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 Rehfeld J.F., Thorpe A.;  
 RA "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated calliFMRPamides) from the blowfly  
 Calliphora vomitoria".  
 RL Proc Natl Acad Sci U.S.A. 89:2326-2330(1992).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC PIR: C44787; C44787.  
 DR Neuropeptide; Amidation.  
 KW MOD\_RES 10 10  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1156 MW; 22810399C44AB6D8 CRC64;  
 Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NF 5  
 ||  
 Db 6 NF 7

RESULT 66  
 GON3 ONCKE  
 ID GON3 ONCKE STANDARD; PRT; 10 AA.  
 AC P20367; P81751;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (LH-  
 RH III) (Luliberin III).  
 [1]  
 RN

GN GNRH3.  
OS Oncorhynchus keta (Chum salmon), and  
OC Clupea pallasii (Pacific herring).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8018, 30724;  
RN  
RP SEQUENCE.  
RC SPECIES=O.keta;  
RA MEDLINE=83195140; PubMed=6341999;  
RX Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;  
RT "Characterization of a teleost gonadotropin-releasing hormone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).  
RN [2]  
RP SEQUENCE AND FUNCTION  
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
RX MEDLINE=20114351; PubMed=10650329;  
RA Carlsfeld J., Powell J.F., Park M., Fischer W.H., Craig A.G.,  
RA Chang J.P., Rivier J.E., Sherwood N.M.;  
RT "Primary structure and function of three gonadotropin-releasing  
hormones, including a novel form, from an ancient teleost, herring.";  
RL Endocrinology 141:505-512(2000).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
the secretion of both luteinizing and follicle-stimulating  
hormones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR: A21114; A21114.  
DR InterPro: IPR002012; GNRH.  
DR Pfam: PF00446; GNRH; 1.  
DR PROSITE: PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 10  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 LP 9  
DB 8 LP 9

RESULT 67  
GNL SQAC  
ID GNL SQAC STANDARD; PRT; 10 AA.  
AC P27429;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH)  
DE (Luliberin).  
OS Squalus acanthias (Spiny dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.  
OX NCBI\_TaxID=7797;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92335300; PubMed=1631133;  
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,  
RA Nanciarik C.S., Peter R.E., Rivier J.E., Sherwood N.M.;  
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in  
dogfish brain provides insight into GNRH evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).  
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR: A46030; A46030.  
DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.  
DR PROSITE: PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 10  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 LP 9  
DB 8 LP 9

RESULT 68  
HTF ROMMI  
ID HTF ROMMI STANDARD; PRT; 10 AA.  
AC P18110;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE RO I (Hypertrehalosaemic factor).  
OS Romalea microptera (Lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Romaleidae; Romalea.  
OX NCBI\_TaxID=7007;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RECH-family from  
the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-688(1988).  
CC -!- FUNCTION: HYPERTREHALSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS  
THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).  
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 10  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 NF 5  
DB 3 NF 4

RESULT 69  
HTF NAUCI  
ID HTF NAUCI STANDARD; PRT; 10 AA.  
AC P10939;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).  
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),  
OS Leucophaea maderae (Madeira cockroach),  
OS Blattella germanica (German cockroach),  
OS Gromphadorina portentosa (Madagascan hissing cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;  
OC Blaberidae; Nauphoeta.  
OX NCBI\_TaxID=6990, 6988, 6973, 36953;

```

RN [1]
RP SEQUENCE.
RC SPECIES=N.cinerea; TISSUE=Corpoca cardiaca;
RX MEDLINE=87100208; PubMed=3801028;
RA Gaede G., Rinehart K.L. Jr.;
RT "Amino acid sequence of a hypertrihaloasemic neuropeptide from the
RL corpus cardiaca of the cockroach, Nauphoeta cinerea.";
RN Biol. Chem. Biophys. Res. Commun. 141:774-781(1986).
RN [2]
RN SEQUENCE.
RC SPECIES=L.maderae; G.portentosa, and B.germanica;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
RN the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RN and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RN Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RN SEQUENCE.
RC SPECIES=B.germanica;
RX MEDLINE=91179584; PubMed=2080017;
RA Veenstra J.A., Camps F.;
RT "Structure of the hypertrihaloasemic neuropeptide of the German
RN cockroach, Blattella germanica.";
RN Neuropeptides 15:107-109(1990).
CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A26381; A26381.
DR PIR; A60421; A60421.
DR PIR; S08997; S08997.
DR PIR; S08998; S08998.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD.RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1092 MW; 05623678675B9C4 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 70
MOSQ CLYJA STANDARD; PRT; 10 AA.
AC P19962;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Gln6]-mosaic.
OS Clypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinozoa; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RN SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K., Kajitara H., Nomura K., Yamaguchi M.;
RT "Purification and structure of mosaic and its derivatives from the
RN egg jelly of the sea urchin Clypeaster japonicus.";
RN Zool. Sci. 4:649-656(1987)
CC -1- FUNCTION: Stimulates sperm respiration and motility.
DR PIR; JN0025; JN0025.

```

```

SQ SEQUENCE 10 AA; 1019 MW; 9AFB032456DDCSBA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QN 4
Db 6 QN 7

RESULT 71
PNEU HUMAN STANDARD; PRT; 10 AA.
ID PNEU HUMAN
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RC TISSUE=Lung;
RA MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RN Regul. Pept. 30:77-87(1990).
CC -1- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
DR PIR; B33143; B33143.
DR GO; GO:0030103; P:vasopressin secretion; NAS.
FT MOD.RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KL 8
Db 5 KL 6

RESULT 72
PNEU RAT STANDARD; PRT; 10 AA.
ID PNEU RAT
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RA MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RN Regul. Pept. 30:77-87(1990).
CC -1- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR; A33143; A33143.
FT MOD.RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;

```



Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8  
||  
Db 5 KL 6

## RESULT 73

RL16\_ACHLA STANDARD; PRT; 10 AA.  
AC P292L1;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE 508 ribosomal protein L16 (fragment).  
GN RPLP.  
OS Acholeplasma laidlawii.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Acholeplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210505; PubMed=1556079;  
RA Lim P.O.; Sears B.B.;  
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like  
organism and Acholeplasma laidlawii deduced from two ribosomal protein  
gene sequences".  
RL J. Bacteriol. 174:2606-2611 (1992).  
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS  
LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER  
(BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M74771; AA021914.1; -;  
DR PDB: F41839; F41839.  
DR InterPro: IPR000114; Ribosomal\_L16.  
DR PROSITE: PS00386; RIBOSOMAL\_L16\_1; PARTIAL.  
DR PROSITE: PS00701; RIBOSOMAL\_L16\_2; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON\_TER 10  
FT SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;  
SQ

Query Match 18.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2  
||  
Db 3 MP 4

## RESULT 74

TEMK\_RANTE STANDARD; PRT; 10 AA.  
AC P56923;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Temporin K.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Skin secretion;  
RX MEDLINE=97175050; PubMed=9022710;  
RA Simmaco M.; Mignogna G.; Canofeni S.; Miele R.; Mangoni M.L.;  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
temporaria".  
RL Eur. J. Biochem. 242:788-792 (1996).  
CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD\_RES 10  
FT SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;  
SQ

Query Match 18.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
||  
Db 2 LP 3

## RESULT 75

TKL2\_LOCM1 STANDARD; PRT; 10 AA.  
AC P16224;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustatachykinin II (TK-II).  
OS Locustatachykinin II (TK-II).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Brain;  
RX MEDLINE=90184489; PubMed=2311766;  
RA Schoofs L.; Holman G.M.; Hayes T.K.; Nachman R.J.; de Loof A.;  
RT "Locustatachykinin I and II, two novel insect neuropeptides with  
homology to peptides of the vertebrate tachykinin family".  
RL FEBS Lett. 261:397-401 (1990).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
OVIDUCT AND FOREGUT.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10  
FT SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;  
SQ

Query Match 18.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6  
||  
Db 6 FY 7

Search completed: November 25, 2003, 18:17:26  
Job time : 6.32447 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 26.5053 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-6

Perfect score: 11

Sequence: 1 MPONFYKLPQM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	19	8 Q9ZY76	Q9ZY76 macroteleia
2	3	27.3	8	2 Q45615	Q45615 bacillus eu
3	3	27.3	8	2 Q9RQ49	Q9RQ49 buchnera ap
4	3	27.3	8	11 Q99B40	Q99B40 mus musculus
5	3	27.3	8	11 Q62527	Q62527 mus spretus
6	3	27.3	9	4 Q14715	Q14715 homo sapien
7	3	27.3	9	8 P92072	P92072 euhadra her
8	3	27.3	9	8 Q94VG2	Q94VG2 varanus ind
9	3	27.3	9	11 Q8CG13	Q8CG13 mus musculus
10	3	27.3	10	2 Q9XBH3	Q9XBH3 bacillus ce
11	3	27.3	11	3 Q9URGL	Q9URGL neurospora
12	3	27.3	12	2 Q51579	Q51579 rhodobacter
13	3	27.3	13	2 Q9P889	Q9P889 streptococc
14	3	27.3	13	11 Q9QVL4	Q9QVL4 rattus sp.
15	3	27.3	14	13 Q91777	Q91777 xenopus lae
16	3	27.3	15	2 Q53580	Q53580 rhodobacter

17	3	27.3	15	2 Q9X637	Q9X637 klebsiella
18	3	27.3	15	2 Q9X635	Q9X635 escherichia
19	3	27.3	15	10 P82331	P82331 piusm sativ
20	3	27.3	15	12 Q66174	Q66174 human coron
21	3	27.3	16	2 Q9F9S4	Q9F9S4 helicobacte
22	3	27.3	16	2 Q9R4X4	Q9R4X4 pseudomonas
23	3	27.3	16	2 Q10748	Q10748 clostridium
24	3	27.3	16	6 Q28324	Q28324 capra hircu
25	3	27.3	16	8 Q34699	Q34699 helianthus
26	3	27.3	17	2 Q9ETL3	Q9ETL3 helicobacte
27	3	27.3	17	6 Q46667	Q46667 mactopus ro
28	3	27.3	17	11 Q9QUY6	Q9QUY6 rattus sp.
29	3	27.3	18	2 Q9ZG42	Q9ZG42 chlamydia t
30	3	27.3	18	4 Q9UC58	Q9UC58 homo sapien
31	3	27.3	18	4 Q16167	Q16167 homo sapien
32	3	27.3	18	10 Q8LNN9	Q8LNN9 oryza sativ
33	3	27.3	18	11 P70649	P70649 mus sp. syn
34	3	27.3	18	11 Q9QV11	Q9QV11 rattus sp.
35	3	27.3	18	11 P70650	P70650 mus sp. syn
36	3	27.3	18	13 Q9PRR7	Q9PRR7 gallus gall
37	3	27.3	19	4 Q8NFL2	Q8NFL2 homo sapien
38	3	27.3	19	4 Q9UD97	Q9UD97 homo sapien
39	3	27.3	19	5 Q9TWD0	Q9TWD0 sphaerechin
40	3	27.3	19	8 Q31687	Q31687 artemia par
41	3	27.3	19	8 Q9XMB5	Q9XMB5 aegilops ta
42	3	27.3	19	13 Q9DPN3	Q9DPN3 gillichthys
43	3	27.3	20	2 Q5X629	Q5X629 pseudomonas
44	3	27.3	20	2 Q9X632	Q9X632 pseudomonas
45	3	27.3	20	2 Q9X634	Q9X634 serratia na
46	3	27.3	20	2 Q9WU7	Q9WU7 escherichia
47	3	27.3	20	2 Q9X630	Q9X630 lechericia a
48	3	27.3	20	2 Q46499	Q46499 desulfovibr
49	3	27.3	20	4 Q8NFW3	Q8NFW3 homo sapien
50	3	27.3	20	4 Q81213	Q81213 homo sapien
51	3	27.3	20	5 Q9TW18	Q9TW18 ceratitlis c
52	3	27.3	20	10 Q9S8A8	Q9S8A8 secalc cere
53	3	27.3	20	13 P83308	P83308 gallus gall
54	2	18.2	7	2 Q50556	Q50556 actinobacil
55	2	18.2	7	2 Q8GL00	Q8GL00 borrelia bu
56	2	18.2	7	8 Q98866	Q98866 spinacia ol
57	2	18.2	7	8 Q95945	Q95945 saccharomyc
58	2	18.2	7	11 Q63668	Q63668 rattus norv
59	2	18.2	7	12 Q62205	Q62205 transmissib
60	2	18.2	7	12 Q68113	Q68113 cherry leaf
61	2	18.2	7	15 Q8UE81	Q8UE81 human immun
62	2	18.2	8	2 Q09258	Q09258 synechococc
63	2	18.2	8	2 Q87471	Q87471 haemophilus
64	2	18.2	8	2 Q9Z1B9	Q9Z1B9 neisseria m
65	2	18.2	8	2 Q9R5K0	Q9R5K0 shigella dy
66	2	18.2	8	3 P87225	P87225 saccharomyc
67	2	18.2	8	4 Q15889	Q15889 homo sapien
68	2	18.2	8	4 Q15895	Q15895 homo sapien
69	2	18.2	8	4 Q15901	Q15901 homo sapien
70	2	18.2	8	4 Q15893	Q15893 homo sapien
71	2	18.2	8	4 Q9HCQ0	Q9HCQ0 homo sapien
72	2	18.2	8	4 Q9P0K3	Q9P0K3 homo sapien
73	2	18.2	8	5 Q9TWH6	Q9TWH6 perinerreis
74	2	18.2	8	5 Q02032	Q02032 lytechinus
75	2	18.2	8	5 Q9TRX8	Q9TRX8 bos taurus
76	2	18.2	8	6 Q9XSV1	Q9XSV1 canis famil
77	2	18.2	8	8 Q9T2Y3	Q9T2Y3 begonia for
78	2	18.2	8	8 Q9T2Y3	Q9T2Y3 varanus yuw
79	2	18.2	8	8 Q9T2Y2	Q9T2Y2 begonia for
80	2	18.2	8	8 Q9T2Y2	Q9T2Y2 locusta mig
81	2	18.2	8	8 Q94VB2	Q94VB2 varanus sal
82	2	18.2	8	8 Q9T2Y2	Q9T2Y2 begonia tai
83	2	18.2	8	8 Q94VA7	Q94VA7 varanus sal
84	2	18.2	8	8 Q94VB5	Q94VB5 varanus sal
85	2	18.2	8	10 Q9T2Y1	Q9T2Y1 begonia apt
86	2	18.2	8	10 Q9XGL9	Q9XGL9 begonia nan
87	2	18.2	8	10 Q9XGL8	Q9XGL8 begonia chi
88	2	18.2	8	10 Q9STD5	Q9STD5 begonia pal
89	2	18.2	8	11 Q9QV15	Q9QV15 rattus sp.

90 2 18.2 8 11 Q99NX9 Q99nx9 hydrochoeru  
 91 2 18.2 8 11 Q9ET21 Q9et21 mus musculus  
 92 2 18.2 8 11 Q9QVK5 Q9qvk5 rattus sp.  
 93 2 18.2 8 12 Q83349 Q83349 murine coro  
 94 2 18.2 8 12 Q89498 Q89498 murine hepa  
 95 2 18.2 8 13 P87488 P87488 oncorhynch  
 96 2 18.2 8 13 Q8J335 Q8j335 ficedula hy  
 97 2 18.2 9 2 Q47556 Q47556 escherichia  
 98 2 18.2 9 2 P72345 P72345 pseudomonas  
 99 2 18.2 9 2 Q9R5R1 Q9r5r1 shigella dy  
 100 2 18.2 9 2 Q46179 Q46179 clostridium

## ALIGNMENTS

RESULT 1  
 Q92Y76 ID Q92Y76 PRELIMINARY; PRT; 19 AA.  
 AC Q92Y76;  
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)  
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)  
 DE Cytochrome oxidase II (Fragment).  
 OS Macroteleia sp.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastridae;  
 OC Scellionidae; Macroteleia.  
 OX NCBI\_TaxID=81090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99152621; PubMed=10028295;  
 RA Dowton M., Austin A.D.;  
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
 the hymenoptera";  
 RL Mol. Biol. Evol. 16:298-309(1999).  
 DR EMBL; AF082925; AAD17785.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 19 AA; 2365 MW; 78C4D5D3A7ABCA1 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0;

QY 4 NFYK 7  
 DB 10 NFYK 13

RESULT 2  
 Q4S615 ID Q4S615 PRELIMINARY; PRT; 8 AA.  
 AC Q4S615;  
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DE GutB protein (Fragment).  
 GN GUTB.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=168;  
 RC MEDLINE=94253000; PubMed=8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis glucitol  
 dehydrogenase gene";  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL; L16626; AAA20875.1; -.  
 FT NON\_TER 8

SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;  
 Query Match 27.3%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0;

QY 2 PQN 4  
 DB 6 PQN 8

RESULT 3  
 Q9RQ49 ID Q9RQ49 PRELIMINARY; PRT; 8 AA.  
 AC Q9RQ49;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)  
 DE Nifs protein homolog (Fragment).  
 GN NIFS.  
 OS Buchnera aphidicola.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=9;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20022990; PubMed=1055290;  
 RA Clark M.A., Moran N.A., Baumann P.;  
 RT "Sequence evolution in bacterial endosymbionts having extreme base  
 compositions";  
 RL Mol. Biol. Evol. 16:1586-1598(1999).  
 DR EMBL; AF130814; AAF13805.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0;

QY 7 KLP 9  
 DB 2 KLP 4

RESULT 4  
 Q99P40 ID Q99P40 PRELIMINARY; PRT; 8 AA.  
 AC Q99P40;  
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
 DE Repressor of GATA (Fragment).  
 GN ROG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57B6;  
 RA Miao S., Ho I.;  
 RT "ROG is a NF-AT target gene that partly rescues the phenotype of NF-  
 ATC2/NF-ATC3 deficient Th cells";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF335542; AAG59843.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0;

QY 1 MPQ 3



Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
|||  
Db 7 FYK 9

RESULT 9  
Q8CG13 PRELIMINARY; PRT; 9 AA.  
AC Q8CG13;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A (Fragment).  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10990;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Wyder K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;  
RT "The mouse orthologue of the human ionotropic glutamate receptor-like gene (GRIN11A) maps to mouse chromosome 9.";  
RL Submitted (DEC-2001) to the EMBL/GenBank/DDJ databases.  
DR EMBL: AF462417; AA015648.1; -;  
DR EMBL: AF462416; AA015648.1; JOINED.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;

Query Match 27.3%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
|||  
Db 7 KLP 9

RESULT 10  
Q9XBH3 PRELIMINARY; PRT; 10 AA.  
AC Q9XBH3;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE cAMP-like protein (Fragment).  
GN CLEF  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 10987;  
RX MEDLINE=99231848; PubMed=10217496;  
RA Oktad O.A., Hegna I., Lindbaeck T., Rishovd A.I., Kolsto A.B.;  
RT "Genome organisation is not conserved between Bacillus cereus and Bacillus subtilis."  
RL Microbiology 145:621-631(1999).  
DR EMBL: AJ000394; CAB40625.1; -;  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1264 MW; D3757EC33339C9D6 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10

Db 1 LPQ 3  
|||

RESULT 11  
Q9URG1 PRELIMINARY; PRT; 11 AA.  
AC Q9URG1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Cytochrome c oxidase subunit 2 (fragment).  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92035059; PubMed=1657411;  
RA Lemire E.G., Percy J.A., Correia J.M., Crowther B.M., Nargang F.E.;  
RT "Alteration of the cytochrome c oxidase subunit 2 gene in the [exn-5] mutant of Neurospora crassa.";  
RL Curr. Genet. 20:121-127(1991).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1222 MW; 936B1558C7605DC5 CRC64;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FQM 11  
|||  
Db 7 FQM 9

RESULT 12  
Q53579 PRELIMINARY; PRT; 12 AA.  
AC Q53579;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Light-harvesting complex I alpha polypeptide (fragment).  
GN PUFA.  
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92234963; PubMed=1569029;  
RA Richter P., Brand M., Drews G.;  
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa mutants.";  
RL J. Bacteriol. 174:3030-3041(1992).  
DR EMBL: S97551; AAC60405.1; -;  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6E8A70532B CRC64;

Query Match 27.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
|||  
Db 4 FYK 6

RESULT 13  
Q9R889 PRELIMINARY; PRT; 13 AA.  
AC Q9R889;

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE C5a peptidase (Fragment).  
 OS SCPA.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 ON NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AP1.  
 RX MEDLINE=98398075; PubMed=9632622;  
 RA Berge A.; Rasmussen M.; Eijck L.;  
 RT "Identification of an insertion sequence located in a region encoding  
 RL virulence factors of Streptococcus pyogenes."  
 DR EMBL; AF064540; AAC38768.1; -.  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1603 MW; 5EDADCDAGCEG723 CRC64;  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 KLP 9  
 Db |||  
 6 KLP 8  
  
 RESULT 14  
 Q9QVL4 PRELIMINARY; PRT; 13 AA.  
 AC Q9QVL4;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE 90 kDa advanced glycosylation ENDPRODUCT binding protein  
 DE (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Rattus.  
 ON NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=S1341412; PubMed=1651976;  
 RA Yang Z.; Makita Z.; Horii Y.; Brunelle S.; Cerani A.; Sehajpal P.;  
 RA Suthanthiran M.; Viassara H.;  
 RT "Two novel rat liver membrane proteins that bind advanced  
 RT glycosylation endproducts: relationship to macrophage receptor for  
 RL glucose-modified proteins."  
 RL J. Exp. Med. 174:515-524(1991).  
 FT NON TER 1 1  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1466 MW; 349E02EEFCFE9AB7 CRC64;  
  
 Query Match 27.3%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 KLP 9  
 Db |||  
 4 KLP 6  
  
 RESULT 15  
 Q91777 PRELIMINARY; PRT; 14 AA.  
 AC Q91777;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE Hypothetical 1.6 kDa protein.

OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 ON NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90231335; PubMed=23300002;  
 RA Kajimoto Y.; Rotwein P.;  
 RT "Evolution of insulin-like growth factor I (IGF-I): structure and  
 RT expression of an IGF-I precursor from Xenopus laevis."  
 RL Mol. Endocrinol. 4:217-226(1990).  
 DR EMBL; M29857; AAA70329.1; -.  
 KW Hypothetical protein  
 SQ SEQUENCE 14 AA; 1627 MW; 3002F6B29B887BD7 CRC64;  
  
 Query Match 27.3%; Score 3; DB 13; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 8 LPQ 10  
 Db |||  
 2 LPQ 4  
  
 RESULT 16  
 Q53580 PRELIMINARY; PRT; 15 AA.  
 AC Q53580;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Light-harvesting complex I alpha polypeptide (Fragment).  
 GN PUFA.  
 OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Rhodobacter.  
 ON NCBI\_TaxID=1061;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92234963; PubMed=1569029;  
 RA Richter P.; Brand M.; Drews G.;  
 RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufla  
 RT mutants."  
 RL J. Bacteriol. 174:3030-3041(1992).  
 DR EMBL; S97552; AAC60406.1; -.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;  
  
 Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 FYK 7  
 Db |||  
 4 FYK 6  
  
 RESULT 17  
 Q9X637 PRELIMINARY; PRT; 15 AA.  
 AC Q9X637;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Mert (Fragment).  
 GN MERT.  
 OS Klebsiella oxytoca.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 ON NCBI\_TaxID=571;  
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=509H;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wierman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=509H;
RX MEDLINE=96027386; PubMed=9361435;
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=509H;
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
RT mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF131272; AAD37141.1; -
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
RT NON_TER 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 4 PQN 6

RESULT 18
ID Q9X635 PRELIMINARY; PRT; 15 AA.
AC Q9X635;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MerT (Fragment).
GN MerT.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=390;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wierman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=390;
RX MEDLINE=96027386; PubMed=9361435;
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=390;
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
RT mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF131271; AAD37139.1; -.
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 4 PQN 6

RESULT 19
ID P82331 PRELIMINARY; PRT; 15 AA.
AC P82331;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT114) (Fragment).
DR EMBL: AF131272; AAD37141.1; -
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
RT NON_TER 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 4 PQN 6

RESULT 19
ID P82331 PRELIMINARY; PRT; 15 AA.
AC P82331;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT114) (Fragment).
DR EMBL: AF131272; AAD37141.1; -
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
RT NON_TER 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 4 PQN 6

RESULT 19
ID P82331 PRELIMINARY; PRT; 15 AA.
AC P82331;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT114) (Fragment).
DR EMBL: AF131272; AAD37141.1; -
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
RT NON_TER 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 27.3%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 8 PQN 10

RESULT 20
ID Q66174 PRELIMINARY; PRT; 15 AA.
AC Q66174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (Fragment).
OS Human coronavirus (strain 229E).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Siddell S.;

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RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA  
 RT 5 unique regions.";  
 RL Nucleic Acids Res. 17:6387-6387 (1989).  
 DR EMBL; X15654; CAA33680.1; -;  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 3 KLP 5

RESULT 21  
 Q9F9S4 PRELIMINARY; PRT; 16 AA.  
 AC Q9F9S4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Methylase HpyI (Fragment).  
 GN M.HPYI  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Helicobacteraceae; Helicobacter.  
 OX NCBI\_TaxID=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Finland 9496;  
 RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,  
 RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;  
 RT "Subtypes of the H. pylori iceA gene in Finnish pediatric patients.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF176822; AAG13123.1; -;  
 DR InterPro; IPR002294; D12N5.mtfrase.  
 DR Pfam; PF02086; MethyitransfD12; 1.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1944 MW; 7306D1D11603768A CRC64;

Query Match 27.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8  
 Db 8 YKL 10

RESULT 22  
 Q9R4X4 PRELIMINARY; PRT; 16 AA.  
 AC Q9R4X4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Exotoxin A (Fragment).  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=94356232; PubMed=8075811;  
 RA Wolz C., Lehmann R., Vasil M.L., Bischoff R., Doring G.;  
 RT "A new extracellular protein of Pseudomonas aeruginosa PA103 regulated  
 by regA.";  
 RL Microbiology 140:1755-1761 (1994).  
 SQ SEQUENCE 16 AA; 1828 MW; D6C94C87E56823274 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 6 KLP 8

RESULT 23  
 Q10748 PRELIMINARY; PRT; 16 AA.  
 AC Q10748;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE 98 kDa cellulosomal protein (Fragment).  
 OS Clostridium thermocellum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1515;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=JW20;  
 RX MEDLINE=96267082; PubMed=8664281;  
 RA Choi S.K., Jungdahl L.G.;  
 RT "Dissociation of the cellulosome of Clostridium thermocellum in the  
 RT presence of ethylenediaminetetraacetic acid occurs with the formation  
 RT of truncated polypeptides.";  
 RL Biochemistry 35:4897-4905 (1996).  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1970 MW; D00573CE23B02A15 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 6 KLP 8

RESULT 24  
 Q28324 PRELIMINARY; PRT; 16 AA.  
 AC Q28324;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Beta-x-globin (Fragment).  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=80227766; PubMed=6248519;  
 RA Haynes J.R., Rostock P.R., Schon E.A., Gallagher P.M., Burks D.J.,  
 RA Smith K., Lingrel J.B.;  
 RT "The isolation of the beta-a-, beta-c-, and gamma-globin genes and a  
 RT presumptive embryonic globin gene from a goat dna recombinant  
 RT library.";  
 RL J. Biol. Chem. 255:6355-6367 (1980).  
 DR EMBL; K00659; AAA30919.1; -;  
 FT NON TER 1  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1784 MW; D027A9E223320213 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5



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Db      12 QNF 14
|||
RESULT 25
Q34699 PRELIMINARY; PRT; 16 AA.
AC Q34699;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cob protein (Fragment).
GN COB
OS Helianthus annuus (Common sunflower).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMSBASO;
RA Koehler R.H.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL: X62592; CAA44477.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 16 AA; 1950 MW; A2980BEE7E26B700 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NPY 6
|||
DB 3 NPY 5

RESULT 26
Q9ETL3 PRELIMINARY; PRT; 17 AA.
ID Q9ETL3;
AC Q9ETL3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Methylase HpyI (Fragment).
GN M.HpyI OR HpyI.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Finland 18696;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "Subtypes of the H. pylori icaA gene in Finnish pediatric patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=7796;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "The subtype of Helicobacter pylori icaA gene in the Finnish pediatric
patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF176823; AAG13125.1; -.
DR EMBL: AF176090; AAG09227.1; -.
DR InterPro: IPR002294; D12N6_mtfrase.
DR Pfam: PF02086; MethyltransfD12; 1.
FT NON_TER
SQ SEQUENCE 17 AA; 2058 MW; B2B306D1D1160376 CRC64;

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Query Match 27.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
|||
DB 8 YKL 10

RESULT 27
Q46667 PRELIMINARY; PRT; 17 AA.
ID Q46667;
AC Q46667;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (fragment).
GN G6PD.
OS Macropus robustus robustus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224585; PubMed=9060417;
RA Loebel D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction.";
RL Mamm. Genome 8:146-147(1997).
DR EMBL: U53779; AAC48792.2; -.
DR EMBL: U53778; AAC48792.2; JOINED.
DR InterPro: IPR001282; G6PD.
DR Pfam: PF02781; G6PD_C; 1.
FT NON_TER
SQ SEQUENCE 17 AA; 2039 MW; 3A5B76F61F908B21 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
DB 14 KLP 16

RESULT 28
Q9QUY6 PRELIMINARY; PRT; 17 AA.
ID Q9QUY6;
AC Q9QUY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=96085162; PubMed=8521863;
RA Schulte S., Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate
RT transporter. Copurification, separation and characterization of the two
RT glycoproteins.";
RL Eur. J. Biochem. 233:947-953(1995).
RN [2]
RP SEQUENCE 17 AA; 2017 MW; 0F92A645FFD7F828 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 LPQ 10  
 DB 5 LPQ 7

RESULT 29  
 Q9ZG42  
 ID Q9ZG42 PRELIMINARY; PRT; 18 AA.  
 AC Q9ZG42  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)  
 DE Proline transport protein (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=12 434E;  
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;  
 RT "Gene identification of Chlamydia trachomatis by random DNA  
 sequencing.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF087325; AAD04100.1; -  
 FT NON TER 1  
 FT NON TER 18  
 SQ SEQUENCE 18 AA; 2236 MW; 55C4N82FD42CC261 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
 DB 10 FYK 12

RESULT 30  
 Q9UC58  
 ID Q9UC58 PRELIMINARY; PRT; 18 AA.  
 AC Q9UC58  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
 DE Uronic-acid-rich protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95406991; PubMed=7676539;  
 RA Atmani F., Khan S.R.;  
 RT "Characterization of uronic-acid-rich inhibitor of calcium oxalate  
 RT crystallization isolated from rat urine.";  
 RL Urol. Res. 23:95-101(1995).  
 SQ SEQUENCE 18 AA; 1867 MW; 15DE1BF37294B836 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 DB 3 LPQ 5

RESULT 31  
 Q16167  
 ID Q16167 PRELIMINARY; PRT; 18 AA.  
 AC Q16167  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 GN SERUM ALBUMIN (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94294404; PubMed=8022807;  
 RA Madison J., Galliano M., Watkins S., Minchiotti L., Porta F.,  
 RA Rossi A., Putnam F.W.;  
 RT "Genetic variants of human serum albumin in Italy: point mutants and a  
 RT carboxyl-terminal variant.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6476-6480(1994).  
 DR EMBL: S70799; AAB31177.1; -  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 18 AA; 2089 MW; 2CCF6CSB0B08690B CRC64;

Query Match 27.3%; Score 3; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 DB 16 KLP 18

RESULT 32  
 Q8LNN9  
 ID Q8LNN9 PRELIMINARY; PRT; 18 AA.  
 AC Q8LNN9;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN OSJNBA0040D23.8.  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,  
 RA Overton II L.H., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,  
 RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,  
 RA Utterback T.T., Feidblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,  
 RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
 RT "Oryza sativa chromosome 10 BAC OSJNBA0040D23 genomic sequence.";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC074196; AAM76354.1; -  
 DR Gramene; Q8LNN9; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 18 AA; 2005 MW; 23DBF28FF63C1608 CRC64;

Query Match 27.3%; Score 3; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 DB 9 KLP 11

RESULT 33  
 P70649  
 ID P70649 PRELIMINARY; PRT; 18 AA.  
 AC P70649;  
 DT 01-FEB-1997 (TRENBLrel. 02, Created)  
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)

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DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Syntaxin 3 isoform D-1 (Fragment).
GN STX3 OR SYN3D.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=95321968; PubMed=7598732;
RA Ibaraki K., Horioka H.P., Morita T., Mori H., Sakimura K.,
RA Mishina M., Saisu H., Abe T.;
RA "Identification of four different forms of syntaxin 3.";
RT Biochem. Biophys. Res. Commun. 211:997-1005(1995).
DR EMBL; S78675; AAC17463.1; -.
DR MGD; MGI:103077; Stx3.
FT NON TER 1
SQ SEQUENCE 18 AA; 2073 MW; 289FBCA5D5495155 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 4 KLP 6

RESULT 34
ID Q9QV11 PRELIMINARY; PRT; 18 AA.
AC Q9QV11;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]_
RP SEQUENCE.
RX MEDLINE=92031479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrase-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 2122 MW; 68FFIABA87E24E49 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 2 KLP 4

RESULT 35
ID P70650 PRELIMINARY; PRT; 18 AA.
AC P70650;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Syntaxin 3 isoform D-2 (Fragment).
GN STX3 OR SYN3D.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=95321968; PubMed=7598732;
RA Ibaraki K., Horioka H.P., Morita T., Mori H., Sakimura K.,
RA Mishina M., Saisu H., Abe T.;
RA "Identification of four different forms of syntaxin 3.";
RT Biochem. Biophys. Res. Commun. 211:997-1005(1995).
DR EMBL; S78677; AAC17462.1; -.
DR MGD; MGI:103077; Stx3.
FT NON TER 1
SQ SEQUENCE 18 AA; 2043 MW; 289FBCA184495155 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 4 KLP 6

RESULT 36
ID Q9PRR7 PRELIMINARY; PRT; 18 AA.
AC Q9PRR7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE OVOFACTOR-1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_
RP SEQUENCE.
RX MEDLINE=96068942; PubMed=8534988;
RA Nakamura T., Saico T., Kitazawa H., Takeuchi S., Itoh T.;
RT "Isolation of a new minor protein (Ovofactor-1), which has a cell
RT growth promoting activity, from hen's egg white by heparin affinity
RT chromatography.";
RL Biochem. Biotechnol. Biochem. 59:1946-1948(1995).
SQ SEQUENCE 18 AA; 2056 MW; 56EE4AEED17C174 CRC64;

Query Match 27.3%; Score 3; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 5 KLP 7

RESULT 37
ID Q8NFL2 PRELIMINARY; PRT; 19 AA.
AC Q8NFL2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Prolyl isomerase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22095969; PubMed=12101225;
RA Ryo A., Liou Y.C., Wulf G., Nakamura M., Lee S.W., Lu K.P.;

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RT "PIN1 Is an E2F Target Gene Essential for Neu/Ras-Induced  
 RT Transformation of Mammary Epithelial Cells.";  
 RL Mol. Cell. Biol. 22:5281-5295 (2002).  
 DR EMBL; AF501321; AAM81970.1; -.  
 KW Isomerase.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2235 MW; 1C4FC381C8A0F17F CRC64;

Query Match 27.3%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 DB 6 KLP 8

RESULT 38  
 Q9UDB7 PRELIMINARY; PRT; 19 AA.  
 AC Q9UDB7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE CD8 BTA chain isoform S BEVA1 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP MEDLINE=93170376; PubMed=8436166;  
 RX DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.; loci."  
 RA "Transcriptional diversity at the duplicated human CD8 beta loci."  
 RL Eur. J. Immunol. 23:320-326 (1993).  
 SQ SEQUENCE 19 AA; 2527 MW; D1405FE2CEEBA419 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
 DB 17 FYK 19

RESULT 39  
 Q9TWD0 PRELIMINARY; PRT; 19 AA.  
 AC Q9TWD0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Sialoprotein I (Fragment).  
 OS Sphaerecthinus granulatus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;  
 OC Sphaerecthinus.  
 OX NCBI\_TaxID=39374;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP MEDLINE=96428846; PubMed=8831948;  
 RX Karamanos N.K., Manouras A., Anagnostides S., Makatsori E.,  
 RA Tsengidis T., Antonopoulos C.A.;  
 RT "Isolation, biochemical and immunological characterization of two sea  
 RT urchin glycoproteins bearing sulphated poly(sialic acid)  
 RT polysaccharides rich in N-glycolyl neuraminic acid."  
 RL Biochimie 78:171-182 (1996).  
 SQ SEQUENCE 19 AA; 2265 MW; 38FFDEB1A033E850 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6  
 DB 5 NFY 7

RESULT 40  
 Q31687 PRELIMINARY; PRT; 19 AA.  
 ID Q31687;  
 AC Q31687;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ATPase subunit 8 (Fragment).  
 GN ATP8.  
 GN Artemia parthenogenetica.  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;  
 OC Artemiidae; Artemia.  
 OX NCBI\_TaxID=6663;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP STRAIN=La Mata;  
 RX MEDLINE=94223692; PubMed=8169960;  
 RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;  
 RT "Speciation in the artemia genus: mitochondrial DNA analysis of  
 RT bisexual and parthenogenetic brine shrimps.";  
 RL J. Mol. Evol. 38:156-168 (1994).  
 DR EMBL; X67263; CAA47685.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PQM 11  
 DB 2 PQM 4

RESULT 41  
 Q9XMB5 PRELIMINARY; PRT; 19 AA.  
 ID Q9XMB5;  
 AC Q9XMB5;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE ORF165 (Fragment).  
 OS Aegilops tauschii (Aegilops squarrosa).  
 OG Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Aegilops.  
 OX NCBI\_TaxID=37682;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP STRAIN=KU29;  
 RA Tsukamoto N., Asakura N., Takumi S., Mori N., Nakamura C.;  
 RT "The presence of paternal sub-genomic mitochondrial DNA copies in the  
 RT nucleus-cytoplasm hybrids of tetraploid wheat with the cytoplasm of  
 RT Aegilops squarrosa.";  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF42479; AAD3734.1; -.  
 DR InterPro; IPR003319; YMF19.  
 DR Pfam; PF02326; YMF19; 1.  
 KW Mitochondrion.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2394 MW; F435DB3B595D3ADC CRC64;

Query Match 27.3%; Score 3; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3  
|||  
Db 1 MQP 3

RESULT 42

Q9DFN3 PRELIMINARY; PRT; 19 AA.

AC Q9DFN3;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Glycogen myosphorylase (Fragment).  
OS Gillichthys mirabilis (Long-jawed mudsucker).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidae;  
OC Gobiidae; Gillichthys.  
OX NCBI\_TaxID=8222;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Tissue=Skeletal white muscle;  
RX MEDLINE=21117151; PubMed=1172064;  
RA Gracey A.Y., Troll J.V., Somero G.N.;  
RT "Hypoxia-induced gene expression profiling in the euryoxic fish Gillichthys mirabilis."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).  
DR EMBL; AF266202; AAG13322.1; -.  
FT NON TER 1  
SQ SEQUENCE 19 AA; 2215 MW; 3554ECD38909FBAA CRC64;

Query Match 27.3%; Score 3; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
|||  
Db 13 KLP 15

RESULT 43

Q9X629 PRELIMINARY; PRT; 20 AA.

AC Q9X629;  
DT 01-NOV-1999 (TRENBLrel. 12, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
DE MerT (Fragment).  
GN MERT.  
OS unidentified enterobacterium 2705A.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae;  
OX NCBI\_TaxID=93168;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=2705A;  
RX MEDLINE=9708220; PubMed=9055422;  
RA Liebert C.A., Wierman J., Smith T., Summers A.O.;  
RT "Phylogeny of mercury resistance (mer) operons of gram-negative bacteria isolated from the fecal flora of primates."  
RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=2705A;  
RX MEDLINE=98027386; PubMed=9361435;  
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;  
RT "Association of mercury resistance with antibiotic resistance in the gram-negative fecal bacteria of primates."  
RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
RN [3]

RP SEQUENCE FROM N.A.  
RC STRAIN=2705A;  
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;  
RT "15-bp tandem repeats occur at a sharp transition in gc content in the mer operon."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF131264; AAD37125.1; -.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4  
|||  
Db 9 PQN 11

RESULT 44

Q9X632 PRELIMINARY; PRT; 20 AA.

AC Q9X632;  
DT 01-NOV-1999 (TRENBLrel. 12, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)  
DE MerT (Fragment).  
GN MERT.  
OS Pseudomonas aeruginosa.  
OG Plasmid pCER100.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97208220; PubMed=9055422;  
RA Liebert C.A., Wierman J., Smith T., Summers A.O.;  
RT "Phylogeny of mercury resistance (mer) operons of gram-negative bacteria isolated from the fecal flora of primates."  
RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98027386; PubMed=9361435;  
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;  
RT "Association of mercury resistance with antibiotic resistance in the gram-negative fecal bacteria of primates."  
RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Wierman J., Liebert C.A., Smith T., Summers A.O.;  
RT "15-bp tandem repeats occur at a sharp transition in gc content in the mer operon."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF131269; AAD37135.1; -.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4  
|||  
Db 9 PQN 11

RESULT 45

Q9X634 PRELIMINARY; PRT; 20 AA.

AC Q9X634;  
DT 01-NOV-1999 (TRENBLrel. 12, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

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DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE MerT (Fragment).
GN MERT.
OS Serratia marcescens.
OG Plasmid pR831b.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1] _TaxID=615;
RP SEQUENCE FROM N.A.
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF131270; AAD37137.1; -.
KW Plasmid.
FT NON-TER 20 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 9 PQN 11

RESULT 46
Q9WVU7 PRELIMINARY; PRT; 20 AA.
AC Q9WVU7
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE MERT (Fragment).
GN MERT.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1] _TaxID=562;
RP SEQUENCE FROM N.A.
RX STRAIN=92H, 2701, 343, and 47H;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=92H, 2701, 343, and 47H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=92H, 2701, 343, and 47H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF131267; AAD37131.1; -.
FT NON-TER 20 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 9 PQN 11

RESULT 47
Q9X630 PRELIMINARY; PRT; 20 AA.
AC Q9X630
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE MERT (Fragment).
GN MERT.
OS Lacteria adecarboxylata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Lactercia.
OX NCBI_TaxID=83655;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=533H;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=533H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=533H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF131267; AAD37131.1; -.
FT NON-TER 20 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 9 PQN 11

RESULT 48
Q46499 PRELIMINARY; PRT; 20 AA.
ID Q46499

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RC STRAIN=92H, 2701, 343, and 47H;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF131268; AAD37133.1; -.
DR EMBL; AF131263; AAD37124.1; -.
DR EMBL; AF131265; AAD37127.1; -.
DR EMBL; AF131266; AAD37129.1; -.
FT NON-TER 20 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 9 PQN 11

RESULT 47
Q9X630 PRELIMINARY; PRT; 20 AA.
AC Q9X630
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE MERT (Fragment).
GN MERT.
OS Lacteria adecarboxylata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Lactercia.
OX NCBI_TaxID=83655;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=533H;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=533H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=533H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF131267; AAD37131.1; -.
FT NON-TER 20 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
Db 9 PQN 11

RESULT 48
Q46499 PRELIMINARY; PRT; 20 AA.
ID Q46499

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AC Q45499;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLrel. 01, Last annotation update)
DE Periplasmic (Fragment).
OS Desulfobivrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobivriales;
OC Desulfobivriaceae; Desulfobivrio.
OX NCBI_TaxID=876;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M6;
RA Lim S.K., Lee S.J., Kim B.H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49192; AAA91808.1; -.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 1996 MW; E93207D26C22999B CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
DB 9 LPQ 11

RESULT 49
Q8NFW3 PRELIMINARY; PRT; 20 AA.
ID Q8NFW3
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Synovial sarcoma SVT/SSX1 fusion protein (Fragment).
GN SVT/SSX1 FUSION.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tamborini E., Agus V., Pierotti M.A., Pilotti S., Rosai J.;
RT "Diversity of both fusion transcripts and rearrangement type in
RT synovial sarcoma.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402619; AAM95901.1; -.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2377 MW; F1534C73F9108E83 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
DB 12 PQN 14

RESULT 50
Q81Z13 PRELIMINARY; PRT; 20 AA.
ID Q81Z13
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE LEF1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Filali M., Cheng N., Abbot D., Leontiev V., Engelhardt J.F.;
RT "Wnt-3A/b-Catenin Signaling Induces Transcription from the LEF-1
RT Promoter.";
RL J. Biol. Chem. 0:0-0(2002).
DR EMBL; AV129650; AAN06089.1; -.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 1761 MW; E4F1891E56FBA675 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQ 3
DB 1 MPQ 3

RESULT 51
Q9TW18 PRELIMINARY; PRT; 20 AA.
ID Q9TW18
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Major cuticular protein (Fragment).
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritoidea; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE.
RX MEDLINE=95279142; PubMed=759285;
RX Tsiliras A., Koromantzou E., Allen G., Dimitriadis G.;
RT "Partial N-terminal sequences of larval cuticular proteins from the
RT dipteran Ceratitis capitata.";
RL Hereditas 122:79-83(1995).
SQ SEQUENCE 20 AA; 2408 MW; 2BC25E2F9ECL5A80 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NPY 6
DB 17 NPY 19

RESULT 52
Q9S8A8 PRELIMINARY; PRT; 20 AA.
ID Q9S8A8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (Fragment)
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RX Rocher A., Calero M., Soriano F., Mendez E.;
RT "Identification of major rye secalins as coeliac immunoreactive
RT proteins.";
RL Biochim. Biophys. Acta 1295:113-22(1996).
SQ SEQUENCE 20 AA; 2249 MW; 96D3DA4098BB5C80 CRC64;

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Query Match 27.3%; Score 3; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 ||  
 Db 18 LPQ 20

RESULT 53  
 P83308 PRELIMINARY; PRT; 5 AA.  
 AC P83308; 2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE FMRamide-like neuropeptide (LPLRF-amide).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX PubMed=6137771;  
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRamide."  
 RL Nature 305:328-330(1983).  
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 ||  
 Db 1 LP 2

RESULT 54  
 O50556 PRELIMINARY; PRT; 7 AA.  
 AC O50556;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE GLYA (Fragment).  
 GN GLYA.  
 OS Actinobacillus actinomycetemcomitans (Haemophilus  
 OS actinomycetemcomitans).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OX NCBI\_TaxID=714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33384;  
 RX MEDLINE=96355846; PubMed=8751884;  
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
 RA Kraig E.;  
 RT "cis Elements and trans factors are both important in strain-specific  
 RT regulation of the leukotoxin gene in Actinobacillus  
 RT actinomycetemcomitans."  
 RL Infect. Immun. 64:3451-3460(1996).  
 DR EMBL; U51862; AAB88721.1; -.  
 FT NON-TER 1  
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 ||  
 Db 3 LP 4

RESULT 55  
 O8GL00 PRELIMINARY; PRT; 7 AA.  
 AC O8GL00; 2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE PF-50 protein (Fragment).  
 GN PF-50.  
 OS Borrelia burgdorferi ( Lyme disease spirochete).  
 OG Plasmid group cp32-13.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CA15;  
 RA Stevenson B., Miller J.C.;  
 RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
 RT prophages: conservation amidst diversity.";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY142106; AANI7857.1; -.  
 KW Plasmid.  
 FT NON-TER 1  
 SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8  
 ||  
 Db 5 KL 6

RESULT 56  
 O98866 PRELIMINARY; PRT; 7 AA.  
 AC O98866;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE Cytochrome b/f subunit IV (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86120353; PubMed=3003688;  
 RA Siljeh-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;  
 RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal  
 RT protein S11 and RNA polymerase alpha-subunit.";  
 RL Nucleic Acids Res. 14:1029-1044(1986).  
 DR EMBL; X03496; CAA27215.1; -.  
 KW Chloroplast.  
 FT NON-TER 1  
 SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 4 NF 5  
 Db 1 NF 2

## RESULT 57

Q95945 PRELIMINARY; PRT; 7 AA.  
 AC Q95945;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Inside intron 5 (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OG Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D273-10B;  
 RX MEDLINE=8106985; PubMed=6254986;  
 PA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
 RT "Assembly of the mitochondrial membrane system: Structure and  
 RT nucleotide sequence of the gene coding for subunit 1 of yeast  
 RT cytochrome oxidase.";  
 RL J. Biol. Chem. 255:11927-11941(1980).  
 DR EMBL; V00694; CAA24066.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 859 MW; 75E7232362CDC460 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8  
 Db 5 KL 6

## RESULT 58

Q63668 PRELIMINARY; PRT; 7 AA.  
 AC Q63668;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF2 protein.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
 EX MEDLINE=96396550; PubMed=7667072;  
 PA Mandon B., Bellanger A.C., Elalouf J.M.;  
 RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin  
 RT V2 receptor gene.";  
 RL Flieders Arch. 430:112-18(1995).  
 DR EMBL; X83264; CAA58237.1; -.  
 SQ SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 Db 5 LP 6

## RESULT 59

Q66205 PRELIMINARY; PRT; 7 AA.  
 AC Q66205;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Membrane protein (1 is 3rd base in codon) (Fragment).  
 OS Transmissible gastroenteritis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirus.  
 OX NCBI\_TaxID=11149;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FS772/70;  
 RX MEDLINE=8216185; PubMed=2835592;  
 PA Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;  
 RT "Sequence of the Nucleoprotein Gene from a Virulent British Field  
 RT Isolate of Transmissible Gastroenteritis Virus and its Expression in  
 RT Saccharomyces Cerevisiae.";  
 RL Mol. Microbiol. 2:89-99(1988).  
 DR EMBL; Y00542; CAA68606.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8  
 Db 2 KL 3

## RESULT 60

Q66113 PRELIMINARY; PRT; 7 AA.  
 AC Q66113;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE C-terminus of the viral replicase (Fragment).  
 OS Cherry leaf roll virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
 OC Nepovirus.  
 OX NCBI\_TaxID=12615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Walnut;  
 RA Borja M.;  
 RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Walnut;  
 RX MEDLINE=96124520; PubMed=8560786;  
 RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;  
 RT "Long, nearly identical untranslated sequences at the 3' terminal  
 RT regions of the genomic RNAs of cherry leafroll virus (walnut  
 RT strain).";  
 RL Virus Genes 10:245-252(1995).  
 DR EMBL; Z34265; CAA84019.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
 Db 5 LP 6

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RESULT 61
QJUEB1 PRELIMINARY; PRT; 7 AA.
ID Q8UEB1
AC Q8UEB1
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4874;
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
approach to predicting phenotype from genotype.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAC32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 18.2%; Score 2; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3
Db 1 PQ 2

RESULT 62
O09258 PRELIMINARY; PRT; 8 AA.
ID O09258
AC O09258
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE NifH (Fragment).
GN NIFH.
OS Synechococcus sp. (strain PCC 8801 / RP-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RP-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RP-1.";
RT Microbiology 145:743-753(1999).
DR EMBL; AF001780; AAC33369.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
Db 6 FY 7

RESULT 63
O87471 PRELIMINARY; PRT; 8 AA.
ID O87471
AC O87471
DT 01-NOV-1998 (TREMELrel. 08, Created)

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DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
DE HiFA (Fragment).
GN HiFA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Eagan;
RX MEDLINE=98389689; PubMed=9721313;
RA Mhlanga-Mutagadura T., Morlin G., Smith A.L., Eisenstark A.,
Golomb M.;
RT "Evolution of the major pilus gene cluster of haemophilus
RT influenzae.";
RT J. Bacteriol. 180:4693-4703(1998).
DR EMBL; AF071762; AAC35830.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
Db 2 KL 3

RESULT 64
Q9ZIE9 PRELIMINARY; PRT; 8 AA.
ID Q9ZIE9
AC Q9ZIE9
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMELrel. 10, Last annotation update)
DE Carbamoyl-phosphate synthase subunit B (Fragment).
GN CARB.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1527;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billows F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RT Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1527;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029363; AAC78449.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
Db 1 MP 2

RESULT 65

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Q9R5R0
ID Q9R5R0 PRELIMINARY; PRT; 8 AA.
AC Q9R5R0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11,500 DA product of ORF4 (Fragment).
OS Shigella dysenteriae
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]_
RP SEQUENCE.
RX MEDLINE=9208268; PubMed=1660923;
RA Polard P., Prere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUG codon
RT in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 66
P87225 PRELIMINARY; PRT; 8 AA.
ID P87225
AC P87225;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GINII protein (Fragment).
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Scharfe M., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]_
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73169; CAA97518.2; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 67
Q15889 PRELIMINARY; PRT; 8 AA.
ID Q15889
AC Q15889;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP15H8) (Fragment).
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32070; AAA73879.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
DB 5 KL 6

RESULT 68
Q15895 PRELIMINARY; PRT; 8 AA.
ID Q15895
AC Q15895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

RESULT 69
Q15901 PRELIMINARY; PRT; 8 AA.
ID Q15901
AC Q15901;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP7B11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32070; AAA73879.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
DB 5 KL 6

RESULT 68
Q15895 PRELIMINARY; PRT; 8 AA.
ID Q15895
AC Q15895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

RESULT 69
Q15901 PRELIMINARY; PRT; 8 AA.
ID Q15901
AC Q15901;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP7B11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; U32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

```

RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries.";  
RL Hum. Mol. Genet. 0:0-0(1995).  
FR EMBL; L32080; AAA73891.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 860 MW; 37D72878676729CB CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
DB 3 LP 4

RESULT 70  
Q15893 PRELIMINARY; PRT; 8 AA.  
AC Q15893;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE (Clone XP587A) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries.";  
RL Hum. Mol. Genet. 0:0-0(1995).  
FR EMBL; L32073; AAA73883.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4  
DB 2 QN 3

RESULT 71  
Q9HCO0 PRELIMINARY; PRT; 8 AA.  
AC Q9HCO0;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).  
GN HSPDE10A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20453115; PubMed=10998054;

RA Fujishige K., Kotera J., Yuasa K., Omori K.;  
RT "The human phosphodiesterase PDE10A gene. Genomic organization and  
RT evolutionary relatedness with other PDEs containing GAP domains.";  
RL Eur. J. Biochem. 267:5943-5951(2000).  
FR EMBL; AB041779; BAB16368.1; -.  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3  
DB 3 PQ 4

RESULT 72  
Q9P0K3 PRELIMINARY; PRT; 8 AA.  
AC Q9P0K3;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE cGMP-specific phosphodiesterase PDE5A2 (Fragment).  
GN PDE5A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2045478; PubMed=10679249;  
RA Lin C.S., Lau A., Tu R., Lue T.F.;  
RT "Identification of three alternative first exons and an intronic  
RT promoter of human PDE5A gene.";  
RL Biochem. Biophys. Res. Commun. 268:596-602(2000).  
FR EMBL; AF155195; AAF40302.1; -.  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 908 MW; E8A33AA879D76726 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9  
DB 2 LP 3

RESULT 73  
Q9TWH6 PRELIMINARY; PRT; 8 AA.  
AC Q9TWH6;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.  
OS Perinereis vancaurica.  
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;  
OC Phyllocorida; Nereididae; Perinereis.  
OX NCBI\_TaxID=6355;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=95323338; PubMed=7599797;  
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,  
RA Fujita T., Minakata H., Nomoto K.;  
RT "Isolation and characterization of four novel bioactive peptides from  
RT a polychaete annelid, Perinereis vancaurica.";  
RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-  
RL 304(1995).  
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LP 2

Search completed: November 25, 2003, 18:25:21  
 Job time : 28.5553 secs

Oy 5 FY 6  
 ||  
 Db 1 FY 2

## RESULT 74

002032 PRELIMINARY; PRT; 8 AA.  
 AC 002032;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Metallothionein (Fragment).  
 GN LPM2.  
 OS Lytechinus pictus (Painted sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;  
 OC Lytechinus.  
 OX NCBI\_TaxID=7653;  
 RN [1]\_TaxID=7653;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97264487; PubMed-9110313;  
 RA Cserjesi P., Fang H., Brandhorst B.P.;  
 RT "Metallothionein gene expression in embryos of the sea urchin  
 Lytechinus pictus.";  
 RL Mol. Reprod. Dev. 47:39-46(1997).  
 DR EMBL; U83400; AAB58320.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MP 2  
 ||  
 Db 1 MP 2

## RESULT 75

Q9TRX8 PRELIMINARY; PRT; 8 AA.  
 AC Q9TRX8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Osteopontin (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]\_TaxID=9913;  
 RP SEQUENCE.  
 RX MEDLINE-91282766; PubMed=1676261;  
 RA Prince C.W., Dickie D., Krundieck C.L.;  
 RT "Osteopontin, a substrate for transglutaminase and factor XIII  
 activity.";  
 RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 LP 9  
 |||

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 35.633 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-6  
Perfect score: 11  
Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length DB	ID	Description
1	11	100.0	11	22	AA872251	Colostrinin derivate
2	11	100.0	11	22	AA872505	Colostrinin peptid
3	11	100.0	11	22	AA872537	Colostrinin peptid
4	11	100.0	11	22	AA875311	Ewe colostrinin pe
5	11	100.0	11	23	AAE20233	Colostrinin consti
6	11	100.0	11	23	AAE51041	Colostrinin consti
7	11	100.0	11	23	AAO14582	Neural cell regula
8	11	100.0	12	22	AA859342	Ewe colostrinin pe
9	5	45.5	20	23	AAU86137	Insulin/insulin li

10	4	36.4	4	24	ABJ36686	G protein coupled
11	4	36.4	5	18	AAW12496	Interleukin-6 anta
12	4	36.4	7	19	AAW48024	AE114 analogue eff
13	4	36.4	7	19	AAW47992	AE114 analogue eff
14	4	36.4	7	23	AB890641	Clostridium botuli
15	4	36.4	8	20	AAV53386	E6 protein epitope
16	4	36.4	8	20	AAV40373	Amino acid sequenc
17	4	36.4	8	20	AAV426724	HPV-derived lipope
18	4	36.4	8	20	AAV10348	T cell epitope/MHC
19	4	36.4	8	22	ABP11965	HIV A02 super moti
20	4	36.4	8	22	ABP18445	HIV B62 super moti
21	4	36.4	8	23	ABG90030	MHC class I molecu
22	4	36.4	9	14	AA843729	MHC class I allele
23	4	36.4	9	15	AA859196	Peptide fragment (
24	4	36.4	9	17	AAW49468	Human leucocyte an
25	4	36.4	9	18	AAW39512	HPV16 E6-encoded C
26	4	36.4	9	19	AAW78890	Human papillomavir
27	4	36.4	9	19	AAW54754	Peptide from HPV 1
28	4	36.4	9	19	AAW54509	Synthetic polypept
29	4	36.4	9	20	AAV53385	E6 protein epitope
30	4	36.4	9	20	AAV40372	Amino acid sequenc
31	4	36.4	9	20	AAV26723	HPV-derived lipope
32	4	36.4	9	20	AAV10560	HLA class I motif
33	4	36.4	9	21	AA833702	MHC class I associ
34	4	36.4	9	21	AAV66471	HLA-A2-binding HPV
35	4	36.4	9	22	AAE07583	Human PUMP-1 pepti
36	4	36.4	9	22	AAK23452	HIV peptide SEQ ID
37	4	36.4	9	22	AAK23484	HIV peptide SEQ ID
38	4	36.4	9	22	AA893798	Human papilloma vi
39	4	36.4	9	22	AA895948	MHC class-I associ
40	4	36.4	9	23	AB880243	MHC class I molecu
41	4	36.4	9	23	AA880674	Human tumour-associ
42	4	36.4	9	24	AAO22817	HPV-16 E6 peptide,
43	4	36.4	9	24	ABU20153	MHC binding peptid
44	4	36.4	9	24	ABU03246	Human expressed pr
45	4	36.4	9	24	AB899353	Peptide derived fr
46	4	36.4	10	14	AAK43905	HIV-1 IIIB gp120 m
47	4	36.4	10	19	AAW76930	Fusion immunoglob
48	4	36.4	10	20	AAW52988	Human papillomavir
49	4	36.4	10	22	AAU70117	Human calcitonin D
50	4	36.4	11	13	AAK28392	Bradykinin recepto
51	4	36.4	11	19	AAW76927	Fusion immunoglob
52	4	36.4	12	18	AAW15279	Salmonella secreta
53	4	36.4	12	23	ABP46973	Human BlyS binding
54	4	36.4	12	24	AB897425	HA186/CD147 prote
55	4	36.4	14	20	AA868428	Human guanine nucl
56	4	36.4	14	22	AAW97223	Human peptide #498
57	4	36.4	14	23	AAU69635	Cell death protect
58	4	36.4	15	9	AA81956	Peptide immunogen
59	4	36.4	15	14	AAK43901	HIV-1 IIIB gp120 m
60	4	36.4	15	14	AAK43907	HIV-1 RF gp120 mon
61	4	36.4	15	16	AAK72007	Biologically activ
62	4	36.4	15	20	AAW99862	HIV-1 gp120 V1/V2
63	4	36.4	15	20	AAW87621	Epitope of HIV-1 g
64	4	36.4	15	20	AAW72822	HIV-1 gp120 monocl
65	4	36.4	15	23	AB898878	Proline rich gamma
66	4	36.4	15	24	AB898946	Translation initia
67	4	36.4	16	20	AAV29841	HIV HXB2 V3 fusion
68	4	36.4	17	19	AAW47339	Apolipoprotein B t
69	4	36.4	17	20	AAV55381	Apolipoprotein fra
70	4	36.4	17	20	AAV23106	Apolipoprotein B tr
71	4	36.4	18	19	AAW23667	Peptide GF52. Syn
72	4	36.4	18	23	ABU00634	B lymphocyte stimu
73	4	36.4	18	23	AB833495	Fusion immunoglob
74	4	36.4	19	21	AAW79176	Immunogenic peptid
75	4	36.4	19	21	AAW85068	Human liver peptid
76	4	36.4	19	22	AB853432	Peptide #6092 enco
77	4	36.4	19	22	AB838586	Human brain expres
78	4	36.4	19	22	AAW59212	Human bone marrow
79	4	36.4	19	22	AAW71747	Human brain marro
80	4	36.4	19	22	AAW32039	Peptide #6076 enco
81	4	36.4	19	23	ABG41561	Human peptide enco
82	4	36.4	19	23	AAU69634	Cell death protect

83	4	36.4	20	14	AA843306	Cl089 epitopic pep
84	4	36.4	20	19	AAW76928	Fusion immunoglob
85	4	36.4	20	19	AAW76929	Fusion immunoglob
86	4	36.4	20	22	AAU12506	Human HIV-1 TH-CTL
87	4	36.4	20	22	AAU12512	Human HIV-1 TH-CTL
88	4	36.4	20	22	AAU12514	Human HIV-1 TH-CTL
89	4	36.4	20	22	AAW95957	HPV 16 E6 protein
90	4	36.4	20	22	AAU69633	Cell death protect
91	3	27.3	4	11	AA804016	Peptidase substrat
92	3	27.3	4	12	AA810877	Peptide component
93	3	27.3	4	12	AA810881	Peptide component
94	3	27.3	4	12	AA811230	Ketone analogue pr
95	3	27.3	4	12	AA811234	Ketone analogue pr
96	3	27.3	4	18	AAW27466	Human tumour supp
97	3	27.3	4	18	AAW33190	Peptide intermedia
98	3	27.3	4	18	AAW32805	Protected oligopep
99	3	27.3	4	18	AAW80258	Oxirane compound w
100	3	27.3	4	21	AA828925	Geminivirus Rep en

```

XX  SQ      Sequence      11 AA;
Query Match      100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MPQNFYKLPQM 11
      |||||
DB      1 MPQNFYKLPQM 11

RESULT 2
AAB72505
ID AAB72505 standard; Peptide; 11 AA.
XX
XX AAB72505;
DT 09-MAY-2001 (first entry)
XX
XX Colostrinin peptide #6.
DE Colostrinin peptide #6.
XX
XX Dermatological; oxidative stress regulator; colostrinin.
XX
XX Unidentified.
XX
XX WO200113650-A2.
XX
XX PN
XX PD 22-FEB-2001.
XX
XX PF 17-AUG-2000; 2000WO-US22665.
XX
XX PR 17-AUG-1999; 99US-0149310.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX
XX DR WPI; 2001-218342/22.
XX
XX PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 25; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.
XX
XX SQ      Sequence      11 AA;
Query Match      100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MPQNFYKLPQM 11
      |||||
DB      1 MPQNFYKLPQM 11

RESULT 3
AAB72537
ID AAB72537 standard; Peptide; 11 AA.
XX
XX AAB72537;
XX
XX DT 09-MAY-2001 (first entry)
XX
XX

```

DE Colostrinin peptide #6.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX Sequence 11 AA;  
 SQ  
 Query Match 100.0%; Score 11; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 |||||  
 DB 1 MPQNFYKLPQM 11  
 |||||  
 RESULT 4  
 AAB59311  
 ID AAB59311 standard; Peptide; 11 AA.  
 XX  
 AC AAB59311;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment A-2.  
 XX  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 KW  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 PN 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REG- ) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis, and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 XX Sequence 11 AA;  
 SQ  
 Query Match 100.0%; Score 11; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 |||||  
 DB 1 MPQNFYKLPQM 11  
 |||||  
 RESULT 5  
 AAE20233  
 ID AAE20233 standard; peptide; 11 AA.  
 XX  
 AC AAE20233;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 XX Colostrinin constituent peptide #6.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulneryary.  
 XX  
 OS Unidentified.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 11 /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 PN 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF 17-AUG-2000; 2000WO-US22776.  
 PR (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 XX Claim 6; Page 25; 51pp; English.  
 PS  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/



CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs) as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11  
 |||||  
 Db 1 MPQNFYKLPQM 11

## RESULT 6

AAW51041  
 ID AAW51041 standard; Peptide; 11 AA.

AC AAW51041;

XX  
 DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "optional C-terminal amidation"

FT  
 FN WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, where the  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-6 and interleukin-10.

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11  
 |||||  
 Db 1 MPQNFYKLPQM 11

## RESULT 7

AAO14582  
 ID AAO14582 standard; peptide; 11 AA.

AC AAO14582;

XX  
 DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 6.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "Optional C-terminal amide"

FT  
 FN WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 |||||  
 Db 1 MPQNFYKLPQM 11  
 RESULT 8  
 ID AAB59342 standard; Peptide; 12 AA.  
 XX  
 AC AAB59342;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrin peptide fragment derived sequence #2.  
 XX  
 KW Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB02128.  
 XX  
 PR 02-JUN-1999; 99GB-0012852.  
 XX  
 PA (REG- ) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 9; Page 27; 63pp; English.  
 CC  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 100.0%; Score 11; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQNFYKLPQM 11  
 |||||  
 Db 2 MPQNFYKLPQM 12  
 RESULT 9  
 ID AAU88197 standard; Peptide; 20 AA.  
 XX  
 DT AAU88197 (first entry)  
 XX  
 DE Insulin/insulin-like growth factor receptor-binding peptide #161.  
 XX  
 DE Cytostatic; antidiabetic; neuroprotective; cerebroprotective;  
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;  
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;  
 KW diabetic retinopathy; neurological diseases; stroke;  
 KW diabetic neuropathy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200172771-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 29-MAR-2000; 2000WO-US08528.  
 XX  
 PR 29-MAR-2000; 2000WO-US08528.  
 XX  
 PA (DGI B-) DGI BIOTECHNOLOGIES LLC.  
 XX  
 PA (NOVO ) NOVO NORDISK AS.  
 XX  
 PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;  
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandelki WS;  
 PI Hansen PH, Ravera M, Hsiao K;  
 XX  
 DR WPI; 2002-025774/03.  
 XX  
 PT Modulating insulin activity in mammalian cells, for treating e.g.  
 PT diabetes and tumours, comprises using peptides that bind to insulin or  
 PT insulin-like growth factor receptors -  
 XX  
 PS Disclosure; Page 44; 390pp; English.  
 CC  
 CC The invention relates to a method of modulating insulin activity in  
 CC mammalian cells by administering a peptide that binds the insulin  
 CC receptor (IR). A composition containing a peptide, optionally expressed  
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
 CC agonist are useful for treating diabetes. Also, peptides that are  
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours  
 CC (e.g. of prostate and breast) and diabetic retinopathy. While IGF-1  
 CC receptor agonists are useful for treating neurological diseases,  
 CC including stroke and diabetic neuropathy. The peptides are also useful in  
 CC screening for compounds that bind to IR or IGF-1 receptor, potential  
 CC therapeutics and research reagents. AAU88034-AAU90957 represent IR  
 CC and/or IGF-1 receptor-binding peptides and related amino acid sequences  
 CC of the invention.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 45.5%; Score 5; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PONEY 6  
 |||||  
 Db 8 PONEY 12  
 RESULT 10  
 ID ABJ36686 standard; Peptide; 4 AA.  
 XX  
 AC ABJ36686;  
 XX  
 DT 01-MAY-2003 (first entry)  
 XX  
 DE G protein coupled receptor related peptide SEQ ID No 9.

XX Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;  
 KW antibacterial; analgesic; anti-allergic; antiasthmatic; anti-inflammatory;  
 KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;  
 KW G protein coupled receptor signaling inhibitor; GPCR; library;  
 KW high throughput screening assay; stroke; myocardial infarction;  
 KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;  
 KW septic shock; pain; allergic disorder; inflammatory bowel disease;  
 KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;  
 KW schizophrenia; Alzheimer's disease.  
 XX Mammalia sp.  
 OS  
 XX WO200272778-A2.  
 PN  
 XX 19-SEP-2002.  
 PD  
 XX  
 XX 14-MAR-2002; 2002WO-US07561.  
 PF  
 XX 14-MAR-2001; 2001US-275472P.  
 PR  
 XX 11-MAY-2001; 2001US-0852910.  
 PR  
 XX (CUEB-) CUE BIOTECH.  
 PA  
 XX Gilchrist A, Hamm HE;  
 PI  
 XX WPI; 2003-247841/24.  
 DR  
 XX  
 XX Identifying G protein coupled receptor (GPCR) signaling inhibitors,  
 PT useful in screening drugs for treating stroke, cancers or pain, by  
 PT identifying compounds that block GPCR mediated signaling with high  
 PT affinity and specificity -  
 PT  
 XX Disclosure; Page 12; 94pp; English.  
 PS  
 XX The invention relates to a novel method for identifying a G protein  
 CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises  
 CC selecting or identifying a member of a library of peptides and/or  
 CC candidate compounds, having binding to a GPCR of higher affinity than  
 CC that of the native peptide. The peptide library is based on a native GPCR  
 CC binding peptide. The method is useful for identifying inhibitors of a G  
 CC protein coupled receptor (GPCR) signaling. The method is particularly  
 CC useful for identifying drugs that antagonize the binding between a GPCR  
 CC and its extracellular ligand(s). The method is especially useful in  
 CC modern high throughput screening assays for identifying potent lead  
 CC compounds. The compounds, peptides or inhibitors identified by the method  
 CC are useful for preventing, ameliorating or treating diseases in which  
 CC GPCR signaling is a causative factor or in which a specific class of G  
 CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,  
 CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,  
 CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,  
 CC obesity, or psychotic and neurological disorders (e.g. anxiety,  
 CC schizophrenia or Alzheimer's disease). This sequence represents a peptide  
 CC relating to the G protein coupled receptors of the invention.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 36.4%; Score 4; DB 24; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LPQM 11  
 Db |||||  
 1 LPQM 4  
 RESULT 11  
 AAW12496  
 ID AAW12496 standard; peptide; 5 AA.  
 XX  
 XX AAW12496;  
 XX  
 XX 22-APR-1997 (first entry)  
 DT

XX Interleukin-6 antagonist 61.  
 DE  
 XX Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease;  
 KW skin; intestine; systemic lupus erythematosus; chronic rheumatism.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 5  
 FT /note= "amidated"  
 FT  
 XX JP08311098-A.  
 PN  
 XX 26-NOV-1996.  
 PD  
 XX 22-MAY-1995; 95JP-0146742.  
 PF  
 XX 22-MAY-1995; 95JP-0146742.  
 PR  
 XX (DAIL) DAICEL CHEM IND LTD.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 PA  
 XX WPI; 1997-061811/06.  
 DR  
 XX Interleukin-6 antagonistic peptide(s) comprising arginine - useful  
 PT for treating autoimmune, renal, skin and intestinal diseases  
 PT  
 XX Example 61; Page 12; 20pp; Japanese.  
 PS  
 XX The present peptide is a specific example of new interleukin-6  
 CC antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino  
 CC acids or an amino group protecting group; Y is 1-5 amino acids, a  
 CC carboxyl group protecting group or an amide; A is preferably Arg  
 CC having an opt. protected guanidino group but can be any amino acid;  
 CC D is Arg having an opt. protected guanidino group and B is preferably  
 CC a Leu residue but can be any amino acid, including non-natural  
 CC amino acids, opt. having a protected side-chain. The peptides are  
 CC useful for treating autoimmune diseases (e.g. systemic lupus  
 CC erythematosus or chronic rheumatism), renal, skin and intestinal  
 CC diseases.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 36.4%; Score 4; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FYKL 8  
 Db |||||  
 1 FYKL 4  
 RESULT 12  
 AAW48024  
 ID AAW48024 standard; peptide; 7 AA.  
 XX  
 XX AAW48024;  
 AC  
 XX 12-JUN-1998 (first entry)  
 DT  
 XX AE114 analogue effector compound SEQ ID NO:102.  
 DE  
 XX Mammalian II key peptide; mammalian invariant chain protein; allergy;  
 KW immune response; MHC class II; antigenic; autoimmune disease.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "Acylated"  
 FT Modified-site 7  
 FT /note= "Amidated"  
 FT

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XX PN WO9749430-A1.
XX XX
XX PD 31-DEC-1997.
XX PF 09-JUN-1997; 97WO-US09993.
XX PR 26-JUN-1996; 96US-0670605.
XX PA (ANTI-) ANTIGEN EXPRESS INC.
XX PI Adams S, Humphreys RE, Xu M;
XX PI WPI; 1998-076917/07.
XX DR
XX CC The present sequence represents an AEl14 analogue effector compound
XX CC used in the present invention. The present invention describes
XX CC a mammalian invariant chain protein (ii) key peptide of sequence
XX CC LRMLKPKPKPVSKMR and modifications with the exclusion of peptide
XX CC YRMKLKPKPKPVSKMR. MHC class II molecules are synthesised in the
XX CC endoplasmic reticulum with their antigenic peptide sites blocked by the
XX CC invariant chain protein (ii). The products and method can be used for
XX CC the modulation of an immune response for therapeutic or diagnostic
XX CC purposes. The enhancement of immunity can be used in the treatment of
XX CC e.g. malignant or allergic disease. The immunosuppression can be used
XX CC for the treatment of autoimmune disease, e.g. rheumatoid arthritis,
XX CC multiple sclerosis, diabetes mellitus, lupus erythematosus, and
XX CC psoriasis or allograft rejection.
XX SQ Sequence 7 AA;
XX
XX Query Match 36.4%; Score 4; DB 19; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 KLPQ 10
XX DB 4 KLPQ 7
XX
XX RESULT 13
XX ID AAM47992
XX AC AAM47992;
XX DT 12-JUN-1998 (first entry)
XX DE AEl14 analogue effector compound SEQ ID NO:69.
XX KW Mammalian II key peptide; mammalian invariant chain protein; allergy;
XX KW immune response; MHC class II; antigenic; autoimmune disease.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Acylated"
XX FT Modified-site 7 /note= "Amidated"
XX PN WO9749430-A1.
XX XX
XX PD 31-DEC-1997.
XX PF 09-JUN-1997; 97WO-US09993.
XX PT
XX
XX PR 26-JUN-1996; 96US-0670605.
XX PA (ANTI-) ANTIGEN EXPRESS INC.
XX PI Adams S, Humphreys RE, Xu M;
XX PI WPI; 1998-076917/07.
XX DR
XX CC The present sequence represents an AEl14 analogue effector compound
XX CC used in the present invention. The present invention describes
XX CC a mammalian invariant chain protein (ii) key peptide of sequence
XX CC LRMLKPKPKPVSKMR and modifications with the exclusion of peptide
XX CC YRMKLKPKPKPVSKMR. MHC class II molecules are synthesised in the
XX CC endoplasmic reticulum with their antigenic peptide sites blocked by the
XX CC invariant chain protein (ii). The products and method can be used for
XX CC the modulation of an immune response for therapeutic or diagnostic
XX CC purposes. The enhancement of immunity can be used in the treatment of
XX CC e.g. malignant or allergic disease. The immunosuppression can be used
XX CC for the treatment of autoimmune disease, e.g. rheumatoid arthritis,
XX CC multiple sclerosis, diabetes mellitus, lupus erythematosus, and
XX CC psoriasis or allograft rejection.
XX SQ Sequence 7 AA;
XX
XX Query Match 36.4%; Score 4; DB 19; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 YKLP 9
XX DB 3 YKLP 6
XX
XX RESULT 14
XX ID ABB80641
XX AC ABB80641 standard; peptide; 7 AA.
XX DT 15-JUL-2002 (first entry)
XX DE Clostridium botulinum toxin type A leucine based motif.
XX KW Neurotoxin; biological persistence; dysphonia; strabismus; muscle spasm;
XX KW dystonia; pain; blepharospasm; hemifacial spasm; excessive salivation;
XX KW eyelid disorder; cerebral palsy; focal spasticity; spasmodic colitis;
XX KW neurogenic bladder; anismus; limb spasticity; tic; tremor; bruxism;
XX KW anal fissure; achalasia; dysphagia; lacrimation; hyperhidrosis; headache;
XX KW excessive gastrointestinal secretion; leucine-based motif; botulinum.
XX OS Clostridium botulinum.
XX PN WO200208268-A2.
XX PD 31-JAN-2002.
XX PF 20-JUL-2001; 2001WO-US23122.
XX PR 21-JUL-2000; 2000US-0620840.
XX PA (ALLR ) ALLERGAN SALES INC.
XX PI Steward LE, Fernandez-salas E, Herrington TM, Aoki KS;
XX PI WPI; 2002-241566/29.
XX DR
XX PT Novel modified neurotoxin comprising structural modification which

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PT alters the biological persistence and/or biological activity of a  
 PT neurotoxin, useful for treating neuromuscular or autonomic disorder, or  
 PT pain  
 XX  
 PS Claim 28; Page 76; 102pp; English.  
 XX  
 CC The sequence represents a leucine based motif from Clostridium botulinum,  
 CC botulinum toxin type A, which may act as a biological persistence  
 CC enhancing component in a neurotoxin. The invention relates to a novel  
 CC modified neurotoxin including a structural modification, where the  
 CC structural modification is effective to alter the biological persistence,  
 CC or biological activity. The modified neurotoxin is useful for treating  
 CC spasmodic dysphonia, laryngeal dystonia, oromandibular dysphonia, lingual  
 CC dystonia, cervical dystonia, focal hand dystonia, blepharospasm,  
 CC strabismus, hemifacial spasm, eyelid disorder, cerebral palsy, focal  
 CC spasticity, spasmodic colitis, neurogenic bladder, anismus, limb  
 CC spasticity, tics, tremors, bruxism, anal fissure, achalasia, dysphagia,  
 CC lactimation, hyperhidrosis, excessive salivation, excessive  
 CC gastrointestinal secretions, pain from muscle spasms, headache pain, brow  
 CC furrows or skin wrinkles.  
 XX  
 SQ Sequence 7 AA;

Query Match 36.4%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8  
 Db 3 FYKL 6

## RESULT 15

AAV53386  
 ID AAV53386 standard; Protein; 8 AA.

AC AAV53386;

DT 18-JAN-2000 (first entry)

DE E6 protein epitope (aa 8-15) binds HLA.

XX Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;  
 KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;  
 KW human immunodeficiency virus; hepatitis B virus; papilloma virus;  
 KW melanoma; malaria; parasite.

XX Synthetic.

OS Homo sapiens.

XX FR2776926-A1.

XX 08-OCT-1999.

XX 07-APR-1998; 98FR-0004323.

XX 07-APR-1998; 98FR-0004323.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSP ) INST PASTEUR LILLE.

PI Le Gal PA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;

XX WPI; 1999-583113/50.

XX New lipopeptide containing lipid regions and two epitopes, all  
 PT separated by peptide spacers that impart hydrophilicity, useful in  
 PT vaccines -

XX Disclosure; Page 19; 35pp; French.

XX The invention relates to the generation of a lipopeptide comprising at

CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)  
 CC epitope and at least one lipid residue with (i) the epitopes and lipid  
 CC portion and (ii) the epitopes, being separated independently by peptide  
 CC spacers. These spacers comprise sequences of amino acids which carry an  
 CC overall electrical charge in neutral media to ensure that the  
 CC lipopeptide is hydrophilic. The peptides AAV53301-Y53549 represents  
 CC examples of peptide epitopes used to generate the lipopeptides. These are  
 CC used in therapeutic or prophylactic compositions and vaccines to induce  
 CC specific immune responses against human immunodeficiency, hepatitis B or  
 CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPP 10  
 Db 4 KLPP 7

## RESULT 16

AAV40373

ID AAV40373 standard; Peptide; 8 AA.

AC AAV40373;

DT 19-NOV-1999 (first entry)

DE Amino acid sequence of an E6 and E7 protein epitope.

XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
 KW vaccine; tumor; infection; immune response; cytokine profile;  
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
 KW autoimmune disease.

XX Human papillomavirus.

XX FR2774687-A1.

XX 13-AUG-1999.

XX 06-FEB-1998; 98FR-0001439.

XX 06-FEB-1998; 98FR-0001439.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP ) INST PASTEUR LILLE.

PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;

XX WPI; 1999-510734/43.

XX New lipopeptide comprising C-terminal interferon-gamma fragment with  
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating  
 PT cancer or virus infection

XX Disclosure; Page 42; 53pp; French.

XX AAV40123-Y40379 represent epitopes that are able to activate cytotoxic  
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or  
 CC B epitopes recognized by corresponding antibodies. The epitopes may be  
 CC used in the composition of the invention. The specification describes a  
 CC lipopeptide that has a peptide part derived from mammalian interferon  
 CC gamma (IFN $\gamma$ ) and one or more lipophilic parts comprising a linear or  
 CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The  
 CC lipopeptide mimics the activity of IFN $\gamma$ . Compositions comprising the  
 CC lipopeptide are used to treat or prevent any condition that responds  
 CC to IFN $\gamma$ , and as adjuvant for vaccines (particularly those directed  
 CC against tumors, viral or parasitic infections), to stimulate or  
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.

CC Particular applications are treatment of infections (particularly  
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and  
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers  
 CC (particularly of kidney, cutaneous T cells or ovary, chronic  
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune  
 CC diseases.  
 XX  
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
 ||||  
 Db 4 KLPQ 7

RESULT 17  
 AAY26724  
 ID AAY26724 standard; peptide; 8 AA.

XX AC AAY26724;  
 XX DT 14-SEP-1999 (first entry)  
 XX DE HPV-derived lipopeptide epitope (E6 aa8-15) for mixed micelles.  
 XX KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
 KW melanoma; Plasmodium falciparum; malaria.  
 XX OS Synthetic.  
 OS Human papillomavirus.

XX PN FR2771640-A1.  
 XX PD 04-JUN-1999.

XX PF 03-DEC-1997; 97FR-0015246.  
 XX PR 03-DEC-1997; 97FR-0015246.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.

XX PI Bossus M, Bourgault VI, Gras-Kasse H, Guillet JG, Lippens G;  
 PI Tartar A, Wieruszski JM;  
 XX WPI; 1999-349509/30.

XX Immunogenic lipopeptide micelles - comprising lipopeptides  
 PT containing cytotoxic and helper T-lymphocyte epitopes  
 XX Disclosure; Page 32; 60pp; French.

XX The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprising: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HNL (helper T-lymphocyte) epitope and at least one lipid unit  
 CC different from that of the first lipopeptide. This peptide represents  
 CC an example of a lipopeptide epitope used in the invention and is derived  
 CC from the human papilloma virus 56 protein. The immunogenic lipopeptide  
 CC micelles are used in vaccines, especially against HIV, hepatitis B virus  
 CC (HBV), papilloma viruses, p53, melanoma or Plasmodium falciparum malaria.  
 XX

SQ Sequence 8 AA;  
 Query Match 36.4%; Score 4; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 KLPQ 10  
 ||||  
 Db 4 KLPQ 7

RESULT 18  
 AAY10348  
 ID AAY10348 standard; Peptide; 8 AA.

XX AC AAY10348;  
 XX DT 12-MAY-1999 (first entry)  
 XX DE T cell epitope/MHC ligand SEQ ID NO:278.  
 XX KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; hepatitis; AIDS.

XX OS Synthetic.  
 OS Human papillomavirus.

XX PN WO9902183-A2.

XX PD 21-JAN-1999.

XX PF 10-JUL-1998; 98WO-US14289.  
 XX PR 10-DEC-1997; 97US-0988320.  
 PR 10-JUL-1997; 97CA-2209815.

XX PA (CTL-) CTL IMMUNOTHERAPIES CORP.

XX PI Kuendig TW, Simard JLL;

XX DR WPI; 1999-120514/10.

XX Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 34; 199pp; English.

XX The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.

SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
 ||||  
 Db 4 KLPQ 7

```

RESULT 19
ABP11965
ID ABP11965 standard; Peptide; 8 AA.
XX
AC ABP11965;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #22.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 114; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
XX
Query Match 36.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FYKL 8
DB 3 FYKL 6
RESULT 20
ABP18445
ID ABP18445 standard; Peptide; 8 AA.

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XX
AC ABP18445;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV B62 super motif env peptide #20.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 247; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
XX
Query Match 36.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FYKL 8
DB 3 FYKL 6
RESULT 21
ABG80030
ID ABG80030 standard; Peptide; 8 AA.
XX
AC ABG80030;
XX

```

DT 15-NOV-2002 (first entry)  
 DE MHC class I molecule, viral epitope #278.  
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.  
 XX Human papillomavirus 16.  
 OS WO200262368-A2.  
 XX 15-AUG-2002.  
 XX 22-JAN-2002; 2002WO-US02033.  
 XX 02-FEB-2001; 2001US-0776232.  
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 XX Kundig TM, Simard JJL;  
 PI WPI; 2002-657506/70.  
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in  
 PT a mammal, useful for treating a mammal with malignant tumour or  
 PT infectious disease, by directly administering an antigen to the  
 PT lymphatic system of the mammal -  
 XX Disclosure; Page 27; 73pp; English.  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.  
 CC ABG79753-ABG80319 represent viral epitopes on major histocompatibility  
 CC complex (MHC) class I molecules, used in the method of the invention.  
 XX Sequence 8 AA;  
 SQ Query Match 36.4%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLPQ 10  
 ||||  
 Db 4 KLPQ 7  
 RESULT 22  
 AAR43729  
 ID AAR43729 standard; peptide; 9 AA.  
 XX AAR43729;  
 AC 25-MAR-2003 (updated)  
 DT 19-MAY-1994 (first entry)  
 XX MHC Class I allele HLA-A2.1 binding HPV16 E6 peptide.  
 XX Human papilloma virus; major histocompatibility complex; prevention;  
 KW treatment; virus-related diseases; T cell response; cervical; human;  
 KW carcinoma; adenoma; screening tools; diagnostics.

XX Synthetic.  
 OS WO9322338-A1.  
 XX 11-NOV-1993.  
 PD 04-MAY-1993; 93WO-NL00093.  
 XX 05-MAY-1992; 92EP-0201252.  
 FR 10-DEC-1992; 92EP-0203870.  
 FR 01-FEB-1993; 93EP-0200243.  
 FR 05-MAR-1993; 93EP-0200621.  
 XX (UYLE-) RIJKSUNIV LEIDEN.  
 XX Kast WM, Melief CJM, Sette AD, Sidney JC;  
 PI WPI; 1993-368718/46.  
 XX Peptide(s) derived from human papilloma virus - which bind to a  
 PT human major histocompatibility complex class I molecule, used for  
 PT prevention and treatment of virus-related diseases  
 XX Claim 5; Page 51; 64pp; English.  
 XX The sequence is that of a peptide, derived from the E6 protein of  
 CC human papilloma virus (HPV) (residues 18-26), which is able to bind  
 CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell  
 CC response effective against HPV, in partic. a HLA class I-restricted  
 CC CD8+ cytotoxic T cell response. It can be used for prevention and  
 CC treatment of cervical carcinoma and/or adenoma and other HPV-related  
 CC diseases. It can also be used as a screening tool and in diagnostic  
 CC applications.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 9 AA;  
 SQ Query Match 36.4%; Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLPQ 10  
 ||||  
 Db 1 KLPQ 4  
 RESULT 23  
 AAR59196  
 ID AAR59196 standard; peptide; 9 AA.  
 XX AAR59196;  
 AC 25-MAR-2003 (updated)  
 DT 03-MAY-1995 (first entry)  
 XX Peptide fragment (1.0221) of HPV binds HLA-A2.1.  
 XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV; core antigen; surface antigen; pharmaceutical composition;  
 KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;  
 KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;  
 KW human leukocyte antigen.  
 XX Human papilloma virus.  
 OS WO9420127-A1.  
 XX 15-SEP-1994.  
 PD 04-MAR-1994; 94WO-US02353.  
 XX 05-MAR-1993; 93US-0027146.



```

PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Grey HM, Kast WM, Sette A, Sidney J;
XX
XX WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Example 5; Page 103; 138pp; English.
XX
XX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59196
CC has an IC50 of 0.0006 and the sequence occurs at position 18 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 9 AA;
SQ
Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 1 KLPQ 4

RESULT 24
AAW49468
ID AAW49468 standard; peptide; 9 AA.
XX
XX AAW49468;
XX
XX 05-JUN-1998 (first entry)
XX
XX Human leucocyte antigen DQ4 binding peptide #359.
XX
XX Human leucocyte antigen; HLA-DQ4; combinatorial library;
KW autoimmune disease; chronic articular rheumatism.
XX
XX Synthetic.
OS
XX JP08151396-A.
PN
XX 11-JUN-1996.
PD
XX 28-NOV-1994; 9AJP-0292657.
PF
XX 28-NOV-1994; 9AJP-0292657.
PR
XX (TEIJ ) TEIJIN LTD.
PA
XX WPI; 1996-329479/33.
DR
XX
XX HLA-binding oligopeptide and an immuno:regulator contg it - used in
PT the treatment of auto:immune disease
PT
XX
XX Claim 4; Page 42; 61pp; Japanese.
XX
XX This peptide is an example of a peptide which binds to a human leucocyte
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
CC combinatorial library comprising the sequence AAV05953, by screening
CC with an HLA-DQ4 molecule. The peptide is used for the treatment of
CC autoimmune disease, or especially for treatment of viral diseases.

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XX
XX Sequence 9 AA;
SQ
Query Match 36.4%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
DB 3 FYKL 6

RESULT 25
AAW39512
ID AAW39512 standard; peptide; 9 AA.
XX
XX AAW39512;
XX
XX 11-JUN-1998 (first entry)
XX
XX HPV16 E6-encoded CTL epitope 5.
XX
XX T cell epitope; immune response; human leukocyte antigen; HLA Class I;
KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
KW disease; anti-tumour; anti-viral; HPV16 E6.
XX
XX Synthetic.
OS
XX Human Papillomavirus.
XX
XX W09741440-A1.
PN
XX
XX 06-NOV-1997.
PD
XX
XX 28-APR-1997; 97WO-NL00229.
PF
XX
XX 23-DEC-1996; 96EP-0203670.
PR
XX 26-APR-1996; 96EP-0201145.
XX
XX (UYLE-) RIJCSUNIV LEIDEN.
PA
XX (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX
XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX
XX WPI; 1997-549891/50.
XX
XX Method of selecting T cell peptide epitope(s) - by measuring the
PT stability of HLA class I-peptide complexes on intact B cells
PT
XX Example 2; Page 59; 109pp; English.
XX
XX Peptides AAW39430-W39734 are used in a novel method for the selection of
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I
CC peptide. The stability of binding of the peptide and MHC (major
CC histocompatibility complex) class I molecule is measured on intact human
CC B cells carrying the MHC molecule at their cell surfaces. The method can
CC be used to select peptide epitopes for generating vaccines against a
CC disease associated with the polypeptide, e.g. cancers or AIDS. The
CC peptide epitopes are especially T-cell peptide epitopes with strong
CC anti-tumour and anti-viral immune responses. Peptide AAW39512 is a HPV16
CC E6 encoded cytotoxic T lymphocyte (CTL) epitope used in a binding assay
CC to test for binding to HLA-A*0201 at different temperatures for different
CC incubation times.
XX
XX Sequence 9 AA;
SQ
Query Match 36.4%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10

```

```

Db      |||||
        1 KLPQ 4

RESULT 26
AAW78890
ID   AAW78890 standard; peptide; 9 AA.
XX   AC   AAW78890;
XX   DT   17-NOV-1998 (first entry)
XX   DE   Human papillomavirus 16 E6 protein fragment 18-26.
XX   KW   Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
XX   KW   class II associated peptide; pathogen; gene therapy; genetic disease;
XX   KW   infection; downregulation; immune response.
XX   OS   Human papillomavirus.
XX   OS   Synthetic.
XX   PN   WO9831398-A1.
XX   PD   23-JUL-1998.
XX   PF   22-JAN-1998; 98WO-US01499.
XX   PR   06-JAN-1998; 98US-0003253.
XX   PR   22-JAN-1997; 97US-0787547.
XX   PA   (PANG-) PANGAEA PHARM INC.
XX   PI   Curley JM, Hedley ML, Langer RS, Lunsford LB;
XX   DR   WPI; 1998-427556/36.
XX   PT   New preparations of microparticles - comprising a synthetic polymer
XX   PT   matrix and nucleic acid comprising an expression vector for use in
XX   PT   gene therapy
XX   PS   Disclosure; Page 10; 101pp; English.
XX   CC   A microparticle preparation (MP) has been developed, consisting of
XX   CC   microparticles having a diameter of less than 100 nm, the MP
XX   CC   comprises: (a) a polymeric matrix (PM) consisting of one or more
XX   CC   synthetic polymers having a solubility in water of less than 1 mg/l; and
XX   CC   (b) an expression vector selected from RNA molecules (at least 50% of
XX   CC   which are closed circles), or circular plasmid DNA (at least 50% of which
XX   CC   are supercoiled). Also described is a MP of at most 20 microns in
XX   CC   diameter, comprising: (a) a PM; and (b) a NAM comprising an expression
XX   CC   control sequence operatively linked to a coding sequence, where the
XX   CC   coding sequence encodes an expression product selected from: (i) a
XX   CC   polypeptide at least 7 amino acids in length, having a sequence identical
XX   CC   to the sequence of: (i) a fragment of a naturally-occurring mammalian
XX   CC   protein; or (ii) a fragment of a naturally-occurring protein from an
XX   CC   infectious agent which infects a mammal; (2) a peptide having a length
XX   CC   and sequence which permits it to bind to an MHC class I or II molecule;
XX   CC   and (3) the polypeptide or the peptide linked to a trafficking sequence.
XX   CC   AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for
XX   CC   use in the present invention. The MPs are highly effective vehicles for
XX   CC   the delivery of polynucleotides into phagocytic cells. They can be used
XX   CC   for gene therapy, e.g. for treating genetic diseases, infections or
XX   CC   tumours or for downregulating an immune response.
XX   SQ   Sequence 9 AA;

Query Match      36.4%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      7 KLPQ 10
        |||||
Db      1 KLPQ 4

RESULT 28
AAW54509
ID   AAW54509 standard; peptide; 9 AA.
XX   AC   AAW54509;
XX   DT   01-SEP-1998 (first entry)
XX   DE   Synthetic polypeptide HPV 16 E6 18-26.
XX   KW   Carbohydrate-specific; cytolytic T cell; therapeutic; tumour;
XX   KW   major histocompatibility complex; vaccine; protective immune response;
XX   KW   pathogenic bacteria; virus; CTL response.
XX   OS   Carbohydrate-specific; cytolytic T cell; therapeutic; tumour;
XX   OS   major histocompatibility complex; vaccine; protective immune response;
XX   OS   pathogenic bacteria; virus; CTL response.
XX   PN   WO9813378-A1.
XX   PD   02-APR-1998.
XX   PF   25-SEP-1997; 97WO-NL00536.
XX   PR   26-SEP-1996; 96EP-0202701.
XX   PR   (UYLE-) RIJKSUNIV LEIDEN.
XX   PI   Drijfhout JW, Koning F;
XX   DR   WPI; 1998-230631/20.
XX   PT   Increasing uptake and presentation of antigen(s) - by adding mannose
XX   PT   residue(s) to antigen for increasing T cell response, useful in,
XX   PT   e.g. vaccines against viral infection(s)
XX   PS   Disclosure; Page 36; 47pp; English.
XX   CC   The peptides AAW54559-W54809 are examples of peptides to which at least
XX   CC   1 (preferably 2) mannose can be attached to increase their uptake as
XX   CC   antigens by antigen-presenting cells. Uptake of agonist mannoseylated
XX   CC   peptides will increase the T cell response, whereas uptake of antagonist
XX   CC   peptides blocks the T cell response. Blocking binding of immunogenic
XX   CC   autoantigens can be used in treatment of type I diabetes, rheumatoid
XX   CC   arthritis, graft rejection etc.; also to induce T-cell non-
XX   CC   responsiveness. Vaccines containing mannoseylated antigen are used to
XX   CC   prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
XX   CC   and parasites.
XX   SQ   Sequence 9 AA;

Query Match      36.4%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      7 KLPQ 10
        |||||
Db      1 KLPQ 4

RESULT 28
AAW54509
ID   AAW54509 standard; peptide; 9 AA.
XX   AC   AAW54509;
XX   DT   01-SEP-1998 (first entry)
XX   DE   Synthetic polypeptide HPV 16 E6 18-26.
XX   KW   Carbohydrate-specific; cytolytic T cell; therapeutic; tumour;
XX   KW   major histocompatibility complex; vaccine; protective immune response;
XX   KW   pathogenic bacteria; virus; CTL response.
XX   OS   Carbohydrate-specific; cytolytic T cell; therapeutic; tumour;
XX   OS   major histocompatibility complex; vaccine; protective immune response;
XX   OS   pathogenic bacteria; virus; CTL response.
XX   PN   WO9813378-A1.
XX   PD   02-APR-1998.
XX   PF   25-SEP-1997; 97WO-NL00536.
XX   PR   26-SEP-1996; 96EP-0202701.
XX   PR   (UYLE-) RIJKSUNIV LEIDEN.
XX   PI   Drijfhout JW, Koning F;
XX   DR   WPI; 1998-230631/20.
XX   PT   Increasing uptake and presentation of antigen(s) - by adding mannose
XX   PT   residue(s) to antigen for increasing T cell response, useful in,
XX   PT   e.g. vaccines against viral infection(s)
XX   PS   Disclosure; Page 36; 47pp; English.
XX   CC   The peptides AAW54559-W54809 are examples of peptides to which at least
XX   CC   1 (preferably 2) mannose can be attached to increase their uptake as
XX   CC   antigens by antigen-presenting cells. Uptake of agonist mannoseylated
XX   CC   peptides will increase the T cell response, whereas uptake of antagonist
XX   CC   peptides blocks the T cell response. Blocking binding of immunogenic
XX   CC   autoantigens can be used in treatment of type I diabetes, rheumatoid
XX   CC   arthritis, graft rejection etc.; also to induce T-cell non-
XX   CC   responsiveness. Vaccines containing mannoseylated antigen are used to
XX   CC   prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
XX   CC   and parasites.
XX   SQ   Sequence 9 AA;

Query Match      36.4%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      7 KLPQ 10
        |||||
Db      1 KLPQ 4

```

OS Synthetic.  
 XX WO9815286-A1.  
 XX  
 XX PD 16-APR-1998.  
 XX  
 XX PF 08-OCT-1997; 97WO-US18146.  
 XX  
 XX PR 08-OCT-1996; 96US-0028260.  
 XX  
 XX PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.  
 XX  
 XX PI Grey H;  
 XX  
 XX DR WPI; 1998-240595/21.  
 XX  
 XX PT Composition for stimulating carbohydrate-specific cytotoxic T  
 PT lymphocytes - comprises synthetic peptide with attached carbohydrate  
 PT haptan, designed to bind to class I molecule, used in vaccines  
 PT against cancer or infectious disease  
 XX  
 XX PS Disclosure; Page 18; 64pp; English.  
 XX  
 CC The peptides AAW5491-W54531 and AAW54533-W54534 are examples of  
 CC polypeptides tested and used in the production of a synthetic  
 CC polypeptide, for stimulating a carbohydrate-specific cytolytic T cell  
 CC (CTL) response. The polypeptide should be at least 8 amino acids, 2 of  
 CC which are anchor residues. The polypeptide binds to the binding groove  
 CC of a major histocompatibility complex class I molecule and a carbohydrate  
 CC molecule which is linked to an internal amino acid of the polypeptide  
 CC extends beyond the groove. This stimulates T cells which are able to  
 CC lyse specifically cells that express carbohydrate residues on their  
 CC surface. The polypeptides are used as vaccines to generate therapeutic  
 CC or protective immune responses, particularly against tumours but also  
 CC against pathogenic bacteria and viruses (e.g. mycobacteria that cause  
 CC leprosy and tuberculosis).  
 XX  
 XX SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 7 KLPQ 10  
 DB 1 KLPQ 4  
 RESULT 29  
 AAY53385  
 ID AAY53385 standard; Protein; 9 AA.  
 XX  
 XX AC AAY53385;  
 XX  
 XX DT 18-JAN-2000 (first entry)  
 XX  
 XX DE B6 protein epitope (aa 18-26) binds HLA.  
 XX  
 XX KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;  
 KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;  
 KW human immunodeficiency virus; hepatitis B virus; papilloma virus;  
 KW melanoma; malaria; parasite.  
 XX  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX PN FR2776926-A1.  
 XX  
 XX PD 08-OCT-1999.  
 XX  
 XX PF 07-APR-1998; 98FR-0004323.  
 XX  
 XX PR 07-APR-1998; 98FR-0004323.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 XX PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;  
 XX  
 XX DR WPI; 1999-583113/50.  
 XX  
 XX PT New lipopeptide containing lipid regions and two epitopes, all  
 PT separated by peptide spacers that impart hydrophilicity, useful in  
 PT vaccines  
 XX  
 XX PS Disclosure; Page 19; 35pp; French.  
 XX  
 CC The invention relates to the generation of a lipopeptide comprising at  
 CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)  
 CC epitope and at least one lipid residue with (i) the epitopes and lipid  
 CC portion and (ii) the epitopes, being separated independently by peptide  
 CC spacers. These spacers comprise sequences of amino acids which carry an  
 CC overall electrical charge in neutral media to ensure that the  
 CC lipopeptide is hydrophilic. The peptides AAY5301-Y53549 represents  
 CC examples of peptide epitopes used to generate the lipopeptides. These are  
 CC used in therapeutic or prophylactic compositions and vaccines to induce  
 CC specific immune responses against human immunodeficiency, hepatitis B or  
 CC papilloma viruses; p53 of melanoma or the malaria parasite.  
 XX  
 XX SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 7 KLPQ 10  
 DB 1 KLPQ 4  
 RESULT 30  
 AAY40372  
 ID AAY40372 standard; Peptide; 9 AA.  
 XX  
 XX AC AAY40372;  
 XX  
 XX DT 19-NOV-1999 (first entry)  
 XX  
 XX DE Amino acid sequence of an E6 and E7 protein epitope.  
 XX  
 XX KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
 KW vaccine; tumor; infection; immune response; cytokine profile;  
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
 KW autoimmune disease.  
 XX  
 XX OS Human papillomavirus.  
 XX  
 XX PN FR2774687-A1.  
 XX  
 XX PD 13-AUG-1999.  
 XX  
 XX PF 06-FEB-1998; 98FR-0001439.  
 XX  
 XX PR 06-FEB-1998; 98FR-0001439.  
 XX  
 XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 XX PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;  
 XX  
 XX DR WPI; 1999-510734/43.  
 XX  
 XX PT New lipopeptide comprising C-terminal interferon-gamma fragment with  
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating



CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.  
 XX  
 XX  
 SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10  
 DB 1 KLPQ 4

RESULT 33  
 AAB33702  
 ID AAB33702 standard; Peptide; 9 AA.  
 XX  
 AC AAB33702;  
 XX  
 XX 26-JAN-2001 (first entry)  
 DT  
 DE MHC class I associated immunogenic peptide SEQ ID 101.  
 XX  
 XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;  
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..  
 XX  
 XX Unidentified.  
 OS  
 XX WO200053161-A2.  
 PN  
 PD 14-SEP-2000.  
 XX  
 XX 10-MAR-2000; 2000WO-US06578.  
 XX  
 XX 11-MAR-1999; 99US-0266463.  
 PR 27-MAY-1999; 99US-0321346.  
 XX  
 XX (ZYCO-) ZYCOS INC.  
 PA  
 XX  
 PI Lunsford LB, Putnam D, Hedley ML;  
 XX  
 DR WPI; 2000-638130/61.  
 XX  
 PT Microparticles useful for administering a nucleic acid into the mucosal  
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric  
 PT matrix, a lipid and a nucleic acid molecule -  
 XX  
 PS Disclosure; Page 16; 96pp; English.  
 XX  
 CC The present invention relates to microparticles which are less than 20  
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a  
 CC nucleic acid molecule. The microparticle is specifically not  
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide  
 CC sequence encodes an expression product that binds to major  
 CC histocompatibility complex (MHC) type I or II molecules. Peptides  
 CC AAB33602-B33647 represent MHC class II associated immunogenic peptides,  
 CC and AAB33648-B33710 represent MHC class I associated immunogenic  
 CC peptides. The peptides are examples of the expression products of the  
 CC nucleotide sequences which can be included in the microparticles of the  
 CC invention. Sequences AAB33711-B33716 represent alternative expression  
 CC products and nuclear localisation signals also used in the invention. The  
 CC microparticles are useful for administering a nucleic acid into the  
 CC mucosal tissue preferably vaginal tissue of an animal.  
 XX  
 XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10  
 DB 1 KLPQ 4

RESULT 34  
 AAY66471  
 ID AAY66471 standard; Peptide; 9 AA.  
 XX  
 AC AAY66471;  
 XX  
 DT 22-FEB-2000 (first entry)  
 XX  
 DE HLA-A2-binding HPV type 16 E6 conserved peptide #273.  
 XX  
 XX Human papillomavirus; HPV; MHC; major histocompatibility complex;  
 KW Class I; HLA-A2; human leukocyte antigen; epitope; allele; binding;  
 KW conserved; genome; peptide; targeting; toxic; drug; antibody; antigen;  
 KW antiviral; molecular conjugate therapeutic; diagnosis; treatment;  
 KW pathogen; localisation; quantification; detection; infection;  
 KW drug resistance; immune response.  
 XX  
 XX Human papillomavirus.  
 OS  
 XX WO9949893-A1.  
 PN  
 PD 07-OCT-1999.  
 XX  
 PF 31-MAR-1999; 99WO-US07111.  
 XX  
 PR 31-MAR-1998; 98US-0052530.  
 XX  
 XX (UYBO-) UNIV BOSTON.  
 PA  
 XX  
 PI Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;  
 XX  
 DR WPI; 2000-038361/03.  
 XX  
 PT Novel methods for designing molecular conjugate therapeutics which are  
 PT used for diagnosis, imaging and treatment against pathogens -  
 XX  
 XX Example 4; Page 54; 62pp; English.  
 PS  
 XX  
 CC AAY66462-Y66474 are peptides derived from conserved portions of the  
 CC human papillomavirus genome (HPV) that are presented by HLA-A2 MHC  
 CC (major histocompatibility complex) Class I molecules. The peptides are  
 CC used to construct targeting antigens comprising one or more peptides  
 CC bound to the corresponding MHC Class I molecule, which can be used to  
 CC raise antibodies. The antibody may then be used as a targeting vehicle  
 CC to deliver a potentially toxic drug to its target site of action, rather  
 CC than administering it systemically, which may result in adverse side  
 CC effects. The invention relates to improved methods for the design  
 CC of molecular conjugate therapeutics for the diagnosis and treatment of  
 CC infections caused by pathogens with a high mutation rate (such as  
 CC HPV). This method involves identifying conserved peptide-encoding  
 CC regions among the genomes of multiple variants of a pathogen,  
 CC identifying the Class I MHC molecules which occur with greatest  
 CC frequency in a population of interest (e.g., human sub-populations),  
 CC and determining which of the peptides bind to the Class I MHC  
 CC molecules. The MHC-binding peptides and the corresponding Class  
 CC I MHC molecules are selected and used to construct targeting  
 CC antigens, which are in turn used to produce targeting antibodies.  
 CC The methods may be used in localisation, quantification and in situ  
 CC detection of specific peptide-MHC Class I complexes and also to  
 CC detect and treat viral infection. The methods of the invention  
 CC mitigate against the development of viral resistance to drugs and  
 CC to the immune response, as well as providing a solution for  
 CC targeting toxic compounds to destroy viruses sequestered in sites not  
 CC accessible to T cells. In addition, the methods eliminate the virus,  
 CC whereas current therapies only arrest viral replication.  
 XX  
 XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
 ||||  
 Db 1 KLPQ 4

RESULT 35  
 AA07583  
 ID AA07583 standard; peptide; 9 AA.  
 AC AA07583;  
 XX  
 XX 06-NOV-2001 (first entry)  
 XX  
 XX Human PUMP-1 peptide (residues 238-246).  
 XX  
 XX PUMP-1 protease; cancer; neoplastic state; malignancy; ovary; lung;  
 KW prostate; colon; cytostatic; gene therapy; vaccine; immunogen; human.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WC200154712-A1.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 26-JAN-2001; 2001WO-US02698.  
 XX  
 XX 27-JAN-2000; 2000US-0492543.  
 XX  
 XX (UYAR-) UNIV ARKANSAS.  
 XX  
 XX O'Brien TU;  
 XX  
 XX WPI; 2001-496835/54.  
 XX  
 XX Diagnosing cancer in an individual, useful for early detection of  
 PT ovarian cancer, lung cancer or prostate cancer, comprises determining  
 PT the presence of PUMP-1 protease in biological sample obtained from  
 PT individual -  
 XX  
 XX Example 20; Page 65; 145pp; English.

CC The patent discloses compositions and methods for the early diagnosis  
 CC of ovarian cancer. The method involves obtaining a biological sample  
 CC from an individual and detecting PUMP-1 protease in the sample, where  
 CC the presence of PUMP-1 in the sample is indicative of the presence of  
 CC cancer in the individual and the absence of PUMP-1 is indicative of  
 CC the absence of cancer in the individual. The method is useful for the  
 CC early detection or diagnosis of ovarian cancer and other neoplastic  
 CC state or malignancies (e.g. lung cancer, prostate cancer, colon cancer  
 CC or other cancers in which PUMP-1 is overexpressed). It is also useful  
 CC for diagnosing whether an individual has cancer, is suspected of having  
 CC cancer or is at risk of getting cancer. The method is also used to  
 CC detect and treat malignant hyperplasia. The PUMP-1 proteins are also  
 CC useful for vaccinating against neoplastic states. The oligonucleotide  
 CC is useful for treating neoplastic states such as lung cancer, prostate  
 CC cancer, colon cancer or other cancers in which PUMP-1 is overexpressed.  
 CC The present sequence is PUMP-1 peptide (residues 238-246) from human.  
 CC This peptide is a putative immunogen and binds strongly to HLA A1  
 CC and is used to inoculate an individual against PUMP-1.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5  
 ||||  
 Db 4 PQNF 7

RESULT 36  
 AA07583  
 ID AA07583 standard; Peptide; 9 AA.  
 XX  
 XX AC AA07583;  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX  
 XX HIV peptide SEQ ID NO 1337.  
 DE  
 XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
 KW human immunodeficiency virus; vaccine.  
 XX  
 XX Human immunodeficiency virus.  
 OS  
 XX Synthetic.  
 XX  
 XX WC200155177-A2.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 29-JAN-2001; 2001WO-DK00059.  
 XX  
 XX 28-JAN-2000; 2000EP-0610017.  
 PR  
 XX 31-JAN-2000; 2000US-0179333.  
 XX  
 XX (STAT-) STATENS SERUM INST.  
 PA  
 XX Fomsgaard A, Brunak S, Buus S, Corbet S, Laumoller SL, Hansen J;  
 FI  
 XX WPI; 2001-476184/51.  
 DR  
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in  
 PT anti-HIV vaccines -  
 PT  
 XX Example 4; Page 378; 383pp; English.

XX The invention relates to identification of cytotoxic T cell lymphocyte  
 CC (CTL) epitopes (AA07583-AA07583) that generate anti-HIV activity. CTL  
 CC are a major protective mechanism against viral diseases. Antibodies may  
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
 CC prevent infection of cells in the host, but CTL will limit viral  
 CC production by killing the cell. The CTL epitopes are useful in medicine,  
 CC in the manufacture of vaccines or diagnostic agents.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8  
 ||||  
 Db 3 FYKL 6

RESULT 37  
 AA07583  
 ID AA07583 standard; Peptide; 9 AA.  
 XX  
 XX AC AA07583;  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX  
 XX HIV peptide SEQ ID NO 1369.  
 DE  
 XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
 KW human immunodeficiency virus; vaccine.  
 XX  
 XX Human immunodeficiency virus.  
 OS  
 XX Synthetic.

PN WO200155177-A2.  
 XX 02-AUG-2001.  
 XX 29-JAN-2001; 2001WO-DK00059.  
 XX 28-JAN-2000; 2000EP-0610017.  
 XX 31-JAN-2000; 2000US-0179333.  
 XX (STAT-) STATENS SERUM INST.  
 XX Pomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;  
 XX WPI; 2001-476184/51.  
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in  
 PT anti-HIV vaccines -  
 XX Example 4; Page 383; 383pp; English.  
 XX The invention relates to identification of cytotoxic T cell lymphocyte  
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL  
 CC are a major protective mechanism against viral diseases. Antibodies may  
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
 CC prevent infection of cells in the host, but CTL will limit viral  
 CC production by killing the cell. The CTL epitopes are useful in medicine,  
 CC in the manufacture of vaccines or diagnostic agents.  
 XX SQ Sequence 9 AA;  
 XX Query Match 36.4%; Score 4; DB 22; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FYKL 8  
 DB ||||  
 3 FYKL 6  
 RESULT 38  
 ID AAG93798 standard; Peptide; 9 AA.  
 AC AAG93798;  
 XX 17-SEP-2001 (first entry)  
 XX Human papilloma virus 16 E6 peptide 1.  
 XX Continuous flow production; microparticle; gene therapy;  
 XX antisense therapy; vaccination; treatment; autoimmune disease;  
 XX immune response modulation.  
 XX Human wart virus.  
 XX WO200136583-A1.  
 XX 25-MAY-2001.  
 XX 17-NOV-2000; 2000WO-US31770.  
 XX 19-NOV-1999; 99US-0443654.  
 XX (ZYCO-) ZYCOS INC.  
 XX Hedley ML, Hsu Y, Tyo M;  
 XX WPI; 2001-425203/45.  
 XX Continuous production of microparticles containing nucleic acid for  
 PT e.g. gene therapy, comprises mixing a solution of polymeric material  
 PT and nucleic acid with a surfactant solution, removing solvent and  
 PT drying -

XX Disclosure; Page 12; 47pp; English.  
 XX The present sequence is that of a peptide of the invention.  
 CC The invention relates to a method for scalable, continuous flow  
 CC production of a nucleic acid containing microparticle that maintains the  
 CC structural integrity of the associated nucleic acid and results in a  
 CC microparticle having purity suitable for introduction into an animal  
 CC host. Microparticles prepared according to the method can be used for  
 CC delivery of a nucleic acid for gene therapy, antisense therapy,  
 CC vaccination, treatment of autoimmune disease and either specific or  
 CC non-specific modulation of an immune response. The microparticles may  
 CC also be used to deliver nucleic acid encoding a protein or peptide useful  
 CC in any kind of therapy. The method is economical, aseptic and scalable.  
 CC The method also enables control over the size of microparticles. The  
 CC microparticles produced are free of impurities such as organic solvents  
 CC and are readily dispersed in a wide range of dispersing agents.  
 XX SQ Sequence 9 AA;  
 XX Query Match 36.4%; Score 4; DB 22; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLPQ 10  
 DB ||||  
 1 KLPQ 4  
 RESULT 39  
 ID AAB95948 standard; Peptide; 9 AA.  
 XX AAB95948;  
 XX 25-JUN-2001 (first entry)  
 XX MHC class-I associated HPV epitope SEQ ID 55.  
 XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;  
 XX human papillomavirus-associated disease; condyloma; cervical dysplasia;  
 XX cervical dysplasia; major histocompatibility complex; MHC I.  
 XX Human papillomavirus.  
 XX WO200119408-A1.  
 XX 22-MAR-2001.  
 XX 18-SEP-2000; 2000WO-US25559.  
 XX 16-SEP-1999; 99US-0154665.  
 XX 16-SEP-1999; 99US-0398534.  
 XX 09-DEC-1999; 99US-0169846.  
 XX 09-DEC-1999; 99US-0458173.  
 XX (ZYCO-) ZYCOS INC.  
 XX Hedley ML, Urban RC, Chiciz RM;  
 XX WPI; 2001-265996/27.  
 XX Novel nucleic acids encoding polypeptide polypeptides containing  
 PT multiple epitopes from one or more proteins, useful for treating tumors  
 PT and as vaccines against pathogenic agents -  
 XX Disclosure; Page 8; 64pp; English.  
 XX This invention relates to polynucleotides encoding a hybrid polypeptide  
 CC comprising a signal sequence and three segments that are either  
 CC contiguous or separated by a spacer amino acid or spacer peptide. The  
 CC invention specifically details polynucleotides encoding a polypeptide  
 CC peptide where the peptide segments are tumour antigens or a naturally

CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit  
 CC antiviral and immunostimulatory activity. The polynucleotide and  
 CC polypeptide peptides are useful for eliciting an immune response in a  
 CC mammal. The polynucleotide and protein are useful as vaccines for  
 CC treating tumours and pathogenic infections. The polynucleotide is also  
 CC useful for preventing or treating human papillomavirus (HPV)-associated  
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical  
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV  
 CC infection, cervical dysplasia, high grade squamous intraepithelial  
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are  
 CC useful for generating or enhancing prophylactic or therapeutic immune  
 CC responses against pathogens, tumours or autoimmune diseases in a  
 CC population of individuals having diverse MHC allotypes, as positive  
 CC controls in cell stimulation assays in vitro, and as tools to  
 CC understand processing of epitopes within cells. Peptides  
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major  
 CC histocompatibility complex I (MHC I) associated tumour and pathogen  
 CC antigens. The peptides can be used as part of the polypeptide proteins of  
 CC the invention. Also included are examples of the polypeptide proteins  
 CC represented by AAB96050 - AAB96052, and localisation signal peptides  
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of  
 CC the polypeptide peptides.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
 Db 1 KLPQ 4

RESULT 41

ID AAG80243  
 ID AAG80243 standard; Peptide; 9 AA.

AC AAG80243;

DT 15-NOV-2002 (first entry)

XX MHC class I molecule, viral epitope #491.

XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.

XX Viridae.

XX WO200262368-A2.

XX 15-AUG-2002.

XX 22-JAN-2002; 2002WO-US02033.

XX 02-FEB-2001; 2001US-0776232.

XX (CTLI-) CTL IMMUNOTHERAPIES CORP.

PI Kundig TM, Simard JUL;

DR WP1; 2002-657506/70.

XX Inducing or sustaining immunological cytotoxic T lymphocyte response in  
 PT a mammal, useful for treating a mammal with malignant tumour or  
 PT infectious disease, by directly administering an antigen to the  
 PT lymphatic system of the mammal -

XX Disclosure; Page 40; 73pp; English.

CC The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.  
 CC AAG97733-ABG8019 represent viral epitopes on major histocompatibility  
 CC complex (MHC) class I molecules, used in the method of the invention.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
 Db 1 KLPQ 4

RESULT 41

ID AAG80674  
 ID AAG80674 standard; Protein; 9 AA.

AC AAG80674;

DT 19-MAR-2002 (first entry)

XX Human tumour-associated antigen B132 immunogenic peptide SEQ ID 95.

XX Tumour-associated antigen B132; human; cytostatic; immunotherapy;  
 KW cancer; kidney; lung; colon; breast; carcinoma; tumour proliferation;  
 KW vaccine; diagnosis.

XX Homo sapiens.

XX WO200189281-A2.

XX 29-NOV-2001.

XX 21-MAY-2001; 2001WO-BP05787.

XX 23-MAY-2000; 2000DE-1025521.

XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

XX Adolf G, Heider K, Koenig U, Sommergruber W, Gruenfelder A;  
 PI Abseher R;

XX WP1; 2002-083034/11.

XX New tumor-associated antigen B132, useful for immunotherapy of cancer  
 PT and for identifying antitumour agents, also related nucleic acid and  
 PT antibodies -

XX Claim 5; Page 105; 108pp; German.

XX This invention describes a novel human tumour-associated antigen (Ag),  
 CC designated B132 which has cytostatic activity. The antigen and its  
 CC immunogenic fragments or decomposition products, are useful in vivo  
 CC or ex vivo immunotherapy of cancers, particularly kidney cell, lung,  
 CC colon or breast carcinoma. DNA (I) that encodes antigen can be used  
 CC similarly (also to detect tumour-related mutations), also as a  
 CC therapeutic target to identify inhibitors of tumour proliferation, and  
 CC for monitoring the response of patients, for optimisation of therapy.  
 CC Cells that express B132 are useful in cancer vaccines. Antibodies (Ab)  
 CC raised against the antigen can be used for diagnosis of B132-related



CC tumours, also therapeutically (by delivery of cytotoxic compounds or  
CC radioisotopes). This sequence represents an immunogenic peptide  
CC derived from the human tumour-associated antigen B132 described in the  
CC method of the invention.  
XX  
SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFYK 7  
|||||  
Db 5 NFYK 8

RESULT 42  
AAO22617  
ID AAO22617 standard; Peptide; 9 AA.

XX AC AAO22617;

XX DT 15-MAY-2003 (first entry)

XX DE HPV-16 E6 peptide, SEQ ID No 1.

XX KW Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;  
KW cancer; human papilloma virus; cervix; cell-mediated immune response;  
KW HPV; HPV-16; E6 peptide.

XX OS Human papilloma virus.

XX PN WO2003008649-A1.

XX PD 30-JAN-2003.

XX PF 19-JUL-2002; 2002WO-US23198.

XX PR 20-JUL-2001; 2001US-306809P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Sastry KJ, Tortolero-luna G, Follen M;

XX DR WPI; 2003-239363/23.

XX PT Determining a possible recurrence of a (pre-)cancerous growth in a  
PT patient infected with human papilloma virus (HPV), comprises incubating  
PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated  
PT immune response -

XX PS Example 1; Page 96; 132pp; English.

XX CC The invention relates to a novel method for determining the possibility  
CC of recurrence of a (pre-)cancerous growth in a patient infected with  
CC human papilloma virus (HPV) or suspected of being infected with HPV, and  
CC has or had a (pre-)cancerous growth on or around the cervix. The novel  
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from  
CC the patient, and assaying the sample for a cell-mediated immune response  
CC against the peptide. The method is useful for determining the possibility  
CC and preventing the recurrence of a (pre-)cancerous growth in a patient  
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or  
CC E7 peptides are useful in immunotherapy for the preventing or reducing  
CC the risk of development of (pre-)cancerous growths. This sequence  
CC represents an HPV-16 E6 peptide of the invention.

XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10

Db |||||  
1 KLPQ 4

RESULT 43

ABU20153  
ID ABU20153 standard; Peptide; 9 AA.

XX AC ABU20153;

XX DT 10-APR-2003 (first entry)

XX DE MHC binding peptide SEQ ID No 318.

XX KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
KW antiinflammatory; major histocompatibility complex; MHC;  
KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
KW inflammation; gene therapy; MHC binding peptide.

XX OS Synthetic.

XX PN WO200294981-A2.

XX PD 28-NOV-2002.

XX PF 16-MAY-2002; 2002WO-IL00383.

XX PR 16-MAY-2001; 2001US-290958P.

XX PR 29-MAY-2001; 2001US-0865548.

XX PA (TECR) TECHNION RES & DEV FOUND LTD.

XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;

XX DR WPI; 2003-210043/20.

XX PT Identifying peptides that are capable of binding to major  
PT histocompatibility complex (MHC) molecules of a particular haplotype by  
PT analyzing peptides bound to the soluble and secreted form of the MHC  
PT molecules of the particular haplotype -

XX PS Claim 51; Page 225; 238pp; English.

XX CC The invention relates to a novel method for identifying peptides  
CC originating from a particular cell type, which are capable of binding to  
CC major histocompatibility complex (MHC) molecules of a particular  
CC haplotype. The method comprises analysing peptides bound to the soluble  
CC and secreted form of the MHC molecules of the particular haplotype. The  
CC method is useful for identifying peptides for treating an autoimmune  
CC disease, such as T or B cell, and/or allergic disease or condition,  
CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
CC sequences of the invention may be used in a gene therapy application.  
CC This sequence represents a peptide relating to the method for identifying  
CC MHC binding peptides of the invention.

XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
|||||  
Db 6 FYKL 9

RESULT 44

ABU03246  
ID ABU03246 standard; Protein; 9 AA.

XX AC ABU03246;

```
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #26.
XX KW Translational profiling; expressed protein tag; EPT; kinase;
XX KW phosphatase; protease; protease inhibitor; transporter;
XX KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer;
XX KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
XX KW leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US09671.
XX PR 28-MAR-2001; 2001US-279495P.
XX PR 21-MAY-2001; 2001US-292544P.
XX PR 08-AUG-2001; 2001US-310801P.
XX PR 01-OCT-2001; 2001US-326370P.
XX PR 04-DEC-2001; 2001US-336780P.
XX PR 20-FEB-2002; 2002US-358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PT Chicx RM, Tomlinson AJ, Urban RG;
XX PT WPI; 2003-040607/03.
XX PS Claim 10; SEQ ID No 26; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor.
XX CC The polypeptide is useful as an immunogenic composition for eliciting
XX CC in a mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to
XX CC this polypeptide, is useful for treating cancer. The polypeptide is
XX CC also useful for identifying compounds that binds to a naturally
XX CC processed class I or class II MHC-binding polypeptide. The polypeptides
XX CC and polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling.
XX CC Note: This sequence does not appear in the printed specification but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 5 FYKL 8
XX DB |||||
XX 6 FYKL 9
XX RESULT 45
XX ABB99353
XX ID ABB99353 standard; peptide; 9 AA.
```

```
XX AC ABB99353;
XX DT 29-JAN-2003 (first entry)
XX DE Peptide derived from E6 protein of HPV18.
XX KW E6 protein; HPV; HPV18; human leukocyte antigen; HLA; HPV16;
XX KW immunogenic peptide; cytotoxic T lymphocyte; HPV16 infection; vaccine.
XX OS Human papillomavirus 18.
XX PN WO200277012-A2.
XX PD 03-OCT-2002.
XX PF 22-MAR-2002; 2002WO-US09261.
XX PR 23-MAR-2001; 2001US-278520P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Khleif SN, Berzofsky JA;
XX DR WPI; 2003-029912/02.
XX PT Inducing a cytotoxic T lymphocyte response against human papilloma
XX PT virus 16 (HPV 16), useful for preventing or treating HPV 16 infection,
XX PT comprises contacting the cytotoxic T cells with an immunogenic peptide
XX PT from E6 protein -
XX PS Example 1; Page 41; 61pp; English.
XX CC The present sequence represents a peptide which is derived from the E6
XX CC protein of human papilloma virus 16 (HPV16). The peptide has lower
XX CC affinity for the human leukocyte antigen (HLA)-A2.1 molecule than the
XX CC corresponding epitope from HPV18. The HPV18 immunogenic peptide is used
XX CC in the method of the invention. The specification describes a method for
XX CC inducing a cytotoxic T lymphocyte response against HPV16 in a patient.
XX CC The method comprises contacting cytotoxic T cells from the patient with
XX CC an immunogenic peptide (e.g. HPV18 E6 peptide) of 20 amino acid residues
XX CC or less, and returning the cytotoxic T cells to the patient to induce a
XX CC cytotoxic T cell response. The method is useful for preventing or
XX CC treating HPV16 infection. The HPV18 peptide is also useful as a vaccine.
XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 7 KLPG 10
XX DB |||||
XX 1 KLPG 4
XX RESULT 46
XX AAR43905
XX ID AAR43905 standard; peptide; 10 AA.
XX AC AAR43905;
XX DT 06-JUN-1994 (first entry)
XX DE HIV-1 IIB gp120 monoclonal antibody antigenic peptide A10P.
XX KW Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;
XX KW post-exposure prophylaxis; infection; cytotoxic agent targeting;
XX KW neutralisation domain; G3-136; BAT085.
XX OS Synthetic.
XX PN US5266478-A.
```

XX 30-NOV-1993.  
 PD XX  
 XX PF 25-NOV-1991; 91US-0797692.  
 XX PR 29-MAY-1987; 87US-0057445.  
 PR 24-DEC-1987; 87US-0137861.  
 PR 26-APR-1991; 91US-0692259.  
 PR 26-SEP-1991; 91US-0747533.  
 PR 25-NOV-1991; 91US-0797692.  
 XX (TANO-) TANOX BIOSYSTEMS INC.  
 PA Chang TW, Fung WSC, Sun BNC, Sun CRY;  
 PI WPI; 1993-395339/49.  
 XX Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1  
 PT infection or AIDS, post-exposure prophylaxis and diagnosis of HIV-1  
 PT HIV-1 infection  
 XX Example; Page 8; 9pp; Japanese.  
 XX The sequence is that of a synthetic peptide corresponding to a  
 CC unique neutralisation domain in the V2 region of HIV-1 gp120. It  
 CC showed no reaction with monoclonal antibodies (MAbs) BA1085 and  
 CC G3-136.  
 XX SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; DB 14; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FYKL 8  
 DB 3 FYKL 6  
 RESULT 47  
 ID AAW76930 standard; peptide; 10 AA.  
 XX AAW76930;  
 XX 25-JAN-1999 (first entry)  
 XX Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #70.  
 XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;  
 KW human immune deficiency virus; HIV; tolerance; treatment; therapy;  
 KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;  
 KW microbial infection; autoimmune disease; antibody; apoptosis;  
 KW antiviral T cell immunity.  
 XX Mus sp.  
 OS Homo sapiens.  
 XX WO9836087-A1.  
 XX 20-AUG-1998.  
 XX 13-FEB-1998; 98WO-US02766.  
 XX 13-FEB-1997; 97US-0040581.  
 XX (AMNA-) AMERICAN NAT RED CROSS.  
 XX Scott D, Zambidis E;  
 XX WPI; 1998-506315/43.  
 XX New fusion immunoglobulin heavy chain including gp120 epitopes and

PT related complete antibodies - DNA, vectors and transformed cells,  
 PT used to induce tolerance to the epitopes for treatment of human  
 PT immune deficiency virus infection  
 XX Disclosure; Page 38; 154pp; English.  
 XX This sequence is an epitope used in the construction of a novel fusion  
 CC immunoglobulin heavy chain (IgH) protein with a mammalian, especially  
 CC human, IgH chain fused in frame at its N-terminus to one or more human  
 CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or  
 CC transfected cells are used to tolerate subjects to gp120 epitopes and to  
 CC maintain this tolerance, particularly for treatment of HIV infection,  
 CC optionally together with other therapeutic/prophylactic agents such as  
 CC vaccines, chemotherapeutic agents and immune response modifiers. Such  
 CC proteins can be used against other diseases where an immune response is  
 CC deleterious, e.g. microbial infection, tumours or autoimmune disease.  
 CC Induction of tolerance suppresses production of antibodies against gp120,  
 CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that  
 CC are bound to gp120 protein, maximising induction of protective antiviral  
 CC T cell immunity.  
 XX SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; DB 19; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FYKL 8  
 DB 5 FYKL 8  
 RESULT 48  
 ID AAM52988 standard; peptide; 10 AA.  
 XX AAM52988;  
 XX 12-MAR-2002 (first entry)  
 XX Human papillomavirus type 16 E6 protein peptide P1 (residues 18-27).  
 XX HPV16; E6 protein; cytotoxic T-lymphocyte; CTL; MHC class I;  
 KW major histocompatibility complex; immunomodulator.  
 XX Human papillomavirus type 16.  
 XX KR98020034-A.  
 XX 25-JUN-1998.  
 XX 05-SEP-1996; 96KR-0038373.  
 XX 05-SEP-1996; 96KR-0038373.  
 XX (CHEI-) CHEIL FOODS & CHEM INC.  
 XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.  
 XX Kim HS, Yoo WD, Noh GS, Chung GT, Park SH, Kang BT, Yoon HS;  
 XX Jin SW;  
 XX WPI; 1999-285579/24.  
 XX Peptide for modulating immune response in a human against human  
 PT papilloma virus type 16 E6 protein -  
 XX Example 1; Page 2; 5pp; Korean.  
 XX The invention relates to peptides derived from the human papillomavirus  
 CC type 16 (HPV16) E6 protein (AAM52985-AAM52987). The peptides are  
 CC presented on major histocompatibility complex (MHC) class I molecules and  
 CC act as cytotoxic T-lymphocyte (CTL) epitopes. The peptides of the  
 CC invention may be used for modulating an immune response against HPV16 in

CC a human (e.g., in a vaccine). Sequences AAM52988-AAM52994 represent HPV16  
 CC E6 protein-derived peptides used in an exemplification of the invention.

XX  
 SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10  
 ||||  
 Db 1 KLPQ 4

RESULT 49  
 AAU70117  
 ID AAU70117 standard; Peptide; 10 AA.

XX  
 AC AAU70117;

XX  
 DT 29-JAN-2002 (first entry)

XX  
 DE Human calcitonin DNA encoded HLA-B35 binding peptide #4.

XX Human; tumour rejection antigen precursor; preprocalcitonin; HLA;  
 KW cytolytic T lymphocyte; major histocompatibility complex; alpha-CGRP;  
 KW calcitonin; cellular abnormality; cell lysis; immune responsive cell;  
 KW lung cancer; human leukocyte antigen binding peptide; HLA; CGRP.

XX  
 OS Homo sapiens.

XX  
 PN WO200175179-A2.

XX  
 PD 11-OCT-2001.

XX  
 PP 14-MAR-2001; 2001WO-US40288.

XX  
 PR 31-MAR-2000; 2000US-0539567.

XX  
 PA (LUDW-) LUDWIG INST CANCER RES.

XX  
 PA (INSR) INST ROUSSY GUSTAVE.

XX  
 PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX  
 PI Echchakir H, Mami-Chouaib F, Vergnon I, Chouaib S, Baurain JF;  
 PI Coulie PG, Boon-Falleur T;

XX  
 DR WPI; 2001-648564/74.

XX  
 PT Determining the presence of a transformed cell by assaying for the  
 PT expression of tumour rejection antigen precursors or for the presence of  
 PT T cells specific for a complex between major histocompatibility complex  
 PT and cell surface antigen

XX  
 PS Example 7; Page 16; 33pp; English.

XX  
 CC The invention relates to a method for detecting the presence of a  
 CC transformed cell by assaying a cell sample for expression of nucleotides  
 CC 292-403 of DNA encoding the tumour rejection antigen precursor,  
 CC preprocalcitonin or for the presence of cytolytic T lymphocytes specific  
 CC for a complex between a major histocompatibility complex and a peptide  
 CC sequence found in alpha-CGRP, calcitonin, or preprocalcitonin. The  
 CC sequences of the invention are useful for identifying those individuals  
 CC diagnosed with conditions characterised by cellular abnormalities. A  
 CC subject afflicted with a disorder characterised by inappropriate or  
 CC abnormal amounts of a polypeptide encoded by nucleotides 292-403 of  
 CC preprocalcitonin (such as lung cancer) can be treated by removing an  
 CC immune responsive cell, contacting it with a cell line transfected with a  
 CC nucleic acid molecule coding for the protein expressed by the abnormal  
 CC cells, under conditions favouring the production of cytolytic T cells  
 CC against a peptide derived from the protein, and introducing the T cells  
 CC back to the subject, to lyse the abnormal cells. Sequences  
 CC AAU69966-AAU70143 represent the polypeptides calcitonin and CGRP, a  
 CC fragment of the preprocalcitonin polypeptide and human leukocyte antigen

CC (HLA) binding peptides of the invention.

XX  
 SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQN 4  
 ||||  
 Db 6 MPQN 9

RESULT 50

AAU70117

ID AAR28392 standard; peptide; 11 AA.

XX  
 AC AAR28392;

XX  
 DT 25-MAR-2003 (updated)

XX  
 DT 18-MAR-1993 (first entry)

XX  
 DE Bradykinin receptor antagonist CT-0008.

XX Bradykinin receptor antagonist; heterodimer; higher oligomer;  
 KW potency; duration; CP-0088; burns; migraine; shock CNS injury; asthma;  
 KW rhinitis; premature labour; inflammatory arthritis; homodimer;  
 KW inflammatory bowel disease.

XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Misc-difference 11 /note= "D-form residue"

FT Modified-site 11 /label= Nle

XX  
 PN WO9217201-A1.

XX  
 PD 15-OCT-1992.

XX  
 PP 30-MAR-1992; 92WO-US02431.

XX  
 PR 01-APR-1991; 91US-0677391.

XX  
 PR 27-MAR-1992; 92US-0859582.

XX  
 PA (CORT-) CORTECH INC.

XX  
 PI Allen LG, Blodgett JK, Cheronis JC, Eubanks SR, Nguyen KT;

XX  
 PI Whalley ET;

XX  
 DR WPI; 1992-365995/44.

XX  
 PT Bradykinin antagonists comprising linked bradykinin antagonist  
 PT chains - are for treatment of post-operative pain, asthma and  
 PT aseptic shock

XX  
 PS Disclosure; Page 76; 109pp; English.

XX  
 CC The sequence given is a bradykinin receptor antagonist which can form  
 CC homo- or heterodimers or higher oligomers. It demonstrates greater  
 CC potency and/or duration of action than the parent peptide itself.  
 CC Bradykinin receptors antagonists such as this can be used in the  
 CC treatment of burns, perioperative pain, migraine and other forms of  
 CC pain, shock CNS injury, asthma, rhinitis, premature labour,  
 CC inflammatory arthritis, inflammatory bowel disease etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 11 AA;  
SQ

Query Match 36.4%; Score 4; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNF 5  
Db |||||  
4 PQNF 7

## RESULT 51

AAW76927 ID AAW76927 standard; peptide; 11 AA.

XX AC AAW76927;

XX 25-JAN-1999 (first entry)

XX Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #67.

XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;

XX human immune deficiency virus; HIV; tolerance; treatment; therapy;

XX prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;

XX microbial infection; autoimmune disease; antibody; apoptosis;

XX antiviral T cell immunity.

XX Mus sp.

XX Homo sapiens.

XX WO9836087-A1.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-US02766.

XX 13-FEB-1997; 97US-0040581.

XX (AMNA-) AMERICAN NAT RED CROSS.

XX Scott D, Zambidis E;

XX WPI; 1998-506315/43.

XX New fusion immunoglobulin heavy chain including gp120 epitopes and

XX related complete antibodies - DNA, vectors and transformed cells,

XX used to induce tolerance to the epitopes for treatment of human

XX immune deficiency virus infection

XX Disclosure; Page 38; 154pp; English.

XX This sequence is an epitope used in the construction of a novel fusion

XX immunoglobulin heavy chain (IgH) protein with a mammalian, especially

XX human, IgH chain fused in frame at its N-terminus to one or more human

XX immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or

XX transfected cells are used to tolerate subjects to gp120 epitopes and to

XX maintain this tolerance, particularly for treatment of HIV infection,

XX optionally together with other therapeutic/prophylactic agents such as

XX vaccines, chemotherapeutic agents and immune response modifiers. Such

XX deleterious, e.g. microbial infection, tumours or autoimmune disease.

XX Induction of tolerance suppresses production of antibodies against gp120,

XX so prevents or inhibits 'bystander' apoptosis of uninfected T cells that

XX are bound to gp120 protein, maximising induction of protective antiviral

XX T cell immunity.

XX Sequence 11 AA;

XX Query Match 36.4%; Score 4; DB 19; Length 11;

XX Best Local Similarity 100.0%; Pred. No. 4e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
Db |||||  
7 FYKL 10

## RESULT 52

AAW15279 ID AAW15279 standard; Peptide; 12 AA.

XX AC AAW15279;

XX 04-AUG-1997 (first entry)

XX DE Salmonella secreted protein Ssp22 N-terminal sequence.

XX Salmonella secreted protein; Ssp22; bacterial-mediated endocytosis;

XX diagnosis; therapy; vaccine; attenuation; virulence.

XX OS Salmonella typhimurium.

XX WO9718225-A1.

XX 22-MAY-1997.

XX 14-NOV-1996; 96WO-US18504.

XX 14-NOV-1995; 95US-0006733.

XX (GEHO) GEN HOSPITAL CORP.

XX Miller SI;

XX WPI; 1997-289217/26.

XX New isolated Salmonella secreted proteins and related genes - used

XX to develop products for the detection, treatment or prevention of

XX Salmonella infections

XX Disclosure; Page 57; 95pp; English.

XX N-terminal sequences are provided (AAW15277-79) for Salmonella

XX secreted proteins Ssp54, Ssp42 and Ssp22, respectively. Ssp

XX proteins (see also AAW15268-71) and nucleic acids are useful for

XX the development of products for the detection, treatment or

XX prevention of Salmonella infections.

XX Sequence 12 AA;

XX Query Match 36.4%; Score 4; DB 18; Length 12;

XX Best Local Similarity 100.0%; Pred. No. 4.2e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNF 5  
Db |||||  
7 PQNF 10

## RESULT 53

ABP46873 ID ABP46873 standard; peptide; 12 AA.

XX AC ABP46873;

XX 19-AUG-2002 (first entry)

XX Human BLys binding scFv VH CDR3 SEQ ID 2884.

XX BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

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XX OS Homo sapiens.
XX FN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US19110.
XX PR 16-JUN-2000; 2000US-212210P.
XX PR 17-OCT-2000; 2000US-240816P.
XX PR 16-MAR-2001; 2001US-276248P.
XX PR 21-MAR-2001; 2001US-277379P.
XX PR 25-MAY-2001; 2001US-293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX FA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX PT the diagnosis and treatment of cancers and immune disorders -
XX PS Claim 2; Page 3071; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
XX CC and so may be used to detect and quantitate the presence of Blys in
XX CC biological samples and may be used in this way to diagnose disease
XX CC associated with aberrant expression of Blys. They may also be
XX CC administered to treat diseases associated with aberrant Blys expression
XX CC and activity such as cancer, immune, and autoimmune disorders and
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX CC the antibodies and fragments of the antibodies described in the method
XX CC of the invention.
XX SQ Sequence 12 AA;
Query Match 36.4%; Score 4; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QNFY 6
DB 5 QNFY 8
RESULT 54
ABP97425
ID ABP97425 standard; peptide; 12 AA.
XX AC ABP97425;
XX DT 30-MAY-2003 (first entry)
XX DE HAB18G/CD147 protein antagonist peptide, SEQ ID NO:10.
XX HAB18G/CD147 protein; peptide antagonist;
XX leukocyte differentiation antigen CD147 homologue; PCI-neo/ashAb18G;
XX antitense expression plasmid; gene therapy; antitense therapy;
XX cancer; stomach; liver; lung; oesophagus; recurrence; metastasis;
XX rheumatoid arthritis; osteoarthritis; human immunodeficiency virus;
XX HIV infection; acquired immunodeficiency syndrome; AIDS;
XX arteriosclerosis; ectatic myocardiopathy; cytostatic; antirheumatic;

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KW antiarthritic; anti-HIV; antiarteriosclerotic; cardiant.
XX Synthetic.
XX OS WO200294875-A1.
XX FN 28-NOV-2002.
XX PD 27-MAY-2002; 2002WO-CN00356.
XX PR 25-MAY-2001; 2001CN-0115274.
XX PR 28-SEP-2001; 2001CN-0131735.
XX PA (CHEN/) CHEN Z.
XX PI Chen Z, Shang P, Li Y, Qian A, Zhu P, Xing J;
XX WPI; 2003-140362/13.
XX DR Novel liver cancer tissue-originated protein molecule HAB18G/CD147, its
XX PT antagonists and expression vector for its antisense RNA, applicable in
XX PT treating cancer, tumor recurrence or metastasis, and rheumatoid
XX PT arthritis -
XX PS Claim 3; Page 14; 24pp; Chinese.
XX CC The invention relates to a protein originating in liver cancer tissue
XX CC designated HAB18G/CD147 (ABP97416) which is capable of promoting tumour
XX CC metastasis. HAB18G/CD147 is encoded by a gene sequence homologous with
XX CC that of the leukocyte differentiation antigen CD147 and is a member of
XX CC the CD147 family, and can be isolated by using liver cancer-specific
XX CC monoclonal antibody HAB18G affinity chromatography. The invention
XX CC also encompasses an HAB18G/CD147 antisense expression plasmid
XX CC PCI-neo/ashHAB18G which can inhibit HAB18G/CD147 mRNA translation, and 9
XX CC HAB18G/CD147 peptide antagonists (ABP97417-ABP97425). The HAB18G/CD147
XX CC protein, its peptide antagonists and antisense expression vector may be
XX CC used in the prevention and treatment of cancer (including cancers of the
XX CC stomach, liver, lung or oesophagus), tumour recurrence or metastasis,
XX CC rheumatoid arthritis, osteoarthritis, human immunodeficiency virus
XX CC (HIV) infection and acquired immunodeficiency syndrome (AIDS),
XX CC arteriosclerosis, and ectatic myocardiopathy. Sequences
XX CC ABP97417-ABP97425 represent specifically claimed peptide antagonists of
XX CC the HAB18G/CD147 protein.
XX SQ Sequence 12 AA;
Query Match 36.4%; Score 4; DB 24; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YKLP 9
DB 1 YKLP 4
RESULT 55
AAW88298
ID AAW88298 standard; Peptide; 14 AA.
XX AC AAW88298;
XX DT 12-APR-1999 (first entry)
XX DE Human guanine nucleotide exchange factor Rac-GEF peptide.
XX Rac-GEF; guanine nucleotide exchange factor; human; cancer;
XX metastasis; cell proliferation; apoptosis; haemostasis;
XX bone resorption; clot retraction; morphogenesis; inflammation;
XX therapy; diagnosis; antibody.
XX OS Homo sapiens.
XX PA WO9857950-A2.

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XX PD 23-DEC-1998.  
 XX PF 15-JUN-1998; 98WO-US12391.  
 XX PR 17-JUN-1997; 97US-0049879.  
 XX (ONYX-) ONYX PHARM INC.  
 XX PI Bollag G, Crompton A, North A, Roscoe W, Sharma S;  
 XX WPI; 1999-095328/08.  
 XX New isolated Rac-guanine nucleotide exchange factor - used to  
 PT develop products for treating conditions involving e.g. cell  
 PT proliferation (e.g. cancer), programmed cell death, haemostasis or  
 PT bone resorption  
 XX Claim 55; Page 50; 62pp; English.  
 XX This peptide corresponds to amino acid residues 372-378 and 403-409  
 CC of human guanine nucleotide exchange factor Rac-GEF (see AAM80995).  
 CC A claimed antibody that is specific for Rac-GEF binds to an amino  
 CC acid sequence selected from a group comprising this peptide and 2  
 CC other Rac-GEF peptides (see AAM88297 and AAM88299). Such antibodies  
 CC may be used to detect the presence of an epitope in a sample, e.g.  
 CC in a sample of tissue containing Rac-GEF gene product. Rac-GEF  
 CC polypeptides, nucleic acids, ligands and modulators are used in  
 CC methods of treating pathological conditions associated or related  
 CC to a Ras superfamily GTPase such as Rac, e.g. to treat cell  
 CC proliferation (cancer), apoptosis, haemostasis, bone resorption,  
 CC etc.  
 XX SQ Sequence 14 AA;  
 Query Match 36.4%; Score 4; DB 20; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 YKLP 9  
 Db 6 YKLP 9  
 RESULT 56  
 AAM97223  
 ID AAM97223 standard; Peptide; 14 AA.  
 XX AC AAM97223;  
 XX DT 24-JAN-2002 (first entry)  
 XX DE Human peptide #498 encoded by a SNP oligonucleotide.  
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; G-protein coupled receptor;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX OS Homo sapiens.  
 XX PN WO200147944-A2.  
 XX PD 05-JUL-2001.  
 XX PF 28-DEC-2000; 2000WO-US35498.  
 XX PR 28-DEC-1999; 99US-0173419.  
 XX PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.  
 XX PI Shimkets RA, Leach M;  
 XX WPI; 2001-465210/50.  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX Disclosure; Page 3777; 4143pp; English.  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.  
 XX SQ Sequence 14 AA;  
 Query Match 36.4%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KUPQ 10  
 Db 1 KUPQ 4  
 RESULT 57  
 AAU69635  
 ID AAU69635 standard; Protein; 14 AA.  
 XX AC AAU69635;  
 XX DT 30-JAN-2002 (first entry)  
 XX DE Cell death protective sequence CNI-00726, protein #14.  
 XX Human; protective sequence; cell death; cerebral oedema; infection;  
 KW meningitis; degenerative disease; Alzheimer's disease; heart disease;  
 KW motor neuron disease; demyelinating disease; multiple sclerosis; asthma;  
 KW nutritional condition; peripheral nervous system disorder; ischaemia;  
 KW diabetic neuropathy; autoimmune haemolytic anaemia; respiratory system;  
 KW oral cavity; gastrointestinal tract; liver; cirrhosis; pancreatitis;  
 KW polycystic renal disease; urinary tract; genitalia; endometriosis;  
 KW breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis;  
 KW adrenal gland; skin; psoriasis; muscular atrophy; bone marrow;  
 KW osteoporosis; cancer; autoimmune disease.  
 XX OS Homo sapiens.  
 XX PN WO200176532-A2.  
 XX PD 18-OCT-2001.  
 XX PF 09-APR-2001; 2001WO-US11655.  
 XX PR 11-APR-2000; 2000US-0547596.  
 XX (COGE-) COSENT NEUROSCIENCE INC.

XX PI Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC;  
 XX WPI; 2002-017408/02.  
 DR N-PSDB; AAS63035.  
 XX Novel nucleic acids referred as protective sequences and their encoded  
 PT products for diagnosing, treating diseases involving cell death,  
 PT including neurological disorders e.g. stroke and for identifying  
 PT modulators -  
 XX Claim 17; Figure 7N; 256pp; English.  
 XX The invention relates to isolated protective sequence polypeptides (I)  
 CC and polynucleotides (II). (I) is useful for transferring a protective  
 CC sequence into a cell, which delays and/or prevents the cell from  
 CC undergoing cell death. Protective sequences, their products or  
 CC antibodies are useful diagnostically, prophylactically, therapeutically  
 CC or as targets for treatment and diagnosis of conditions, disorders or  
 CC diseases involving cell death. The protective sequences and their  
 CC products are useful for preventing or treating disorders of the central  
 CC nervous system including neurological and psychiatric conditions,  
 CC cerebral oedema, infections such as meningitis, degenerative diseases  
 CC such as Alzheimer's and motor neuron disease, demyelinating diseases such  
 CC as multiple sclerosis, nutritional conditions, disorders of the  
 CC peripheral nervous system including diabetic neuropathy, disorders  
 CC which cause cell death in organ systems including blood vessels, heart  
 CC (ischaemia), blood cells (autoimmune haemolytic anaemia), respiratory  
 CC system (asthma), oral cavity, gastrointestinal tract, liver (cirrhosis),  
 CC pancreatitis, polycystic renal disease, urinary tract, genitalia  
 CC (congenital anomalies), endometriosis, breast (chronic mastitis), thyroid  
 CC gland (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis),  
 CC musculoskeletal system (muscular atrophy), bone marrow or bone  
 CC (osteoporosis). The compositions promote cell death and are useful for  
 CC treating and/or ameliorating cancer and autoimmune diseases. The  
 CC compounds are further useful for treating physiological impacts on  
 CC organs caused by infection which induce cell death. (I) is useful to  
 CC raise an immune response, as a reagent in assays designed to  
 CC quantitatively determine levels of the protein in biological fluids, as  
 CC markers for tissues in which the corresponding protein is expressed and  
 CC to isolate receptors or ligands. AAU69571-AAU69736 represent the  
 CC protective polypeptide sequences as described in the invention.  
 XX Sequence 14 AA;  
 SQ Query Match 36.4%; Score 4; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 KLPQ 10  
 Db |||||  
 2 KLPQ 5  
 RESULT 58  
 AAP81956  
 ID AAP81956 standard; protein, 15 AA.  
 AC AAP81956;  
 XX 25-MAR-2003 (updated)  
 DT 16-OCT-1990 (first entry)  
 XX Peptide immunogen for HPV.  
 DE Human papilloma virus; immunogen; antibody; antigen; cervical carcinoma;  
 KW HPV-16; early reading frame; E6.  
 XX Synthetic.  
 OS EP257754-A.  
 PN 02-MAR-1988.  
 PD

XX 09-JUL-1987; 87EP-0306061.  
 XX 10-JUL-1986; 86US-0884184.  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA Schoolinik GK, Palefsky JM;  
 PI WPI; 1988-057971/09.  
 XX Synthetic peptide(s) of human papilloma virus - corresp. to amino  
 PT acid sequence region having at least one reverse turn and predicted  
 PT hydrophilicity.  
 XX Claim 8; Page 13; 27pp; English.  
 XX The peptide corresponds to amino acids 9-23 of the E6 early open  
 CC reading frame of HPV-16. It can be used to raise antibodies for  
 CC vaccines or to heighten the immune response to an HPV infection  
 CC already present.  
 CC See also AAP81955-71.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 15 AA;  
 SQ Query Match 36.4%; Score 4; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 KLPQ 10  
 Db |||||  
 10 KLPQ 13  
 RESULT 59  
 AAR43901  
 ID AAR43901 standard; peptide, 15 AA.  
 XX AAR43901;  
 AC AAR43901;  
 XX 06-JUN-1994 (first entry)  
 DT HIV-1 IIIB gp120 monoclonal antibody antigenic peptide VI5P.  
 DE Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;  
 XX post-exposure prophylaxis; infection; cytotoxic agent targeting;  
 KW neutralisation domain; BAT085; G3-136.  
 XX Synthetic.  
 OS US5266478-A.  
 XX 30-NOV-1993.  
 XX 25-NOV-1991; 91US-0797692.  
 XX 29-MAY-1987; 87US-0057445.  
 XX 24-DEC-1987; 87US-0137861.  
 XX 26-APR-1991; 91US-0692299.  
 XX 26-SEP-1991; 91US-0767533.  
 XX 25-NOV-1991; 91US-0797692.  
 XX (TANO-) TANOX BIOSYSTEMS INC.  
 PA Chang TW, Fung MSC, Sun BNC, Sun CRY;  
 PI WPI; 1993-395339/49.  
 XX Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1  
 PT infection or AIDS, post-exposure prophylaxis and diagnosis of HIV-1



PT HIV-1 infection

PS Example; Page 8; 9pp; Japanese.

XX The sequence is that of a synthetic peptide V1SP corresponding to a  
 CC unique neutralisation domain in the V2 region of HIV-1 gp 120, it  
 CC can be used in the prodn. of monoclonal antibodies (MAbs) BAT085  
 CC and G3-136. The MAbs may be used for therapy of HIV-1 infection or  
 CC AIDS, post-exposure prophylaxis and diagnosis of HIV-1 infection and  
 CC to reduce or eliminate virus infected T-cells by antibody-dependent  
 CC cellular cytotoxicity, complement-mediated cytotoxicity or other  
 CC cytolytic or regulatory immune mechanisms. The Mab can also be  
 CC used for targeting cytotoxic agents to HIV-1 infected cells.

XX Sequence 15 AA;

Query Match 36.4%; Score 4; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 8 FYKL 11

RESULT 60

AAR43907

ID AAR43907 standard; peptide; 15 AA.

AC AAR43907;

XX

DT 06-JUN-1994 (first entry)

DE HIV-1 RF gp120 monoclonal antibody antigenic peptide T1SP.

XX Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;  
 KW post-exposure prophylaxis; infection; cytotoxic agent targeting;  
 KW neutralisation domain; G3-136; BAT085.

XX Synthetic.

XX US266478-A.

XX 30-NOV-1993.

XX 25-NOV-1991; 91US-0797692.

XX 29-MAY-1987; 87US-0057445.

XX 24-DEC-1987; 87US-0137861.

XX 26-APR-1991; 91US-0692299.

XX 26-SEP-1991; 91US-0767533.

XX 25-NOV-1991; 91US-0797692.

XX (TANO-) TANOX BIOSYSTEMS INC.

XX Chang TW, Fung MSC, Sun BNC, Sun CRY;

XX WPI; 1993-395339/49.

XX Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1  
 PT infection or AIDS, post-exposure prophylaxis and diagnosis of HIV-1  
 PT HIV-1 infection

XX Example; Page 9; 9pp; Japanese.

XX The sequence is that of a synthetic peptide corresponding to a  
 CC unique neutralisation domain in the V2 region of HIV-1 gp 120. It  
 CC showed no reaction with monoclonal antibody (MAb) BAT085 but  
 CC reacted with MAb G3-136.

XX Sequence 15 AA;

Query Match 36.4%; Score 4; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 8 FYKL 11

RESULT 61

AAR72007

ID AAR72007 standard; peptide; 15 AA.

AC AAR72007;

DT 25-MAR-2003 (updated)

DT 20-NOV-1995 (first entry)

DE Biologically active lipopolysaccharide binding protein deriv.

XX Lipopolysaccharide; binding; protein; LBP; inhibitor; toxic; shock;  
 KW Gram; negative.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 15

FT /note= "amidated"

XX MO9508560-A1.

XX 30-MAR-1995.

XX 22-SEP-1994; 94WO-US10760.

XX 24-SEP-1993; 93US-0126326.

XX (CENZ ) CENTOCOR INC.

XX Heavner GA, Sherries D, Taylor AH;

XX WPI; 1995-139546/18.

XX Novel peptide inhibitors of lipo:polysaccharide binding protein  
 PT (LBP) - prevent binding of lipo:polysaccharide to LBP, useful for  
 PT treatment and prevention of Gram-negative toxic shock

XX Claim 4; Page 56; 74pp; English.

XX AAR71993-R72053 are novel peptides which are specifically claimed  
 CC examples of a highly generic sequence derived from portions of the  
 CC 95-104 amino acid sequence region of LBP. Peptides corresp. to the  
 CC generic formula are inhibitors of lipopolysaccharide binding to LBP.  
 CC Such peptides may be useful in the prevention and treatment  
 CC of Gram-negative septic shock.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 15 AA;

Query Match 36.4%; Score 4; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 4 FYKL 7

RESULT 62

AAW99862

ID AAW99862 standard; peptide; 15 AA.

AC AAW99862;

XX

DT XX 09-JUN-1999 (first entry)  
DE XX HIV-1 gp120 V1/V2 domain peptide p8.  
XX XX HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;  
KW KW infection; antibody; immunoassay.  
XX OS Human immunodeficiency virus type 1.  
XX XX WO9912556-A1.  
XX XX 18-MAR-1999.  
XX XX 08-SEP-1998; 98WO-US18679.  
XX XX 08-SEP-1997; 97US-0058155.  
XX XX (PINTV) PINTER A.  
XX XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.  
XX XX Pinter A;  
PI XX  
XX XX WPI; 1999-229137/19.  
XX XX New gp120 V1/V2 fusion proteins  
XX XX Disclosure; Page 18; 64pp; English.  
XX XX The present invention describes a novel protein (A) comprising a gp120  
XX XX V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain  
XX XX of an HIV-1 strain, where the protein does not bind CD4 the gp120 V1/V2  
XX XX domain of the protein displaying an epitope which is recognized by an  
XX XX antibody which neutralizes at least one HIV-1 primary isolate with a  
XX XX ND90 of at most 100 ml/9/ml. The present sequence represents an HIV-1  
XX XX gp120 V1/V2 domain peptide from the present invention. The novel  
XX XX proteins can be used for stimulating the formation of antibodies capable  
XX XX of neutralising infection by an HIV viral isolate in mammals. They can  
XX XX also be used for therapeutic treatment of subjects already infected with  
XX XX HIV. They can also be used in immunoassays for anti-HIV antibodies and  
XX XX for the production of anti-HIV antiserum.  
XX XX  
XX XX Sequence 15 AA;  
XX XX  
XX XX Query Match 36.4%; Score 4; DB 20; Length 15;  
XX XX Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
XX XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX XX  
XX XX 5 FYKL 8  
XX XX ||||  
XX XX 5 FYKL 8  
XX XX  
XX XX RESULT 63  
XX XX AAW87621  
XX XX ID AAW87621 standard; peptide; 15 AA.  
XX XX AC AAW87621;  
XX XX DT 20-MAR-2003 (updated)  
XX XX DT 03-MAR-1999 (first entry)  
XX XX  
XX XX Epitope of HIV-1 gp120 protein which binds antibody BAT085.  
XX XX  
XX XX Epitope; gp120 protein; monoclonal antibody; HIV-1; antibody BAT123;  
XX KW antibody BAT267; antibody BAT085; T cell infection inhibition;  
XX KW syncytia formation; acquired immune deficiency syndrome; AIDS;  
XX KW AIDS-related complex; passive immunisation; antiviral; cytotoxic;  
XX KW viral load measurement; vaccine.  
XX XX  
XX XX Human immunodeficiency virus type 1.  
XX XX US5854400-A.  
XX XX

PD XX 29-DEC-1998.  
XX XX 22-SEP-1992; 92US-0950571.  
XX XX 24-DEC-1987; 87US-0137861.  
XX PR 29-MAY-1987; 87US-0057445.  
XX PR 26-SEP-1991; 91US-0767533.  
XX XX (TANO-) TANOX INC.  
XX XX Chang NT, Chang TW, Fung MSC, Sun BNC, Sun CRY;  
XX XX WPI; 1999-095002/08.  
XX XX Monoclonal antibodies directed against regions of gp120 of human  
XX XX immune deficiency virus-1 - are neutralising and able to inhibit  
XX XX infection of T cells and formation of syncytia, used for treatment,  
XX XX prevention or diagnosis of acquired immune deficiency syndrome  
XX XX Claim 8; Column 9; 16pp; English.  
XX XX The present sequence represents an epitope of the gp120 protein of  
XX XX human immune deficiency virus (HIV)-1. The sequence comprises  
XX XX amino acids 169 to 183 of gp120. The specification describes  
XX XX monoclonal antibodies which bind to epitopes of the gp120 protein.  
XX XX Specifically, these antibodies are designated BAT123, 267 and 085.  
XX XX Monoclonal antibodies neutralise HIV-1 inhibiting both infection  
XX XX of T cells and formation of syncytia, so are used to treat acquired  
XX XX immune deficiency syndrome (AIDS) and AIDS-related complex, by  
XX XX passive immunisation, as carriers of cytotoxic or antiviral agents,  
XX XX and in extracorporeal systems. They can also be used as immunoassay  
XX XX reagents (for diagnosis or measurement of viral load) and to screen  
XX XX for neutralising epitopes, potentially useful in vaccine development.  
XX XX (Updated on 20-MAR-2003 to correct PR field.)  
XX XX  
XX XX Sequence 15 AA;  
XX XX  
XX XX Query Match 36.4%; Score 4; DB 20; Length 15;  
XX XX Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
XX XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX XX  
XX XX 5 FYKL 8  
XX XX ||||  
XX XX 8 FYKL 11  
XX XX  
XX XX RESULT 64  
XX XX AAW72822  
XX XX ID AAW72822 standard; peptide; 15 AA.  
XX XX AC AAW72822;  
XX XX DT 13-JAN-1999 (first entry)  
XX XX  
XX XX HIV-1 gp120 monoclonal antibody BAT085 residue 178 to 192.  
XX XX  
XX KW HIV-1; gp120; epitope; monoclonal antibody; envelope; neutralise;  
XX KW inhibit; infection; T-cell; inhibit syncytium formation; AIDS.  
XX XX Human immunodeficiency virus type 1.  
XX XX US5834599-A.  
XX XX  
XX XX 10-NOV-1998.  
XX XX  
XX XX 04-MAR-1993; 93US-0026276.  
XX XX  
XX XX 04-MAR-1993; 93US-0026276.  
XX PR 29-MAY-1987; 87US-0057445.  
XX PR 24-DEC-1987; 87US-0137861.  
XX PR 25-APR-1989; 89US-0343540.  
XX PR 05-JUN-1992; 92US-0895197.  
XX XX

PA (TANO-) TANOX BIOSYSTEMS INC.  
 XX Chang NT, Chang T, Fung SC, Kim YW, Sun BN, Sun CR;  
 XX WPI; 1999-008810/01.  
 XX Antibody conjugate comprising monoclonal antibody - which binds to  
 PT epitope within amino acid residue of gp120 which neutralises HIV-1  
 PT conjugated with, e.g. cytotoxic agent  
 XX Example 4; Column 25; 22pp; English.  
 CC The present invention describes an antibody conjugate comprising an  
 CC antibody (Ab) which binds to an epitope within amino acid residue  
 CC 308-322 of gp120 and neutralises HIV-1, conjugated with a cytotoxic  
 CC agent, an anti-viral agent or an agent which facilitates passage through  
 CC the blood brain barrier. Also described is an antibody conjugate as  
 CC above but where the Ab binds to an epitope within amino acid residue  
 CC 298-312 of gp120 which neutralises HIV-1. The present sequence represents  
 CC an HIV-1 gp120 monoclonal antibody BAT085 residue 178 to 192 from an  
 CC example of the present invention. The Ab are monoclonal Ab which bind  
 CC to the gp120 protein on the envelope of HIV-1. They inhibit the  
 CC infection of T-cells and also inhibit syncytium formation. The  
 CC antibodies are group specific and neutralise different strains and  
 CC isolates of HIV-1. The antibodies have a variety of uses, including the  
 CC treatment and prevention of AIDS and AIDS related complex. They are  
 CC especially used to kill infected T-cells.  
 XX Sequence 15 AA;  
 SQ Query Match 36.4%; Score 4; DB 20; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FYKL 8  
 DB 8 FYKL 11  
 RESULT 65  
 ABB98878  
 ID ABB98878 standard; Peptide; 15 AA.  
 XX AC ABB98878;  
 XX DT 25-MAR-2003 (first entry)  
 XX DE Proline rich gamma carboxyl glutamic protein 9.13 peptide fragment.  
 XX KW Proline rich gamma carboxyl glutamic protein 9.13;  
 KW blood coagulation disorder; tumour; developmental disorder;  
 KW inflammation; immunological disease.  
 XX OS Unidentified.  
 XX PN CN1352002-A.  
 XX PD 05-JUN-2002.  
 XX PF 02-NOV-2000; 2000CN-0127180.  
 XX PR 02-NOV-2000; 2000CN-0127180.  
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX PI Mao Y, Xie Y;  
 XX WPI; 2002-699440/76.  
 XX New proline containing rich gamma carboxyl glutamic protein 9.13  
 PT polypeptide for treating blood coagulation, tumors, a development  
 PT disorder, inflammations, and immunological diseases -

PS Example 5; Page 19 (Disclosure); 34pp; Chinese.  
 XX The present invention relates to proline rich gamma carboxyl glutamic  
 CC protein 9.13 (see ABB98877). The protein can be used for treating  
 CC various diseases, such as blood coagulation disorders, tumours,  
 CC developmental disorders, inflammations and immunological diseases.  
 CC The present sequence is an N-terminal peptide fragment of the protein,  
 CC which was used in an example from the invention.  
 XX Sequence 15 AA;  
 SQ Query Match 36.4%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KL PQ 10  
 DB 4 KL PQ 7  
 RESULT 66  
 ABB98946  
 ID ABB98946 standard; Peptide; 15 AA.  
 XX AC ABB98946;  
 XX DT 14-APR-2003 (first entry)  
 XX DE Translation initiation factor eIF-2-11.44 peptide fragment.  
 XX KW Translation initiation factor eIF-2-11.44; diabetes; tumour; infection;  
 KW cytosstatic.  
 XX OS Unidentified.  
 XX PN CN1355189-A.  
 XX PD 26-JUN-2002.  
 XX PF 01-DEC-2000; 2000CN-0127631.  
 XX PR 01-DEC-2000; 2000CN-0127631.  
 XX PA (UYFU-) UNIV FUDAN.  
 XX PI Mao Y, Xie Y;  
 XX WPI; 2003-000126/01.  
 XX PT Polypeptide-translation initiation factor eIF-2-11.44 and  
 PT polynucleotide for coding it -  
 XX Example 5; Page 18 (Disclosure); 33pp; Chinese.  
 XX The present invention relates to translation initiation factor  
 CC eIF-2-11.44 (see ABB98945). The protein can be used for treating diseases  
 CC such as diabetes, tumours and infections. The present sequence is an  
 CC N-terminal peptide fragment of the protein, which was used in an example  
 CC from the invention.  
 XX Sequence 15 AA;  
 SQ Query Match 36.4%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPQN 4  
 DB 1 MPQN 4  
 RESULT 67  
 AAY29641

ID XX AAY29841 standard; peptide; 16 AA.  
 AC AAY29841;  
 DT 16-NOV-1999 (first entry)  
 XX  
 DE HIV HXB2 V3 fusion peptide #1.  
 XX  
 KW Fusion glycoprotein; env polypeptide; SU domain; expression vector;  
 KW retrovirus; surface protein; murine leukaemia virus; MuLV; immunoassay;  
 KW envelope protein; immunogen; vaccines HIV.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 FN US952474-A.  
 XX  
 PD 14-SEP-1999.  
 XX  
 PF 01-JUL-1997; 97US-0886642.  
 XX  
 PR 20-AUG-1993; 93US-0110300.  
 XX  
 PR 28-AUG-1992; 92US-0938100.  
 XX  
 PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.  
 XX  
 PI Pinter A, Kayman S;  
 XX  
 XX WPI; 1999-550490/46.  
 DR  
 XX Fusion glycoprotein comprising active polypeptide and retroviral  
 PT envelope protein useful in immunoassays and as immunogens, especially  
 PT for anti-human immune deficiency vaccines -  
 XX  
 PS Example; Column 17; 48pp; English.  
 XX  
 CC The present invention describes a fusion glycoprotein (I) containing the  
 CC N-terminal globular domain of a retroviral envelope (env) surface protein  
 CC linked to a glycopeptide. (I) is expressed by a vector comprising a  
 CC biologically active amino acid sequence (II) from a protein lacking a  
 CC hydrophobic glycosylation signal (HGS) located about 7 residues  
 CC N-terminal to a Cys-Tyr-Leu-Cys sequence. (II) is operably linked to  
 CC the C-terminus of a polypeptide sequence (III) from a retroviral env  
 CC protein. (III) is an N-terminal fragment of env and includes all Cys  
 CC residue with the N-terminal globular domain with a N-glycan attachment  
 CC site with an HGS located within 7 residues N-terminal to a  
 CC Cys-Tyr-Leu-Cys sequence. (II) particularly includes an epitope and can  
 CC then be used in immunoassays for diagnostic detection of antibodies,  
 CC receptors or other binding partners, in affinity chromatography, or as  
 CC immunogens, particularly in protective vaccines or for production of  
 CC monoclonal antibodies. Most particularly (I) is used to raise  
 CC neutralising antibodies against human immune deficiency virus (HIV)-1.  
 CC Vectors used to express (I) can be constructed in bacteria to generate  
 CC stable cell lines and can be used to infect a wide variety of cells.  
 CC (I)-expressing cell cultures can be made quickly (without use of a  
 CC selection marker) and the level of expression in mammalian cells is high,  
 CC allowing simple and quick analysis during vaccine development. The  
 CC present sequence represents a peptide, which is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 16 AA;  
 SQ  
 Query Match 36.4%; Score 4; DB 20; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 FYKL 8  
 DB 12 FYKL 15  
 RESULT 68  
 AAY29841

ID XX AAW47339 standard; peptide; 17 AA.  
 AC AAW47339;  
 DT 01-JUN-1998 (first entry)  
 XX  
 DE Apolipoprotein B tryptic peptide.  
 XX  
 KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;  
 KW vascular injury; elastin; collagen; prevention; treatment;  
 KW vascular disease; atherosclerosis; apolipoprotein B; apoB;  
 KW tryptic peptide.  
 XX  
 OS Homo sapiens.  
 OS  
 FN US5726153-A.  
 XX  
 PD 10-MAR-1998.  
 XX  
 PF 06-JUN-1995; 95US-0468543.  
 XX  
 PR 06-JUN-1995; 95US-0469692.  
 PR 02-MAY-1988; 88US-0189130.  
 PR 03-MAY-1990; 90US-0518142.  
 PR 03-MAY-1990; 90US-0518215.  
 PR 02-MAY-1991; 91US-0694929.  
 PR 16-APR-1993; 93US-0048569.  
 PR 24-FEB-1994; 94US-0201057.  
 PR 28-FEB-1995; 95US-0398046.  
 PR 06-JUN-1995; 95US-0468543.  
 XX  
 XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.  
 XX  
 PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;  
 XX  
 DR WPI; 1998-192802/17.  
 XX  
 CC Inhibiting binding of low-density lipoprotein to vascular walls - by  
 CC administering peptide with affinity for vascular injury sites  
 PS Disclosure; Column 10; 31pp; English.  
 XX  
 CC A novel method for inhibiting the binding of a low-density  
 CC lipoprotein (LDL) to vascular walls in vivo, comprises  
 CC administering a synthetic water soluble peptide containing an  
 CC amphiphilic domain and having affinity for sites of vascular  
 CC injury, e.g. derived from the present peptide.  
 CC The peptide inhibits the binding of LDL to vascular wall  
 CC components, e.g. elastin and collagen, and so can be used to  
 CC prevent or treat vascular diseases, e.g. atherosclerosis.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 36.4%; Score 4; DB 19; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLPQ 10  
 DB 1 KLPQ 4  
 RESULT 69  
 AAY55881  
 ID AAY55881 standard; peptide; 17 AA.  
 XX  
 AC AAY55881;  
 DT 01-FEB-2000 (first entry)  
 XX  
 DE Apolipoprotein fragment peptide #31 for vascular disease imaging.  
 XX  
 KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;

KW detection; imaging; disease; atherosclerosis; apolipoprotein.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX US5972890-A.  
 XX PD 26-OCT-1999.  
 XX PF 28-FEB-1995; 95US-0398046.  
 XX PR 02-MAY-1991; 91US-0694929.  
 PR 16-APR-1993; 93US-0048569.  
 PR 24-FEB-1994; 94US-0201057.  
 PR 02-MAY-1988; 88US-0189130.  
 PR 03-MAY-1990; 90US-0518142.  
 PR 03-MAY-1990; 90US-0518215.  
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.  
 XX Lees AM, Fischman A, Shih I, Findeis MA, Lees RS;  
 XX WPI; 1999-632641/54.  
 XX PT New diagnostic synthetic peptides which have affinity for and  
 PT accumulate at a site of vascular injury useful for detection and  
 PT imaging of vascular disease such as atherosclerosis -  
 XX PS Disclosure; Column 10; 30pp; English.  
 XX CC The peptides AAY55851-V55889 represent examples of diagnostic, synthetic  
 CC peptides which carry a detectable label, contain 30 or fewer amino  
 CC acids, are water soluble, contain an amphiphilic domain and have affinity  
 CC for, and propensity to accumulate at, a site of vascular injury. They  
 CC are preferably derived from the amino acid sequence of apolipoprotein.  
 CC The peptides can be used for the detection or imaging of a vascular  
 CC injury or disease, e.g. atherosclerosis.  
 XX SQ Sequence 17 AA;  
 Query Match 36.4%; Score 4; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 5.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLPQ 10  
 DB 1 KLPQ 4  
 RESULT 70  
 AAY33106  
 ID AAY33106 standard; peptide; 17 AA.  
 XX AAY33106;  
 XX DT 15-NOV-1999 (first entry)  
 XX DE Alipoprotein B tryptic peptide 2.  
 KW Alipoprotein B; alipoprotein A1; elastin; vascular imaging; detection;  
 KW injury; vascular system; atherosclerosis; re-endothelializing; noninvasive;  
 KW aortic lesion; trauma; lipoprotein accumulation.  
 XX Synthetic.  
 XX US5955055-A.  
 XX PD 21-SEP-1999.  
 XX PF 06-JUN-1995; 95US-0469692.  
 XX PR 02-MAY-1991; 91US-0694929.  
 PR 02-MAY-1988; 88US-0189130.

PR 03-MAY-1990; 90US-0518142.  
 PR 03-MAY-1990; 90US-0518215.  
 PR 16-APR-1993; 93US-0048569.  
 PR 24-FEB-1994; 94US-0201057.  
 PR 28-FEB-1995; 95US-0398046.  
 PR 06-JUN-1995; 95US-0469692.  
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.  
 XX Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;  
 XX WPI; 1999-539543/45.  
 XX PT Detecting vascular injuries using a labeled peptide useful for the  
 PT diagnosis and monitoring of atherosclerosis  
 XX PS Disclosure; Column 29-30; 31pp; English.  
 XX CC This invention describes a novel method (I) for detecting injuries in a  
 CC vascular system using a labeled synthetic peptide with an affinity for,  
 CC and propensity to accumulate at, a site of vascular injury. The method  
 CC is particularly suitable for detecting and monitoring atherosclerosis.  
 CC It has been found that the synthetic peptide accumulates at the healing  
 CC (re-endothelializing) edge of aortic lesions produced by trauma. These  
 CC lesions resemble human atherosclerosis in many important respects  
 CC (including accumulation of lipoproteins and other pathological changes).  
 CC The ability of the synthetic peptides to localize at the trauma site, and  
 CC and to permit imaging, may be used to visualize vascular disease. The  
 CC method is noninvasive and the peptides used to target vascular lesions  
 CC may be produced inexpensively, quickly and in large quantities.  
 CC AAY3088-13314 represent synthetic peptides derived from apolipoprotein B,  
 CC apolipoprotein A1 and elastin which are used in the method of the  
 CC invention.  
 XX SQ Sequence 17 AA;  
 Query Match 36.4%; Score 4; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 5.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KLPQ 10  
 DB 1 KLPQ 4  
 RESULT 71  
 AAW29567  
 ID AAW29567 standard; peptide; 18 AA.  
 XX AAW29567;  
 XX DT 26-OCT-1998 (first entry)  
 XX DE Peptide GF52.  
 XX KW Immune response; human papillomavirus; HPV; MHC class II; chimeric;  
 KW automated peptide synthesis; solution synthesis; solid phase synthesis;  
 KW B-cell; Cytotoxic T lymphocyte; CTL; HPV16; antigen;  
 KW 9-fluorenylmethoxycarbonyl chemistry; Fmoc; peptide-resin conjugate;  
 KW thioanisole; ethanedithiol; purification; precipitation; ether.  
 XX Synthetic.  
 XX WO9823635-A1.  
 XX PD 04-JUN-1998.  
 XX PF 01-DEC-1997; 97WO-AU00820.  
 XX PR 29-NOV-1996; 96AU-0003903.  
 XX (CSLC-) CSL LTD.  
 PA (UYQU ) UNIV QUEENSLAND.

XX PI Azourey-ziaadeh R, Frazer IH, Tindie R;  
 XX DR WPI; 1998-322657/28.  
 XX  
 XX New peptide(s) comprising promiscuous T helper cell epitopes from  
 PT papilloma virus proteins - used for, e.g. generation of immune  
 PT response, and particularly for treating or preventing papilloma  
 PT virus infection  
 XX  
 XX Disclosure; Figure 1; 70pp; English.  
 XX  
 XX Synthetic peptides AAW29566-W29581 cover the entire HPV16 E6 open  
 CC reading frame, and were constructed to be used as antigens. The  
 CC synthesis of these peptides was performed by using  
 CC 9-fluorenylmethoxycarbonyl (Fmoc) chemistry on an applied biosystems 431A  
 CC peptide synthesizer. This enables peptide-resin conjugates to be  
 CC obtained which can be cleaved by the addition of thioanisole and  
 CC ethanedithiol, thus releasing the peptide. To purify these peptides they  
 CC were precipitated with cold ether. Peptides AAW29572 and AAW29576 both  
 CC contain the t-helper cell epitopes given in AAW60838 and AAW60839  
 CC respectively. These T helper cell epitopes generate an immune response  
 CC against human papillomavirus (HPV), and thus can be used to treat HPV  
 CC infections. These peptides have been found to provide immunity to HPV  
 CC infection across a broad spectrum of MHC backgrounds, therefore they  
 CC would enable a diverse genetically outbred group to be vaccinated.  
 XX  
 XX Sequence 18 AA;  
 SQ

Query Match 36.4%; Score 4; DB 19; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10  
 Db 4 KLPQ 7  
 ||||  
 ||||

RESULT 72  
 ABJ00634  
 ID ABJ00634 standard; Peptide; 18 AA.  
 AC ABJ00634;  
 XX  
 XX 05-SEP-2002 (first entry)  
 XX  
 XX B lymphocyte stimulator protein binding peptide #78.  
 XX  
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;  
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;  
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;  
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;  
 KW antitachmatic; anti-allergic; thyromimetic; antianaemic; haemostatic;  
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;  
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 XX Unidentified.  
 XX  
 XX WC200216411-A2.  
 XX  
 XX 28-FEB-2002.  
 XX  
 XX 17-AUG-2001; 2001WO-US25850.  
 XX  
 XX 18-AUG-2000; 2000US-226700P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B Lymphocyte stimulator binding polypeptide -  
 XX  
 XX Claim 70; Page 194; 387pp; English.  
 XX  
 XX The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells  
 CC of haematopoietic origin; or proliferative disease; and reducing  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of Blys binding polypeptide.  
 CC The Blys binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 XX  
 XX Sequence 18 AA;  
 SQ

Query Match 36.4%; Score 4; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6  
 Db 11 QNFY 14  
 ||||  
 ||||

RESULT 73  
 ABG33495  
 ID ABG33495 standard; Peptide; 18 AA.  
 AC ABG33495;  
 XX  
 XX 15-JUL-2002 (first entry)  
 XX  
 XX B Lymphocyte Stimulator (Blys) binding peptide #83.  
 XX  
 XX B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;  
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;  
 KW synovial fluid; saliva; mucus.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200216412-A2.  
 XX  
 XX 28-FEB-2002.  
 XX  
 XX 17-AUG-2001; 2001WO-US25891.  
 XX  
 XX 18-AUG-2000; 2000US-226489P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX  
 XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;  
 XX  
 XX WPI; 2002-351647/38.  
 XX  
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or  
 PT isolating Blys or Blys-like polypeptide comprises a specified amino  
 PT acid sequence -  
 XX  
 XX Claim 13; Page 74; 269pp; English.  
 XX  
 XX The invention relates to a B Lymphocyte Stimulator (Blys) binding  
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins  
 CC reversibly or irreversibly. The binding peptides are used in detection,  
 CC isolation and/or purification of Blys in a solution such as water or a  
 CC buffer solution, as well as any fluid and/or cell obtained from an  
 CC individual biological fluid, body tissue, body cell, cell line, tissue

CC culture or other source containing Blys or Blys-like polypeptides. The  
CC biological fluids include sera, plasma, lymph, blood, blood fraction,  
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences  
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and  
CC ABG33852-33862 represent Blys binding peptides of the invention.  
XX  
SQ Sequence 18 AA;  
Query Match 36.4%; Score 4; DB 23; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;  
QY 3 QNPFY 6  
DB 11 QNPFY 14  
RESULT 74  
ID AAW79176 standard; peptide; 19 AA.  
XX  
AC AAW79176;  
XX  
DT 25-JAN-1999 (first entry)  
XX  
DE Fusion immunoglobulin heavy chain HIV gp120 T cell epitope #54.  
XX  
DE B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IGH;  
XX human immune deficiency virus; HIV; tolerance; treatment; therapy;  
XX prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;  
XX microbial infection; autoimmune disease; antibody; apoptosis;  
XX antiviral T cell immunity.  
XX  
OS Mus sp.  
OS Homo sapiens.  
XX  
XX WO9836087-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 13-FEB-1998; 98WO-US02766.  
XX  
PR 13-FEB-1997; 97US-0040581.  
XX  
PA (AMNA-) AMERICAN NAT RED CROSS.  
XX  
XX Scott D, Zambidis B;  
XX  
XX WPI; 1998-506315/43.  
XX  
XX New fusion immunoglobulin heavy chain including gp120 epitopes and  
PT related complete antibodies - DNA, vectors and transformed cells,  
PT used to induce tolerance to the epitopes for treatment of human  
PT immune deficiency virus infection  
XX  
PS Disclosure; Page 49; 154pp; English.  
XX  
CC This sequence is an epitope used in the construction of a novel fusion  
CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially  
CC human, IGH chain fused in frame at its N-terminus to one or more human  
CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or  
CC transfected cells are used to tolerate subjects to gp120 epitopes and to  
CC maintain this tolerance, particularly for treatment of HIV infection,  
CC optionally together with other therapeutic/prophylactic agents such as  
CC vaccines, chemotherapeutic agents and immune response modifiers. Such  
CC proteins can be used against other diseases where an immune response is  
CC deleterious, e.g. microbial infection, tumours or autoimmune disease.  
CC Induction of tolerance suppresses production of antibodies against gp120,  
CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that  
CC are bound to gp120 protein, maximising induction of protective antiviral  
CC T cell immunity.  
XX  
SQ Sequence 19 AA;

Query Match 36.4%; Score 4; DB 19; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 FYKL 8  
DB 9 FYKL 12  
RESULT 75  
ID AAY85068 standard; peptide; 19 AA.  
XX  
AC AAY85068;  
XX  
DT 20-JUN-2000 (first entry)  
XX  
DE Immunogenic peptide #6 derived from FMDV non-structural protein 3B.  
XX Foot and mouth disease; FMDV; epitope; anti-FMDV antibody; diagnose;  
XX vaccine; immunoreagent; non-structural protein.  
XX  
OS Foot and mouth disease virus.  
XX  
PN US6048538-A.  
XX  
PD 11-APR-2000.  
XX  
PF 03-OCT-1997; 97US-0943173.  
XX  
PR -03-OCT-1997; 97US-0943173.  
XX  
PA (UNBI-) UNITED BIOMEDICAL INC.  
XX  
XX Yi Wang C, De Chen P, Shen F;  
XX  
XX WPI; 2000-328034/28.  
XX  
PT Peptide from non-structural proteins useful for detecting  
PT foot-and-mouth disease virus infection in animal comprises an  
PT immunogenic epitope specific to antibodies -  
XX  
XX Claim 1; Column 25-26; 23pp; English.  
XX  
CC This sequence represents a peptide derived from the non-structural  
CC protein 3B of the foot and mouth disease virus (FMDV). The amino acid  
CC sequence of the peptide corresponds to an immunodominant region of the  
CC FMDV non-structural protein and is an immunogenic epitope specific for  
CC anti-FMDV antibodies. The invention relates to peptides derived from  
CC three non-structural FMDV proteins. The peptides are useful as  
CC immunoreagents i.e. reagent in an immunoassay in detecting antibodies to  
CC FMDV or diagnosis of FMDV infection. The immunoassays are used to screen  
CC body fluids and tissues for the presence of FMDV-reactive antibodies and  
CC aid in the diagnosis of FMDV infection and differentiate infected from  
CC the vaccinated animals.  
XX  
SQ Sequence 19 AA;  
Query Match 36.4%; Score 4; DB 21; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 KLPQ 10  
DB 5 KLPQ 8  
Search completed: November 25, 2003, 18:15:47  
Job time : 37.633 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 21.883 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-6

Perfect score: 11

Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLIGO  
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Searched: 673684 seqs, 18443283 residues

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Total number of hits satisfying chosen parameters: 139596

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	15	US-10-281-652-6
2	4	36.4	4	11	US-09-852-910-9
3	4	36.4	7	11	US-09-310-346C-7
4	4	36.4	7	12	US-09-261-894-69
5	4	36.4	7	12	US-09-261-894-102
6	4	36.4	9	10	US-09-835-948-73
7	4	36.4	9	10	US-09-835-948-101
8	4	36.4	9	10	US-09-909-460-101
9	4	36.4	9	12	US-10-172-597-73
10	4	36.4	9	12	US-10-172-597-101
11	4	36.4	9	15	US-10-133-210-278
12	4	36.4	10	10	US-09-867-852-99
13	4	36.4	10	15	US-10-062-710-83
14	4	36.4	12	11	US-09-880-748-2884
15	4	36.4	12	11	US-09-845-612B-10
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					Sequence 9, Appli
					Sequence 7, Appli
					Sequence 69, Appl
					Sequence 102, App
					Sequence 73, Appl
					Sequence 101, App
					Sequence 101, App
					Sequence 73, Appl
					Sequence 101, App
					Sequence 278, App
					Sequence 99, Appl
					Sequence 83, Appl
					Sequence 2884, Ap
					Sequence 10, Appli

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18	4	36.4	18	11	US-09-932-613-92
19	4	36.4	18	12	US-09-932-322-92
20	4	36.4	19	9	US-09-864-761-43517
21	4	36.4	20	11	US-09-974-879-610
22	4	36.4	20	11	US-09-305-736-611
23	4	36.4	20	12	US-09-818-683-611
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58	3	27.3	7	9	US-09-832-723-68
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61	3	27.3	7	10	US-09-771-035A-3
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Sequence 59, Appl  
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Sequence 208, App  
Sequence 335, App  
Sequence 27, Appl  
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Sequence 26, Appl  
Sequence 38, Appl  
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Sequence 36, Appl  
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Sequence 17, Appl  
Sequence 18, Appl  
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Sequence 118, App  
Sequence 246, App  
Sequence 17, Appl  
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Sequence 42, App  
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 93 3 27.3 7 12 US-10-086-208-81 Sequence 81, Appl  
 94 3 27.3 7 12 US-10-122-675-11 Sequence 11, Appl  
 95 3 27.3 7 12 US-09-261-894-4 Sequence 4, Appl  
 96 3 27.3 7 12 US-09-261-894-22 Sequence 22, Appl  
 97 3 27.3 7 12 US-09-261-894-23 Sequence 23, Appl  
 98 3 27.3 7 12 US-09-261-894-34 Sequence 34, Appl  
 99 3 27.3 7 12 US-09-261-894-35 Sequence 35, Appl  
 100 3 27.3 7 12 US-09-261-894-36 Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
 US-10-281-652-6  
 ; Sequence 6, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLCISTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; FILE REFERENCE: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-6

Query Match 100.0%; Score 11; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11  
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 Db 1 MPQNFYKLPQM 11

RESULT 2  
 US-09-852-910-9  
 ; Sequence 9, Application US/09852910  
 ; Publication No. US20030096297A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hamm, Heidi  
 ; APPLICANT: Gilchrist, Annette  
 ; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S  
 ; FILE REFERENCE: 2861-101  
 ; CURRENT APPLICATION NUMBER: US/09/852,910  
 ; CURRENT FILING DATE: 2001-09-18  
 ; PRIOR APPLICATION NUMBER: US 60/275,472  
 ; PRIOR FILING DATE: 2001-03-14  
 ; NUMBER OF SEQ ID NOS: 271  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: mammal

; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(4)  
 ; OTHER INFORMATION: PAR-34  
 US-09-852-910-9  
 Query Match 36.4%; Score 4; DB 11; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 LPQM 11  
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 Db 1 LPQM 4

RESULT 3  
 US-09-910-346C-7  
 ; Sequence 7, Application US/09910346C  
 ; Publication No. US20030027752A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STEWARD, LANCE E  
 ; APPLICANT: FERNANDEZ-SALAS, ESTER  
 ; APPLICANT: HERRINGTON, TODD M  
 ; APPLICANT: AOKI, KEI R  
 ; TITLE OF INVENTION: Leucine-based motif and clostridial neurotoxins  
 ; FILE REFERENCE: D-2885CIP  
 ; CURRENT APPLICATION NUMBER: US/09/910,346C  
 ; CURRENT FILING DATE: 2000-07-21  
 ; PRIOR APPLICATION NUMBER: US 09/620,840  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: This fragment may have come from  
 ; OTHER INFORMATION: a rat source.  
 US-09-910-346C-7

Query Match 36.4%; Score 4; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
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 Db 3 FYKL 6

RESULT 4  
 US-09-261-894-69  
 ; Sequence 69, Application US/09261894  
 ; Publication No. US20030207324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Humphreys, Robert E  
 ; APPLICANT: Adams, Sharlene  
 ; APPLICANT: Xu, Minzhen  
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
 ; NUMBER OF SEQUENCES: 165  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kevin M. Farrell, P.C.  
 ; STREET: P.O. Box 999  
 ; CITY: York Harbor  
 ; STATE: ME  
 ; COUNTRY: USA  
 ; ZIP: 03911  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/261,894  
; FILING DATE: March 3, 1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-261-894-69

Query Match 36.4%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKLP 9  
Db 3 YKLP 6

RESULT 5  
US-09-261-894-102  
; Sequence 102, Application US/09261894  
; Publication No. US20030207324A1  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzheng  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/261,894  
; FILING DATE: March 3, 1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-261-894-102

Query Match 36.4%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
Db 4 KLPQ 7

RESULT 6  
US-09-835-948-73  
; Sequence 73, Application US/09835948  
; Patent No. US20020160365A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
; FILE REFERENCE: D6223CIP-B/D  
; CURRENT APPLICATION NUMBER: US/09/835,948  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: US 09/492,543  
; PRIOR FILING DATE: 01-27-2000  
; NUMBER OF SEQ ID NOS: 189  
; SEQ ID NO 73  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein  
US-09-835-948-73

Query Match 36.4%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5  
Db 4 PQNF 7

RESULT 7  
US-09-835-948-101  
; Sequence 101, Application US/09835948  
; Patent No. US20020160365A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
; FILE REFERENCE: D6223CIP-B/D  
; CURRENT APPLICATION NUMBER: US/09/835,948  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: US 09/492,543  
; PRIOR FILING DATE: 01-27-2000  
; NUMBER OF SEQ ID NOS: 189  
; SEQ ID NO 101  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein  
US-09-835-948-101

Query Match 36.4%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5  
Db 4 PQNF 7

RESULT 8  
US-09-909-460-101  
; Sequence 101, Application US/09909460  
; Publication No. US20020182258A1  
; GENERAL INFORMATION:

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; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-909-460-101

Query Match      36.4%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLPQ 10
DB      1 KLPQ 4

RESULT 9
US-10-172-597-73
; Sequence 73, Application US/10172597
; Publication No. US20030180736A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Methods for the Early Diagnosis of Ovarian Cancer
; FILE REFERENCE: D6223CIPB/D/CIP
; CURRENT APPLICATION NUMBER: US/10/172,597
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/835,948
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 189
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-10-172-597-73

Query Match      36.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PQNF 5
DB      4 PQNF 7

RESULT 10
US-10-172-597-101
; Sequence 101, Application US/10172597
; Publication No. US20030180736A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Methods for the Early Diagnosis of Ovarian Cancer
; FILE REFERENCE: D6223CIPB/D/CIP
; CURRENT APPLICATION NUMBER: US/10/172,597
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/835,948
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 189
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-10-172-597-101

Query Match      36.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PQNF 5
DB      4 PQNF 7

RESULT 11
US-10-133-210-278
; Sequence 278, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-095AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 278
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-278

Query Match      36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLPQ 10
DB      1 KLPQ 4

RESULT 12
US-09-867-852-99
; Sequence 99, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RES2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
```

```

; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-99

Query Match          36.4%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 6 KLPQ 9

RESULT 13
US-10-062-710-83
; Sequence 83, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV CTL-Epitopes
US-10-062-710-83

Query Match          36.4%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
DB 4 FYKL 7

RESULT 14
US-09-880-748-2884
; Sequence 2884, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2884
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2884

Query Match          36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6
DB 5 QNFY 8

RESULT 15
US-09-845-612B-10
; Sequence 10, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOCH.
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UMSD:795
; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-10

Query Match          36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLP 9
DB 3 YKLP 6

RESULT 16
US-09-927-734C-10
; Sequence 10, Application US/09927734C
; Publication No. US20030194758A1
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Nakata, Mitsunori
; TITLE OF INVENTION: Method for the Identification of Fungal Glucose Utilization
; TITLE OF INVENTION: Inhibitors and Antifungal Agents
; FILE REFERENCE: MYCOLOGX-06279
; CURRENT APPLICATION NUMBER: US/09/927,734C
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-734C-10

Query Match          36.4%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NPYK 7  
    ||||  
Db 6 NPYK 9

RESULT 17  
US-10-038-407-16  
; Sequence 16, Application US/10038407  
; Publication No. US20030105282A1  
; GENERAL INFORMATION:  
; APPLICANT: Biotex  
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES  
; TITLE OF INVENTION: CAPABLE OF GENERATING NEUTRALIZING ANTIBODIES  
; FILE REFERENCE: 07763-048001  
; CURRENT APPLICATION NUMBER: US/10/038,407  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: 09/508,208  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: PCT/US98/18679  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: 60/038,155  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus (HIV)  
US-10-038-407-16

Query Match 36.4%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8  
    ||||  
Db 5 FYKL 8

RESULT 18  
US-09-932-613-92  
; Sequence 92, Application US/09932613  
; Publication No. US20030091565A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,613  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BlyS binding polypeptide  
US-09-932-613-92

Query Match 36.4%; Score 4; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6  
    ||||  
Db 11 QNFY 14

## RESULT 19

US-09-932-322-92  
; Sequence 92, Application US/09932322  
; Publication No. US20030194743A1  
; GENERAL INFORMATION:  
; APPLICANT: Dyax Corp.  
; APPLICANT: Beltzer, James P.  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Fleming, Tony J.  
; APPLICANT: Ladner, Robert Charles  
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)  
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US  
; CURRENT APPLICATION NUMBER: US/09/932,322  
; CURRENT FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 458  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BlyS binding polypeptide  
US-09-932-322-92

Query Match 36.4%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6  
    ||||  
Db 11 QNFY 14

## RESULT 20

US-09-864-761-43517  
; Sequence 43517, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43517
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002088.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
; OTHER INFORMATION: EST_HUMAN HIT: H56539.1, EVALUATE 6.00e-03
US-09-864-761-43517

```

```

Query Match          36.4%; Score 4; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 7 KLPQ 10
DB 4 KLPQ 7

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```

RESULT 21
US-09-974-879-610
; Sequence 610, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Regen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: PZ020F2
; CURRENT APPLICATION NUMBER: US 09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066,090
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07

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; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 610
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-610

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Query Match          36.4%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 FYKL 8
DB 9 FYKL 12

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RESULT 22
US-09-305-736-611
; Sequence 611, Application US/09305736
; Publication No. US2003008078A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: PZ020F1
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 611
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens

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; MOLECULE TYPE: peptide
US-09-071-838-143

Query Match      27.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 NFY 6
      |||
Db      1 NFY 3

RESULT 26
US-09-784-641-8
; Sequence 8, Application US/09784641
; Publication No. US20030050260A1
; GENERAL INFORMATION:
; APPLICANT: NewMillennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES BY REDUCING IN VIVO CATHEPSIN L ACTI
; FILE REFERENCE: 26748-702
; CURRENT APPLICATION NUMBER: US/09/784,641
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-641-8

Query Match      27.3%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 FYK 7
      |||
Db      1 FYK 3

RESULT 27
US-09-784-642-8
; Sequence 8, Application US/09784642
; Publication No. US20030054984A1
; GENERAL INFORMATION:
; APPLICANT: NewMillennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHOD FOR REDUCING BLOOD INSULIN LEVELS BY REDUCING IN VIVO CAT
; FILE REFERENCE: 26748-703
; CURRENT APPLICATION NUMBER: US/09/784,642
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-642-8

Query Match      27.3%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 FYK 7
      |||
Db      1 FYK 3

RESULT 28
US-10-213-512-143
; Sequence 143, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.

; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; FILE REFERENCE: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-143

Query Match      27.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 NFY 6
      |||
Db      1 NFY 3

RESULT 29
US-10-028-075B-85
; Sequence 85, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pcd/IGBR/IGBR-B
US-10-028-075B-85

Query Match      27.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLP 9
      |||
Db      2 KLP 4

RESULT 30
US-10-029-206A-85
; Sequence 85, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert

```



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; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pdb/1GBR/1GBR-B
US-10-029-206A-85

Query Match      27.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 KLP 9
      |||
Db      2 KLP 4

RESULT 31
US-09-788-006-57
; Sequence 57, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-57

Query Match      27.3%; Score 3; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 YKL 8
      |||
Db      1 YKL 3

RESULT 34
US-10-027-038-18
; Sequence 18, Application US/10027038
; Publication No. US20030159380A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, S.
; TITLE OF INVENTION: Modular peptide-based reagent
; FILE REFERENCE: 1443.026US1
; CURRENT APPLICATION NUMBER: US/10/027,038
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide interactive domain.
US-10-027-038-18

Query Match      27.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 YKL 8
      |||
Db      1 YKL 3

RESULT 35
US-10-235-483-31
; Sequence 31, Application US/10235483
; Publication No. US20030087407A1

```



; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550B  
; FILING DATE:  
; CLASSIFICATION: 435435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 335:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-424-550B-335

Query Match 27.3%; Score 3; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQ 10  
|||  
Db 3 LPQ 5

RESULT 38  
US-09-486-734A-26  
; Sequence 26, Application US/09486734A  
; Patent No. US20020164732A1  
; GENERAL INFORMATION:  
; APPLICANT: Chopin, Marie-Christine  
; APPLICANT: Clier, Florence  
; APPLICANT: Erlich, S. Dusko  
; APPLICANT: Gautier, Michel  
; APPLICANT: Schouler, Catherine  
; APPLICANT: Institut National de la Recherche Agronomique  
; TITLE OF INVENTION: Resistance Mechanisms to IC Type R/M  
; FILE REFERENCE: Bacteriophages of Lactic Acid Bacteria  
; CURRENT APPLICATION NUMBER: 33339/196048  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: PCT/FR98/01873  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR FILING DATE: 1997-09-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HdM subunit  
; US-09-486-734A-26

Query Match 27.3%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7  
|||  
Db 1 FYK 3

RESULT 39  
US-09-523-759-27  
; Sequence 27, Application US/09529759  
; Publication No. US20020192644A1  
; GENERAL INFORMATION:  
; APPLICANT: Vivier, Eric

; APPLICANT: Vely, Frederic  
; TITLE OF INVENTION: DOCUMENTATION MEANS FOR REPERTOIRES OF  
; TITLE OF INVENTION: NKR IMMUNORECEPTORS AND/OR ACTIVATORY OR NON-INHIBITORY  
; FILE REFERENCE: A33131 PCT USA 067858.0101  
; CURRENT APPLICATION NUMBER: US/09/529,759  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: FR 97/13115  
; PRIOR FILING DATE: 1997-10-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-529-759-27

Query Match 27.3%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9  
|||  
Db 1 KLP 3

RESULT 40  
US-09-842-930A-46  
; Sequence 46, Application US/09842930A  
; Publication No. US20020197681A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul  
; TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis  
; FILE REFERENCE: 5820.603  
; CURRENT APPLICATION NUMBER: US/09/842,930A  
; CURRENT FILING DATE: 2001-04-22  
; PRIOR APPLICATION NUMBER: 60/245,320  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 46  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-842-930A-46

Query Match 27.3%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQ 3  
|||  
Db 1 MPQ 3

RESULT 41  
US-09-992-331-26  
; Sequence 26, Application US/09992331  
; Publication No. US20030022186A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, JOHN N.  
; APPLICANT: MINTIER, GABE  
; APPLICANT: RAMANATHAN, CHANDRA S.  
; APPLICANT: RAMANATHAN, DONALD R.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV18,  
; FILE REFERENCE: D0048NP  
; CURRENT APPLICATION NUMBER: US/09/992,331  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/308,540

;  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/261,782  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/248,483  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized  
; OTHER INFORMATION: peptide  
US-09-992-331-26

Query Match 27.3%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5  
Db 1 QNF 3

RESULT 42  
US-09-997-961-38  
; Sequence 38, Application US/0997961  
; Publication No. US20030060613A1  
; GENERAL INFORMATION:  
; APPLICANT: DEPHAR, Shoukat  
; TITLE OF INVENTION: NOVEL USE OF CALRETICULIN IN MODULATING  
; HORMONE RESPONSIVENESS AND NEW PHARMACEUTICALS FOR  
; TREATING CANCER, OSTEOPOROSIS AND CHRONIC INFLAMMATORY  
; DISEASE  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/997 961  
; FILING DATE: 29-Jan-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/169,935  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US/08/377,432  
; FILING DATE: 24-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 007315-005  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-997-961-38

Query Match 27.3%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
Db 3 FYK 5

RESULT 43  
US-09-261-894-24  
; Sequence 24, Application US/09261894  
; Publication No. US20030207324A1  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/261,894  
; FILING DATE: March 3, 1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-261-894-24

Query Match 27.3%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
Db 4 KLP 6

RESULT 44  
US-10-137-967-150  
; Sequence 150, Application US/10137867  
; Publication No. US20030207349A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.

```

; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3390RIC146
; CURRENT APPLICATION NUMBER: US/10/137,867
; PRIOR FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 150
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-150

Query Match 27.3%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
Db 3 LPQ 5

RESULT 45
US-10-036-418-13
; Sequence 13, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INCAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-13

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 4 KLP 6

RESULT 46
US-10-036-418-14
; Sequence 14, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INCAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07

```

```

; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-14

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 3 KLP 5

RESULT 47
US-10-036-418-15
; Sequence 15, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INCAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-15

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 2 KLP 4

RESULT 48
US-10-036-418-16
; Sequence 16, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INCAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-16

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 KLP 9  
|||  
Db 1 KLP 3

## RESULT 49

US-10-156-820-36  
; Sequence 36, Application US/10156820  
; Publication No. US2002015058A1  
; GENERAL INFORMATION:  
; APPLICANT: Boulanger, Pierre  
; APPLICANT: Hong, Saw See  
; APPLICANT: Karavan, Lucie  
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
; FILE REFERENCE: 032751-036  
; CURRENT APPLICATION NUMBER: US/10/156,820  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: PCI/FR98/00184  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: FR 97/01005  
; PRIOR FILING DATE: 1997-01-30  
; PRIOR APPLICATION NUMBER: FR 97/11166  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Phagotope  
US-10-156-820-36

Query Match 27.3%; Score 3; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
|||  
Db 4 KLP 6

## RESULT 50

US-10-121-857-16  
; Sequence 16, Application US/10121857  
; Publication No. US20030028923A1  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.143  
; CURRENT APPLICATION NUMBER: US/10/121,857  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mortierella ramanniana  
US-10-121-857-16

Query Match 27.3%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
|||  
Db 1 KLP 3

## RESULT 51

US-10-208-018-16  
; Sequence 16, Application US/10208018  
; Publication No. US20030115632A1  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.155  
; CURRENT APPLICATION NUMBER: US/10/208,018  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US 10/121,857  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mortierella ramanniana  
US-10-208-018-16

Query Match 27.3%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
|||  
Db 1 KLP 3

## RESULT 52

US-10-262-313-26  
; Sequence 26, Application US/10262313  
; Publication No. US20030129653A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP8MW18, EXPRESSED HIGH  
; FILE REFERENCE: D0048 CIP  
; CURRENT APPLICATION NUMBER: US/10/262,313  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: U.S. 09/992,331  
; PRIOR FILING DATE: 2001-11-14  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-262-313-26

Query Match 27.3%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5  
|||  
Db 1 QNF 3

## RESULT 53

```

US-10-305-346-1
; Sequence 1, Application US/10305346
; Publication No. US20030130195A1
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57*US*-1
; CURRENT APPLICATION NUMBER: US/10/305,346
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins
US-10-305-346-1

Query Match      27.3%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPQ 10
      |||
Db      2 LPQ 4

RESULT 54
US-09-821-380-9
; Sequence 9, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/????.???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-9

Query Match      27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPQ 10
      |||
Db      5 LPQ 7

RESULT 55
US-09-822-270-5
; Sequence 5, Application US/09822270
; Patent No. US20020068697A1
; GENERAL INFORMATION:
; APPLICANT: TOURNAIRE, ROSELYNE
; APPLICANT: DEMANGEL, CAROLINE
; APPLICANT: DERBIN, CLAUDE
; APPLICANT: PERRET, GERARD
; APPLICANT: MAZIE, JEAN-CLAUDE
; APPLICANT: PLOUET, JEAN
; APPLICANT: VASSAY, ROGER
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA
; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS
; FILE REFERENCE: 2050600US
; CURRENT APPLICATION NUMBER: US/09/822,270
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,396
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PPT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-822-270-5

Query Match      27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 YKL 8
      |||
Db      5 YKL 7

RESULT 56
US-09-749-234A-18
; Sequence 18, Application US/09749234A
; Patent No. US20020068817A1
; GENERAL INFORMATION:
; APPLICANT: HOFMANN, Joachim
; APPLICANT: SCHMID, Karlheirich
; APPLICANT: PAULI, Admette
; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
; TITLE OF INVENTION: DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,234A
; FILING DATE: 27-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/403,092
; FILING DATE: 199-10-15
; APPLICATION NUMBER: DE 197 15 586.3
; FILING DATE: 15-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 038311/0103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399

```

```
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-749-234A-18

Query Match          27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PON 4
Db 4 PON 6

RESULT 57
US-09-832-723-17
; Sequence 17, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides screened from a phage display random
; OTHER INFORMATION: Peptide library
US-09-832-723-17

Query Match          27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
Db 5 KLP 7

RESULT 58
US-09-832-723-68
; Sequence 68, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides screened from a phage display random
; OTHER INFORMATION: Peptide library
US-09-832-723-68

Query Match          27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
Db 5 KLP 7

RESULT 59
US-09-947-137-3
; Sequence 3, Application US/09947137
; Patent No. US20020137023A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Bruce F.
; APPLICANT: Samoilova, Tatiana
; TITLE OF INVENTION: Methods and Compositions for Targeting
; FILE REFERENCE: 5721-8
; CURRENT APPLICATION NUMBER: US/09/947,137
; CURRENT FILING DATE: 2001-09-05
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phage display library peptides
US-09-947-137-3

Query Match          27.3%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
Db 5 KLP 7

RESULT 60
US-09-771-415-13
; Sequence 13, Application US/09771415
; Patent No. US20020164326A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Koenig, Scott
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies
; FILE REFERENCE: 469201-520
; CURRENT APPLICATION NUMBER: US/09/771,415
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```



OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
 OTHER INFORMATION: sequence present in high affinity complementarity  
 OTHER INFORMATION: determining regions of antibodies of the invention  
 US-09-771-415-13

Query Match 27.3%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKL 8  
 |||  
 Db 3 YKL 5

RESULT 61  
 US-09-771-035A-5  
 ; Sequence 5, Application US/09771035A  
 ; Patent No. US20020165370A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KUMAGAI, Monto H.  
 ; APPLICANT: ROBERTS, Peter D.  
 ; APPLICANT: VAEWHONGS, Andy A.  
 ; TITLE OF INVENTION: CYTOPLASMIC GENE INHIBITION OR GENE  
 ; FILE REFERENCE: 008010137CPTS04  
 ; CURRENT APPLICATION NUMBER: US/09/771,035A  
 ; CURRENT FILING DATE: 2001-01-21  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: PCT/ US 00/20261  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Pea Early Browning Virus  
 US-09-771-035A-5

Query Match 27.3%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQ 3  
 |||  
 Db 1 MPQ 3

RESULT 62  
 US-09-771-035A-8  
 ; Sequence 6, Application US/09771035A  
 ; Patent No. US20020165370A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KUMAGAI, Monto H.  
 ; APPLICANT: ROBERTS, Peter D.  
 ; APPLICANT: VAEWHONGS, Andy A.  
 ; TITLE OF INVENTION: CYTOPLASMIC GENE INHIBITION OR GENE  
 ; FILE REFERENCE: 008010137CPTS04  
 ; CURRENT APPLICATION NUMBER: US/09/771,035A  
 ; CURRENT FILING DATE: 2001-01-21  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: PCT/ US 00/20261  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Nicotiana benthamiana  
 US-09-771-035A-8

Query Match 27.3%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQ 3  
 |||  
 Db 1 MPQ 3

RESULT 63  
 US-09-996-288-102  
 ; Sequence 102, Application US/09996288  
 ; Patent No. US20020177126A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi  
 ; FILE REFERENCE: 10271-047-999  
 ; CURRENT APPLICATION NUMBER: US/09/996,288  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 102  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-996-288-102

Query Match 27.3%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9  
 |||  
 Db 4 KLP 6

RESULT 64  
 US-09-996-288-118  
 ; Sequence 118, Application US/09996288  
 ; Patent No. US20020177126A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi  
 ; FILE REFERENCE: 10271-047-999  
 ; CURRENT APPLICATION NUMBER: US/09/996,288  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 118  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-996-288-118

Query Match 27.3%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9  
 |||  
 Db 4 KLP 6

RESULT 65  
 US-09-884-767A-23  
 ; Sequence 23, Application US/09884767A  
 ; Publication No. US20020192789A1

; GENERAL INFORMATION:  
 ; APPLICANT: DYAX Corp.  
 ; APPLICANT: Ley, Arthur C.  
 ; APPLICANT: Luneau, Christopher J.  
 ; APPLICANT: Ladner, Robert C.  
 ; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
 ; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
 ; CURRENT APPLICATION NUMBER: US/09/884,767A  
 ; CURRENT FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 09/597,321  
 ; PRIOR FILING DATE: 2000-06-19  
 ; NUMBER OF SEQ ID NOS: 217  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 23  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
 US-09-884-767A-23

Query Match 27.3%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 6e+05; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MPQ 3  
 DB 2 MPQ 4

## RESULT 66

US-09-229-751A-28  
 ; Sequence 28, Application US/09229751A  
 ; Publication No. US20030044838A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turbough, Charles K  
 ; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES  
 ; NUMBER OF SEQUENCES: 80  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Glenna Hendricks  
 ; STREET: P.O. Box 2509  
 ; CITY: Fairfax  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22031

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/09/229,751A  
 ; FILING DATE: 14-Jan-1999  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hendricks, Glenna M  
 ; REGISTRATION NUMBER: 32,535  
 ; REFERENCE/DOCKET NUMBER: turn  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 425-8405  
 ; TELEFAX: (703) 425-8406

; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; TYPE: amino acid  
 ; LENGTH: 7 amino acids  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
 US-09-229-751A-28

Query Match 27.3%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 6e+05; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 PQN 4  
 DB 5 PQN 7

## RESULT 67

US-09-845-612B-18  
 ; Sequence 18, Application US/09845612B  
 ; Publication No. US20030083261A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YU, HONGTAO  
 ; APPLICANT: TANG, XUELIAN  
 ; APPLICANT: LUO, XUELIAN  
 ; APPLICANT: RIZO-REY, JOSE  
 ; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOTIC  
 ; FILE REFERENCE: UTSID:795  
 ; CURRENT APPLICATION NUMBER: US/09/845,612B  
 ; CURRENT FILING DATE: 2001-04-27  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 18  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (4)..(5)  
 ; OTHER INFORMATION: X is any  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)..(7)  
 ; OTHER INFORMATION: Synthetic Peptide  
 US-09-845-612B-18

Query Match 27.3%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 6e+05; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 YKL 8  
 DB 2 YKL 4

## RESULT 68

US-09-996-265-102  
 ; Sequence 102, Application US/09996265  
 ; Publication No. US20030091584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi  
 ; FILE REFERENCE: 10271-048-999  
 ; CURRENT APPLICATION NUMBER: US/09/996,265  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 102  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-996-265-102

Query Match 27.3%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 6e+05; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KLP 9  
 Db 4 KLP 6

## RESULT 69

US-09-996-265-118  
 ; Sequence 118, Application US/09996265  
 ; Publication No. US20030091584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
 ; FILE REFERENCE: 10271-048-999  
 ; CURRENT APPLICATION NUMBER: US/09/996,265  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 118  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-996-265-118

Query Match 27.3%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 4 KLP 6

## RESULT 70

US-09-954-385-81  
 ; Sequence 81, Application US/09954385  
 ; Publication No. US20030100467A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aehle, Wolfgang  
 ; APPLICANT: Baldwin, Toby L.  
 ; APPLICANT: Van Gastel, Franciscus J.C.  
 ; APPLICANT: Janssen, Giselle G.  
 ; APPLICANT: Murray, Christopher J.  
 ; APPLICANT: Wang, Huang  
 ; APPLICANT: Winetzk, Deborah S.  
 ; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
 ; FILE REFERENCE: GC690  
 ; CURRENT APPLICATION NUMBER: US/09/954,385  
 ; CURRENT FILING DATE: 2001-09-12  
 ; NUMBER OF SEQ ID NOS: 433  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 81  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: binding peptide  
 US-09-954-385-81

Query Match 27.3%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 Db 1 LPQ 3

## RESULT 71

US-10-052-578-246  
 ; Sequence 246, Application US/10052578  
 ; Publication No. US20030134787A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloan-Kettering Institute for Cancer Research  
 ; APPLICANT: Rothman, James E.  
 ; APPLICANT: Mayhew, Mark  
 ; APPLICANT: Hoe, Mee H.  
 ; APPLICANT: Houghton, Alan  
 ; APPLICANT: Hartl, Ulrich  
 ; APPLICANT: Ouerfelli, Ouathhek  
 ; APPLICANT: Moroi, Yoichi  
 ; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
 ; FILE REFERENCE: 11746/46003  
 ; CURRENT APPLICATION NUMBER: US/10/052,578  
 ; CURRENT FILING DATE: 2002-01-17  
 ; PRIOR APPLICATION NUMBER: 08/961,707  
 ; PRIOR FILING DATE: 1997-10-31  
 ; NUMBER OF SEQ ID NOS: 321  
 ; SOFTWARE: WordPerfect 8.0 for Windows  
 ; SEQ ID NO 246  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: peptide in m13 coliphage  
 US-10-052-578-246

Query Match 27.3%; Score 3; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 1 KLP 3

## RESULT 72

US-10-303-331-17  
 ; Sequence 17, Application US/10303331  
 ; Publication No. US20030152976A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janssen, Giselle G.  
 ; APPLICANT: Murray, Christopher J.  
 ; APPLICANT: Winetzk, Deborah S.  
 ; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
 ; FILE REFERENCE: GC617-3  
 ; CURRENT APPLICATION NUMBER: US/10/303,331  
 ; CURRENT FILING DATE: 2002-11-25  
 ; PRIOR APPLICATION NUMBER: US 09/832,723  
 ; PRIOR FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: US 60/197,259  
 ; PRIOR FILING DATE: 2000-04-14  
 ; NUMBER OF SEQ ID NOS: 125  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: peptides screened from a phage display random  
 ; OTHER INFORMATION: peptide library  
 US-10-303-331-17

Query Match 27.3%; Score 3; DB 12; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 Db 5 KLP 7

## RESULT 73

```

US-10-303-331-68
; Sequence 68, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-68

```

```

Query Match      27.3%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MPQ 3
      |||
DB      1 MPQ 3

```

## RESULT 74

```

US-10-293-371-4
; Sequence 4, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-4

```

```

Query Match      27.3%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MPQ 3
      |||
DB      5 MPQ 7

```

## RESULT 75

```

US-10-293-371-7
; Sequence 7, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-7

```

```

Query Match      27.3%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MPQ 3
      |||
DB      5 MPQ 7

```

```

Search completed: November 25, 2003, 20:25:32
Job time : 22.883 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 11.9947 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-6  
Perfect score: 11  
Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

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4: /cgm2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgm2\_6/prodata/1/iaa/PCFUS\_COMB.pep:\*  
6: /cgm2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	4	US-09-641-803-6
2	4	36.4	7	2	US-08-968-676-69
3	4	36.4	7	2	US-08-968-676-102
4	4	36.4	9	1	US-08-787-547-101
5	4	36.4	9	4	US-08-492-543-73
6	4	36.4	9	4	US-09-492-543-101
7	4	36.4	10	1	US-07-797-692-5
8	4	36.4	10	2	US-08-310-912A-99
9	4	36.4	10	3	US-08-841-089-99
10	4	36.4	10	3	US-08-301-085-99
11	4	36.4	10	5	PCT-US95-04570-99
12	4	36.4	10	5	PCT-US95-04589-99
13	4	36.4	15	1	US-07-797-692-1
14	4	36.4	15	1	US-07-797-692-7
15	4	36.4	15	1	US-07-909-122-2
16	4	36.4	15	1	US-08-709-047-11
17	4	36.4	15	1	US-08-410-360-11
18	4	36.4	15	1	US-08-707-804A-11
19	4	36.4	15	1	US-08-709-006-11
20	4	36.4	15	1	US-08-711-175-11
21	4	36.4	15	2	US-07-950-571A-4
22	4	36.4	15	3	US-08-075-541D-4
23	4	36.4	16	1	US-08-110-300A-22
24	4	36.4	16	2	US-08-886-642-22
25	4	36.4	17	1	US-08-468-543-19
26	4	36.4	17	1	US-08-469-692-19
27	4	36.4	17	2	US-08-398-046-19

28	4	36.4	19	3	US-08-943-173-9	Sequence 9, Appli
29	4	36.4	20	2	US-08-934-915-158	Sequence 158, App
30	4	36.4	20	2	US-08-934-915-159	Sequence 159, App
31	3	27.3	4	2	US-08-667-001-6	Sequence 6, Appli
32	3	27.3	4	3	US-08-974-549A-182	Sequence 182, App
33	3	27.3	4	3	US-09-177-249-143	Sequence 143, App
34	3	27.3	4	6	5258287-45	Patent No. 5258287
35	3	27.3	5	1	US-08-014-979-41	Sequence 41, Appli
36	3	27.3	5	1	US-08-014-979-42	Sequence 42, Appli
37	3	27.3	5	2	US-08-447-010-22	Sequence 22, Appli
38	3	27.3	5	2	US-08-667-001-11	Sequence 11, Appli
39	3	27.3	5	3	US-08-981-122-4	Sequence 4, Appli
40	3	27.3	5	3	US-08-652-877-81	Sequence 81, Appli
41	3	27.3	5	3	US-08-476-515A-81	Sequence 81, Appli
42	3	27.3	5	4	US-09-381-244B-17	Sequence 17, Appli
43	3	27.3	5	4	US-08-766-596A-31	Sequence 31, Appli
44	3	27.3	5	4	US-09-043-877-21	Sequence 21, Appli
45	3	27.3	6	1	US-08-106-493A-3	Sequence 3, Appli
46	3	27.3	6	1	US-08-429-264-3	Sequence 3, Appli
47	3	27.3	6	1	US-08-260-199A-27	Sequence 27, Appli
48	3	27.3	6	1	US-08-532-065B-5	Sequence 5, Appli
49	3	27.3	6	1	US-07-923-724-62	Sequence 62, Appli
50	3	27.3	6	2	US-08-609-426A-62	Sequence 62, Appli
51	3	27.3	6	2	US-08-374-652C-57	Sequence 57, Appli
52	3	27.3	6	2	US-08-377-432-38	Sequence 38, Appli
53	3	27.3	6	2	US-08-968-676-24	Sequence 24, Appli
54	3	27.3	6	2	US-08-819-444-3	Sequence 3, Appli
55	3	27.3	6	2	US-08-819-444-5	Sequence 5, Appli
56	3	27.3	6	3	US-09-186-934-6	Sequence 6, Appli
57	3	27.3	6	3	US-08-803-346-76	Sequence 76, Appli
58	3	27.3	6	4	US-09-155-613A-36	Sequence 36, Appli
59	3	27.3	6	4	US-09-581-944A-30	Sequence 30, Appli
60	3	27.3	6	4	US-08-000-286A-2	Sequence 2, Appli
61	3	27.3	6	4	US-08-469-260A-208	Sequence 208, App
62	3	27.3	6	4	US-08-469-260A-335	Sequence 335, App
63	3	27.3	6	4	US-09-492-766-1	Sequence 1, Appli
64	3	27.3	6	4	US-08-900-241-38	Sequence 38, Appli
65	3	27.3	6	4	US-09-209-676-40	Sequence 40, Appli
66	3	27.3	6	4	US-09-555-352-26	Sequence 26, Appli
67	3	27.3	6	4	US-08-488-446-208	Sequence 208, App
68	3	27.3	6	4	US-08-488-446-335	Sequence 335, App
69	3	27.3	6	4	US-08-467-344A-208	Sequence 208, App
70	3	27.3	6	4	US-08-467-344A-335	Sequence 335, App
71	3	27.3	6	5	PCT-US93-01669-10	Sequence 26, Appli
72	3	27.3	7	1	US-08-127-499A-10	Sequence 10, Appli
73	3	27.3	7	1	US-08-482-847-10	Sequence 14, Appli
74	3	27.3	7	1	US-08-537-069-14	Sequence 14, Appli
75	3	27.3	7	2	US-08-177-109A-5	Sequence 5, Appli
76	3	27.3	7	2	US-08-893-853-72	Sequence 72, Appli
77	3	27.3	7	2	US-08-893-853-76	Sequence 76, Appli
78	3	27.3	7	2	US-08-893-853-78	Sequence 78, Appli
79	3	27.3	7	2	US-08-893-853-81	Sequence 81, Appli
80	3	27.3	7	2	US-08-968-676-4	Sequence 4, Appli
81	3	27.3	7	2	US-08-968-676-22	Sequence 22, Appli
82	3	27.3	7	2	US-08-968-676-23	Sequence 23, Appli
83	3	27.3	7	2	US-08-968-676-34	Sequence 34, Appli
84	3	27.3	7	2	US-08-968-676-35	Sequence 35, Appli
85	3	27.3	7	2	US-08-968-676-36	Sequence 36, Appli
86	3	27.3	7	2	US-08-968-676-37	Sequence 37, Appli
87	3	27.3	7	2	US-08-968-676-38	Sequence 38, Appli
88	3	27.3	7	2	US-08-968-676-39	Sequence 39, Appli
89	3	27.3	7	2	US-08-968-676-40	Sequence 40, Appli
90	3	27.3	7	2	US-08-968-676-41	Sequence 41, Appli
91	3	27.3	7	2	US-08-968-676-42	Sequence 42, Appli
92	3	27.3	7	2	US-08-968-676-43	Sequence 43, Appli
93	3	27.3	7	2	US-08-968-676-44	Sequence 44, Appli
94	3	27.3	7	2	US-08-968-676-59	Sequence 59, Appli
95	3	27.3	7	2	US-08-968-676-60	Sequence 60, Appli
96	3	27.3	7	2	US-08-968-676-61	Sequence 61, Appli
97	3	27.3	7	2	US-08-968-676-62	Sequence 62, Appli
98	3	27.3	7	2	US-08-968-676-63	Sequence 63, Appli
99	3	27.3	7	2	US-08-968-676-64	Sequence 64, Appli
100	3	27.3	7	2	US-08-968-676-65	Sequence 65, Appli

## ALIGNMENTS

## RESULT 1

US-09-641-803-6  
 ; Sequence 6, Application US/09641803  
 ; Patent No. 6500798  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/09/641.803  
 ; CURRENT FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-641-803-6

Query Match 100.0%; Score 11; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11  
 |||||  
 DB 1 MPQNFYKLPQM 11

## RESULT 2

US-08-968-676-69  
 ; Sequence 69, Application US/08968676  
 ; Patent No. 5913639  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Humphreys, Robert E  
 ; APPLICANT: Adams, Shariene  
 ; APPLICANT: Xu, Minzhen  
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
 ; NUMBER OF SEQUENCES: 165  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kevin M. Farrell, P.C.  
 ; STREET: P.O. Box 999  
 ; CITY: York Harbor  
 ; STATE: ME  
 ; COUNTRY: USA  
 ; ZIP: 03911  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Farrell, Kevin M  
 ; REGISTRATION NUMBER: 35,505  
 ; REFERENCE/DOCKET NUMBER: REH-9601  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (207) 363-0558  
 ; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 69:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-968-676-69

Query Match 36.4%; Score 4; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLP 9  
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 DB 3 YKLP 6

## RESULT 3

US-08-968-676-102  
 ; Sequence 102, Application US/08968676  
 ; Patent No. 5913639  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Humphreys, Robert E  
 ; APPLICANT: Adams, Shariene  
 ; APPLICANT: Xu, Minzhen  
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
 ; NUMBER OF SEQUENCES: 165  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kevin M. Farrell, P.C.  
 ; STREET: P.O. Box 999  
 ; CITY: York Harbor  
 ; STATE: ME  
 ; COUNTRY: USA  
 ; ZIP: 03911  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Farrell, Kevin M  
 ; REGISTRATION NUMBER: 35,505  
 ; REFERENCE/DOCKET NUMBER: REH-9601  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (207) 363-0558  
 ; TELEFAX: (207) 363-0528  
 ; INFORMATION FOR SEQ ID NO: 102:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-968-676-102

Query Match 36.4%; Score 4; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10  
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 DB 4 KLPQ 7

## RESULT 4

US-08-787-547-101  
 ; Sequence 101, Application US/08787547  
 ; Patent No. 5783567

```

; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Gurley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-787-547-101

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Query Match 36.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

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QY 7 KLPQ 10
Db 1 KLPQ 4

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RESULT 5
US-09-492-543-73
; Sequence 73, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B
; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
; US-09-492-543-73

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Query Match 36.4%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 2 PQNF 5
Db 4 PQNF 7

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```

RESULT 6
US-09-492-543-101
; Sequence 101, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B
; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
; US-09-492-543-101

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Query Match 36.4%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 2 PQNF 5
Db 4 PQNF 7

```

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RESULT 7
US-07-797-692-5
; Sequence 5, Application US/07797692
; Patent No. 5266478
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C.; Sun, Cecily R.Y.; Sun, Bill N.C.
; TITLE OF INVENTION: Products which target a Neutralization Site Within the Second
; TITLE OF INVENTION: Region of Human Immunodeficiency Virus Type 1 gp120
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,692
; FILING DATE: 19911125
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/767,533; 07/692,299
; FILING DATE: 9/26/1991; 4/25/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211

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REFERENCE/DOCKET NUMBER: TXN91-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 664-2288  
TELEFAX: (713) 664-8914  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-797-692-5

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8  
Db 3 FYKL 6

RESULT 8  
US-08-310-912A-99  
; Sequence 99, Application US/08310912A  
; Patent No. 5981730  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RP52 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
; NUMBER OF SEQUENCES: 208  
; TITLE OF INVENTION: METHODS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; FILING DATE: September 22, 1994  
; APPLICATION NUMBER: US/08/310,912A  
; CLASSIFICATION: S36  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/227,360  
; FILING DATE: April 13, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lech, Karen F.  
; REGISTRATION NUMBER: 35,238  
; REFERENCE/DOCKET NUMBER: 00786/254001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-310-912A-99

Query Match 36.4%; Score 4; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 KLPQ 10  
Db 6 KLPQ 9

RESULT 9  
US-08-841-089-99  
; Sequence 99, Application US/08841089  
; Patent No. 6127607  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RP52 GENE AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/841,089  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,360  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/230001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-841-089-99

Query Match 36.4%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 KLPQ 10  
Db 6 KLPQ 9

RESULT 10  
US-09-301-085-99  
; Sequence 99, Application US/09301085  
; Patent No. 6262248  
; GENERAL INFORMATION:



```

; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER FILING DATE: 1994-09-22
; EARLIER FILING DATE: 1994-09-22
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-99

```

```

Query Match          36.4%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 KLPQ 10
        ||||
Db      6 KLPQ 9

```

```

RESULT 11
PCT-US95-04570-99
; Sequence 99, Application PC/TUS9504570
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04570-99

```

```

Query Match          36.4%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04570-99

```

```

Query Match          36.4%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 KLPQ 10
        ||||
Db      6 KLPQ 9

```

```

RESULT 12
PCT-US95-04589-99
; Sequence 99, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 201
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04589-99

```

```

Query Match          36.4%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 KLPQ 10  
 Db ||||  
 6 KLPQ 9

## RESULT 13

US-07-797-692-1  
 ; Sequence 1, Application US/07797692  
 ; Patent No. 5266478  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fung, Michael S.C.; Sun, Cecily R.Y.; Sun, Bill N.C.  
 ; TITLE OF INVENTION: Products which target a Neutralization Site within the Second  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Tanox Biosystems, Inc.  
 ; STREET: 10301 Stella Link Rd.  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77025  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: DOS 3.30  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/797,692  
 ; FILING DATE: 19911125  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/767,533; 07/692,299  
 ; FILING DATE: 9/26/1991; 4/25/91  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mirabel, Eric P.  
 ; REGISTRATION NUMBER: 31,211  
 ; REFERENCE/DOCKET NUMBER: TNX91-6  
 ; TELEPHONE: (713) 664-2288  
 ; TELEFAX: (713) 664-8914  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; US-07-797-692-1

Query Match 36.4%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
 Db ||||  
 8 FYKL 11

## RESULT 14

US-07-797-692-7  
 ; Sequence 7, Application US/07797692  
 ; Patent No. 5266478  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fung, Michael S.C.; Sun, Cecily R.Y.; Sun, Bill N.C.  
 ; TITLE OF INVENTION: Products which target a Neutralization Site within the Second  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Tanox Biosystems, Inc.  
 ; STREET: 10301 Stella Link Rd.  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77025

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: DOS 3.30  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/797,692  
 ; FILING DATE: 19911125  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/767,533; 07/692,299  
 ; FILING DATE: 9/26/1991; 4/25/91  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mirabel, Eric P.  
 ; REGISTRATION NUMBER: 31,211  
 ; REFERENCE/DOCKET NUMBER: TNX91-6  
 ; TELEPHONE: (713) 664-2288  
 ; TELEFAX: (713) 664-8914  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; US-07-797-692-7

Query Match 36.4%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
 Db ||||  
 8 FYKL 11

## RESULT 15

US-07-909-122-2  
 ; Sequence 2, Application US/07909122  
 ; Patent No. 5415995  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SCHOOLNIK, GARY K.  
 ; APPLICANT: PALEFSKY, JOEL M.  
 ; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA  
 ; TITLE OF INVENTION: VIRUS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/909,122  
 ; FILING DATE: 19920706  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENZ, WILLIAM H.  
 ; REGISTRATION NUMBER: 25,952  
 ; REFERENCE/DOCKET NUMBER: 28600-20105.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: AMINO ACID

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-2

Query Match          36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 10 KLPQ 13

RESULT 16
US-08-709-047-11
; Sequence 11, Application US/08709047
; Patent No. 5652333
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Limiting
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,047
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TXN95-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-709-047-11

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,047
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/410,360
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirabel, Eric P.
REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TXN95-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 664-2288
TELEFAX: (713) 664-8914
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-709-047-11

Query Match          36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
DB 8 FYKL 11

RESULT 17
US-08-410-360-11
; Sequence 11, Application US/08410360
; Patent No. 5691447
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Limiting
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,

```

```

; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TXN95-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-410-360-11

Query Match          36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
DB 8 FYKL 11

RESULT 18
US-08-707-801A-11
; Sequence 11, Application US/08707801A
; Patent No. 5728814
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Limiting
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,801A
; FILING DATE: 09/04/1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE: 03/24/1995

```

ATTORNEY/AGENT INFORMATION:  
 NAME: Mirabel, Eric P.  
 REGISTRATION NUMBER: 31,211  
 REFERENCE/DOCKET NUMBER: TNX95-1A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (713) 664-2288  
 TELEFAX: (713) 664-8914  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-707-801A-11

Query Match 36.4%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
 ||||  
 DB 8 FYKL 11

RESULT 19  
 US-08-709-006-11  
 Sequence 11, Application US/08709006  
 Patent No. 5731428  
 GENERAL INFORMATION:  
 APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y.,  
 TITLE OF INVENTION: THE 9C1q RECEPTOR, HIV-1 gp120 REGION BINDING  
 TITLE OF INVENTION: THERETO, AND RELATED PEPTIDES AND TARGETING  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Tanox Biosystems, Inc.  
 STREET: 10301 Stella Link Rd.  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77025

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: DOS 3.30  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/709,006  
 FILING DATE: 09-SEP-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/410,360  
 FILING DATE: 24-MAR-1995  
 NAME: Mirabel, Eric P.  
 REGISTRATION NUMBER: 31,211  
 REFERENCE/DOCKET NUMBER: TNX95-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (713) 664-2288  
 TELEFAX: (713) 664-8914  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-709-006-11

Query Match 36.4%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
 ||||

DB 8 FYKL 11

RESULT 20  
 US-08-711-175-11  
 Sequence 11, Application US/08711175  
 Patent No. 5739306  
 GENERAL INFORMATION:  
 APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y.,  
 TITLE OF INVENTION: THE 9C1q RECEPTOR, HIV-1 gp120 REGION BINDING  
 TITLE OF INVENTION: THERETO, AND RELATED PEPTIDES AND TARGETING  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Tanox Biosystems, Inc.  
 STREET: 10301 Stella Link Rd.  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77025

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: DOS 3.30  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/711,175  
 FILING DATE: 09-SEP-1996  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/410,360  
 FILING DATE: 24-MAR-1995  
 NAME: Mirabel, Eric P.  
 REGISTRATION NUMBER: 31,211  
 REFERENCE/DOCKET NUMBER: TNX95-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (713) 664-2288  
 TELEFAX: (713) 664-8914  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-711-175-11

Query Match 36.4%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
 ||||  
 DB 8 FYKL 11

RESULT 21  
 US-07-950-571A-4  
 Sequence 4, Application US/07950571A  
 Patent No. 5854400  
 GENERAL INFORMATION:  
 APPLICANT: Chang, Tee Wen, Fung, Michael S.C., Sun, Bill N.C., Sun, Cecily R.Y.,  
 TITLE OF INVENTION: Monoclonal Antibodies which Neutralize HIV-1 Infection  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Tanox Biosystems, Inc.  
 STREET: 10301 Stella Link Rd.  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77025

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: 3.5" Hi Density Diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS, Version 3.30
; SOFTWARE: Roxio-Soft 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/950.571A
; FILING DATE: 19920922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5854400 07/767.533
; FILING DATE: 09/26/1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX87-11BBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-664-2288
; TELEFAX: 713-664-8914
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; US-07-950-571A-4

```

```

Query Match          36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

```

QY 5 FYKL 8
DB 8 FYKL 11

```

```

RESULT 22
US-08-075-541D-52
; Sequence 52, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAITICH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

```

```

; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-075-541D-52

```

```

Query Match          36.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 KLPQ 10
DB 10 KLPQ 13

```

```

RESULT 23
US-08-110-300A-22
; Sequence 22, Application US/08110300A
; Patent No. 5643756
; GENERAL INFORMATION:
; APPLICANT: Pitter, Abraham
; APPLICANT: Kanner, Samuel
; TITLE OF INVENTION: FUSION GLYCOPROTEINS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davis Hoxie Faithfull and Hapgood
; STREET: 45 Rockefeller Pl.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,300A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H.
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER: 11698A50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-757-2200
; TELEFAX: 212-586-1461
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..16
; OTHER INFORMATION: /note= "An analogous peptide
; OTHER INFORMATION: matching the consensus sequence for HXB2d V2
; OTHER INFORMATION: domain and homologs with an additional C-terminal
; OTHER INFORMATION:
; OTHER INFORMATION: and AIDS database (ADP 794.1)."
; US-08-110-300A-22

```

```

Query Match          36.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 FYKL 8  
Db 12 FYKL 15

RESULT 24  
US-08-886-642-22  
; Sequence 22, Application US/08886642  
; Patent No. 5952474  
; GENERAL INFORMATION:  
; APPLICANT: Pinter, Abraham  
; APPLICANT: Kayman, Samuel  
; TITLE OF INVENTION: FUSION GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 45 Rockefeller Plaza, Suite 2800  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/886,642  
; FILING DATE: 01-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/110,300  
; FILING DATE: 20-AUG-1993  
; APPLICATION NUMBER: 07/938,100  
; FILING DATE: 28-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hone, William J.  
; REGISTRATION NUMBER: 26,739  
; REFERENCE/DOCKET NUMBER: 07763/010002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212/765-5070  
; TELEFAX: 212/258-2291  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; LOCATION: 1..16  
; OTHER INFORMATION: /note= "An analogous peptide matching the  
; OTHER INFORMATION: consensus sequence for HXB2d V2 domain and homologs with an  
; OTHER INFORMATION: additional C-terminal (Cys) as defined in the Los Alamos Human  
; OTHER INFORMATION: Retrovirus and AIDS database (ADP 794.11.""  
US-08-886-642-22

Query Match 36.4%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8  
Db 12 FYKL 15

RESULT 25  
US-08-468-543-19  
; Sequence 19, Application US/08468543  
; Patent No. 5726153  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Robert S. et al.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING  
; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,543  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/398,046  
; FILING DATE: 02-MAR-1995  
; PRIOR APPLICATION NUMBER: US 08/201,057  
; FILING DATE: 24-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/048,569  
; FILING DATE: 16-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/694,929  
; FILING DATE: 02-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,215  
; FILING DATE: 03-MAY-1990  
; PRIOR APPLICATION NUMBER: US 07/189,130  
; FILING DATE: 02-MAY-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 04547/002003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-468-543-19

Query Match 36.4%; Score 4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10  
Db 1 KLPQ 4

RESULT 26  
US-08-469-692-19  
; Sequence 19, Application US/08469692  
; Patent No. 5955055  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Robert S. et al.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street

```

; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,692
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/398,046
; FILING DATE: 02-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,057
; FILING DATE: 24-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/048,569
; FILING DATE: 16-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/694,929
; FILING DATE: 02-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,215
; FILING DATE: 03-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,142
; FILING DATE: 03-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/189,130
; FILING DATE: 02-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04547/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-469-692-19

Query Match 36.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
Db 1 KLPQ 4

RESULT 27
US-08-398-046-19
; Sequence 19, Application US/08398046
; Patent No. 5972890
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S. et al.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR
; TITLE OF INVENTION: ARTERIAL IMAGING
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

```

```

; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,046
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,057
; FILING DATE:
; APPLICATION NUMBER: US/08/048,569
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/694,929
; APPLICATION NUMBER: 07/517,215
; FILING DATE: May 3, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/518,142
; FILING DATE: May 3, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/189,130
; FILING DATE: May 2, 1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04547/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-398-046-19

Query Match 36.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
Db 1 KLPQ 4

RESULT 28
US-08-943-173-9
; Sequence 9, Application US/08943173
; Patent No. 6048538
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Shen, Fan
; APPLICANT: Chen, Pei De
; TITLE OF INVENTION: PEPTIDES DERIVED
; TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF
; TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,173  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lin, Maria C.H.  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4152  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-943-173-9

Query Match 36.4%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
|||  
Db 5 KLPQ 8

RESULT 29  
US-08-934-915-158  
; Sequence 158, Application US/08934915  
; Patent No. 5932412  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; APPLICANT: DILLNER, LENA  
; APPLICANT: CHENG, HWEE-MING  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,  
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
; NUMBER OF SEQUENCES: 193  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MASON & ASSOCIATES, P.A.  
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
; CITY: CLEARWATER  
; STATE: FLORIDA  
; COUNTRY: U.S.A.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 3.0  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,915  
; FILING DATE: 22-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: 07/949,836  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LOUISE A. FOUTCH  
; REGISTRATION NUMBER: 37,133  
; REFERENCE/DOCKET NUMBER: 1946.6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 813-538-3800  
; TELEFAX: 813-538-3820  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-934-915-158

LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-158  
Query Match 36.4%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
|||  
Db 17 KLPQ 20

RESULT 30  
US-08-934-915-159  
; Sequence 159, Application US/08934915  
; Patent No. 5932412  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; APPLICANT: DILLNER, LENA  
; APPLICANT: CHENG, HWEE-MING  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,  
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
; NUMBER OF SEQUENCES: 193  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MASON & ASSOCIATES, P.A.  
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
; CITY: CLEARWATER  
; STATE: FLORIDA  
; COUNTRY: U.S.A.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 3.0  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,915  
; FILING DATE: 22-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: 07/949,836  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LOUISE A. FOUTCH  
; REGISTRATION NUMBER: 37,133  
; REFERENCE/DOCKET NUMBER: 1946.6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 813-538-3800  
; TELEFAX: 813-538-3820  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 159:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-934-915-159

Query Match 36.4%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10  
|||  
Db 2 KLPQ 5

RESULT 31



US-08-667-001-6  
; Sequence 6, Application US/08667001  
; Patent No. 5827827  
; GENERAL INFORMATION:  
; APPLICANT: Janda, Kim D.  
; APPLICANT: Wirsching, Peter  
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,001  
; FILING DATE: 20-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/335,039  
; FILING DATE: 16-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lewis, Donald G.  
; REGISTRATION NUMBER: 28,636  
; REFERENCE/DOCKET NUMBER: TSRI 282.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "sequence = Y1 in formula  
; OTHER INFORMATION: (III A) and (III B)"  
US-08-667-001-6  
Query Match 27.3%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 QNF 5  
DB 2 QNF 4  
RESULT 32  
US-08-974-549A-182  
; Sequence 182, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 182:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-974-549A-182  
Query Match 27.3%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 NPY 6  
DB 2 NPY 4  
RESULT 33  
US-09-177-249-143  
; Sequence 143, Application US/09177249  
; Patent No. 6229064

```

; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramon
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; US-09-177-249-143

```

```

Query Match      27.3%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      4 NFY 6
Db      1 NFY 3

```

```

RESULT 34
5258287-45
; Patent No. 5258287
; APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.
; TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
; OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
; NUMBER OF SEQUENCES: 58
; CURRENT APPLICATION DATA:
; APPLICANT: Lam, Kit S. et al.
; FILING DATE: 22-MAR-1988
; SEQ ID NO:45:
; LENGTH: 4
5258287-45

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```

Query Match      27.3%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 FYK 7
Db      2 FYK 4

```

```

RESULT 35
US-08-014-979-41
; Sequence 41, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-014-979-41

```

```

Query Match      27.3%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 PQN 4
Db      3 PQN 5

```

```

RESULT 36
US-08-014-979-42
; Sequence 42, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

```

; MOLECULE TYPE: peptide  
US-08-014-979-42

Query Match 27.3%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4  
|||  
DB 3 PQN 5

RESULT 37  
US-08-447-010-22  
; Sequence 22, Application US/08447010  
; Patent No. 5770718  
; GENERAL INFORMATION:  
; APPLICANT: MOFFATT, BARBARA  
; TITLE OF INVENTION: GENE FOR APPT FROM PLANT TISSUE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SIM & MCBURNEY  
; STREET: 330 University Avenue, Suite 701  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,010  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION NUMBER: US 08/230,695  
; FILING DATE: 21-APR-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION NUMBER: US 07/888,132  
; APPLICATION NUMBER: 24,973  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, MICHAEL I  
; REGISTRATION NUMBER: 1811-183 MIS:vg  
; REFERENCE/DOCKET NUMBER: 1811-183 MIS:vg  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; TELEX: 065-24567 SIMBAS  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-08-447-010-22

Query Match 27.3%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
|||  
DB 1 KLP 3

RESULT 38  
US-08-667-001-11  
; Sequence 11, Application US/08667001

; Patent No. 5827827  
; GENERAL INFORMATION:  
; APPLICANT: Janda, Kim D.  
; APPLICANT: Wirsching, Peter  
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,001  
; FILING DATE: 20-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: US 08/335,039  
; FILING DATE: 16-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lewis, Donald G.  
; REGISTRATION NUMBER: 28,636  
; REFERENCE/DOCKET NUMBER: TSRI 282.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "sequence = Y1 in formula  
; OTHER INFORMATION: (III A) and (III B)"  
US-08-667-001-11

Query Match 27.3%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5  
|||  
DB 3 QNF 5

RESULT 39  
US-08-981-122-4  
; Sequence 4, Application US/08981122B  
; Patent No. 6127339  
; GENERAL INFORMATION:  
; APPLICANT: Hatanaka, Yoshihiro  
; APPLICANT: Arizumi, Masaharu  
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/981,122B  
; CURRENT FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: JP 7-176904  
; PRIOR FILING DATE: 1995-06-21  
; PRIOR APPLICATION NUMBER: PCT/Jp96/01734  
; PRIOR FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4

LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form  
Patent No. 6127339  
OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide  
US-08-981-122-4

Query Match 27.3%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
|||  
Db 2 FYK 4

RESULT 40  
US-08-652-877-81  
; Sequence 81, Application US/08652877  
; Patent No. 6187548  
; GENERAL INFORMATION:  
; APPLICANT: Akerstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjalms, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Rd., 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.5.1  
; SOFTWARE: Word 6.0 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,877  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15203  
; FILING DATE: 22-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,314  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355E-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 81:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO  
; FRAGMENT TYPE: Internal  
US-08-652-877-81  
Query Match 27.3%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 KLP 9  
|||  
Db 3 KLP 5

RESULT 41  
US-08-476-515A-81  
; Sequence 81, Application US/08476515A  
; Patent No. 6239270  
; GENERAL INFORMATION:  
; APPLICANT: Akerstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjalms, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Martin Savitzky  
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
; STREET: 3C43,  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Compaq PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 7.0 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,515A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/SE94/00483  
; FILING DATE: 24-MAY-1993  
; APPLICATION NUMBER: SE 9301764-8  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 81:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: Internal  
US-08-476-515A-81

Query Match 27.3%; Score 3; DB 3; Length 5;

```

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 3 KLP 5

RESULT 42
US-09-381-244B-17
; Sequence 17, Application US/09381244B
; Patent No. 6462170
; GENERAL INFORMATION:
; APPLICANT: BLASI, Francesco
; APPLICANT: FAZIOI, Francesca
; APPLICANT: RESNATI, Massimo
; APPLICANT: NICOLAI, Sidenius
; TITLE OF INVENTION: UPAR Mimicking Peptide
; FILE REFERENCE: 0471-0143P
; CURRENT APPLICATION NUMBER: US/09/381,244B
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/EP98/01547
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide analogue of the human uPAR
US-09-381-244B-17

Query Match 27.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
DB 1 PQN 3

RESULT 43
US-08-766-596A-31
; Sequence 31, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3538
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-31

Query Match 27.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 1 KLP 3

RESULT 44
US-09-043-877-21
; Sequence 21, Application US/09043877
; Patent No. 6495314
; GENERAL INFORMATION:
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Muir, Tom W.
; APPLICANT: Dawson, Philip E.
; APPLICANT: Fitzgerald, Michael C.
; TITLE OF INVENTION: PROTEIN SIGNATURE ANALYSIS
; FILE REFERENCE: GRY0039S
; CURRENT APPLICATION NUMBER: US/09/043,877
; CURRENT FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PCT/US96/15516
; PRIOR FILING DATE: 1996-09-27
; PRIOR APPLICATION NUMBER: 60/004,563
; PRIOR FILING DATE: 1995-09-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
US-09-043-877-21

Query Match 27.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
DB 1 YKL 3

RESULT 45
US-08-106-493A-3
; Sequence 3, Application US/08106493A
; Patent No. 5457049
; GENERAL INFORMATION:
; APPLICANT: Antonio Giordano
; TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRE2,

```

;; TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Temple University of the Commonwealth  
;; STREET: System of Higher Education  
;; CITY: Philadelphia  
;; STATE: Pennsylvania  
;; COUNTRY: U.S.A.  
;; ZIP: 19122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: WordPerfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/106,493A  
;; FILING DATE: August 12, 1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mullins, J.G.  
;; REGISTRATION NUMBER: 33,073  
;; REFERENCE/DOCKET NUMBER: 6056-188  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-8383  
;; TELEFAX: (215) 568-5549  
;; TELEX: No. 5457049e  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; TYPE: amino acid  
;; LENGTH: 6 amino acids  
;; TOPOLOGY: linear  
;; US-08-106-493A-3

Query Match 27.3%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7  
Db 1 FYK 3

RESULT 46  
US-08-429-264-3  
; Sequence 3, Application US/08429264  
; Patent No. 5532340  
; GENERAL INFORMATION:  
; APPLICANT: Antonio Giordano  
; TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN"  
; TITLE OF INVENTION: PRE2"  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavoragna & Monaco, P.C.  
; STREET: 1800 Two Penn Center Plaza  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/429,264  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/106,493  
;; FILING DATE: August 12, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Monaco, D.A.  
;; REGISTRATION NUMBER: 30,480  
;; REFERENCE/DOCKET NUMBER: 6056-188 D11  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-8383  
;; TELEFAX: (215) 568-5549  
;; TELEX: No. 5532340e  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-429-264-3

Query Match 27.3%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7  
Db 1 FYK 3

RESULT 47  
US-08-260-199A-27  
; Sequence 27, Application US/08260199A  
; Patent No. 5738996  
; GENERAL INFORMATION:  
; APPLICANT: Hodges, Robert S.  
; APPLICANT: Irvin, Randall T.  
; APPLICANT: Holm, A  
; APPLICANT: Wong, W.Y.  
; APPLICANT: Sheth, H.B.  
; APPLICANT: Husband, Devon L.  
; TITLE OF INVENTION: Combinatorial Library Composition and  
; TITLE OF INVENTION: Method  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/260,199A  
; FILING DATE: 15-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dehlinger, Peter J.  
; REGISTRATION NUMBER: 28,006  
; REFERENCE/DOCKET NUMBER: 8900-0008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

	ORIGINAL SOURCE:	QNFIPK peptide, . 15			
	INDIVIDUAL ISOLATE:	QNFIPK peptide, . 15			
	US-08-260-199A-27				
	Query Match	27.3%; Score 3; DB 1; Length 6;			
	Best Local Similarity	100.0%; Pred.No. 2.5e+05;			
	Matches	3; Conservative 0; Mismatches 0; Indels 0;			
	Gaps	0;			
QY	3 QNF 5				
DB	1 QNF 3				
RESULT 48					
US-08-532-065B-5					
; Sequence 5, Application US/08532065B					
; Patent No. 5753507					
; GENERAL INFORMATION:					
; APPLICANT: Ohta, Daisaku					
; APPLICANT: Mizutani, Masaharu					
; TITLE OF INVENTION: Plant Geraniol/Nerol 10-Hydroxylase and					
; TITLE OF INVENTION: DNA Coding Therefor					
; NUMBER OF SEQUENCES: 6					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: No. 5753507artis Corporation					
; STREET: 59 Route 10					
; CITY: East Hanover					
; STATE: NJ					
; COUNTRY: USA					
; ZIP: 07936					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: Patentin Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/532.065B					
; FILING DATE: 22-SEP-1995					
; CLASSIFICATION: 800					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Meigs, J. Timothy					
; REGISTRATION NUMBER: 38,241					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: 919-541-8587					
; TELEFAX: 919-541-8689					
; INFORMATION FOR SEQ ID NO: 5:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 6 amino acids					
; TYPE: amino acid					
; STRANDEDNESS: single					
; TOPOLOGY: not relevant					
; MOLECULE TYPE: peptide					
US-08-532-065B-5					
Query Match	27.3%; Score 3; DB 1; Length 6;				
Best Local Similarity	100.0%; Pred.No. 2.5e+05;				
Matches	3; Conservative 0; Mismatches 0; Indels 0;				
Gaps	0;				
QY	7 KLP 9				
DB	1 KLP 3				
RESULT 49					
US-07-923-724-62					
; Sequence 62, Application US/07923724					
; Patent No. 5780292					
; GENERAL INFORMATION:					
; APPLICANT: Nevalainen, Helena K.M.					
; APPLICANT: Paloheimo, Marja T.					
; APPLICANT: Mieltinen-Oinonen, Arja S.K.					
; APPLICANT: Toikkeli, Tuula K.					
; APPLICANT: Cantrell, Michael					
US-07-923-724-62					
Query Match	27.3%; Score 3; DB 1; Length 6;				
Best Local Similarity	100.0%; Pred.No. 2.5e+05;				
Matches	3; Conservative 0; Mismatches 0; Indels 0;				
Gaps	0;				
QY	7 KLP 9				
DB	1 KLP 3				
RESULT 50					
US-08-609-426A-62					
; Sequence 62, Application US/08609426A					
; Patent No. 5830733					
; GENERAL INFORMATION:					
; APPLICANT: Nevalainen, Helena K.M.					
; APPLICANT: Paloheimo, Marja T.					
; APPLICANT: Mieltinen-Oinonen, Arja S.K.					
; APPLICANT: Toikkeli, Tuula K.					
; APPLICANT: Cantrell, Michael					
; APPLICANT: Piddington, Christopher S.					
; APPLICANT: Rambossek, John A.					
; APPLICANT: Turunen, Maria K.					
; APPLICANT: Egerstr m, Richard B.					
; APPLICANT: Houston, Christine S.					
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes					
; TITLE OF INVENTION: in Trichoderma					
; NUMBER OF SEQUENCES: 69					
US-07-923-724-62					
Query Match	27.3%; Score 3; DB 1; Length 6;				
Best Local Similarity	100.0%; Pred.No. 2.5e+05;				
Matches	3; Conservative 0; Mismatches 0; Indels 0;				
Gaps	0;				
QY	8 LPQ 10				</

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-609-426A-62

Query Match 27.3%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQ 10
Db 2 LPQ 4

RESULT 51
US-08-374-652C-57
; Sequence 57, Application US/08374652C
; Patent No. 584286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON

```

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STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-374-652C-57

Query Match 27.3%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQ 10
Db 2 LPQ 4

RESULT 52
US-08-377-432-38
; Sequence 38, Application US/08377432
; Patent No. 5854202
; GENERAL INFORMATION:
; APPLICANT: DEDHAR, Shoukat
; TITLE OF INVENTION: NOVEL USE OF CALRETICULIN IN MODULATING
; TITLE OF INVENTION: HORMONE RESPONSIVENESS AND NEW PHARMACEUTICALS FOR
; TITLE OF INVENTION: TREATING CANCER, OSTEOPOROSIS AND CHRONIC INFLAMMATORY
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,432
FILING DATE: 24-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

```



NAME: Mool, Leslie A  
 REGISTRATION NUMBER: 37,047  
 REFERENCE/DOCKET NUMBER: 007315-005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-377-432-38

Query Match 27.3%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
 |||  
 Db 3 FYK 5

RESULT 53  
 US-08-968-676-24  
 ; Sequence 24, Application US/08968676  
 ; Patent No. 5918639  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Humphreys, Robert E  
 ; APPLICANT: Adams, Shariene  
 ; APPLICANT: Xu, Minzhen  
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
 ; NUMBER OF SEQUENCES: 165  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kevin M. Farrell, P.C.  
 ; STREET: P.O. Box 999  
 ; CITY: York Harbor  
 ; STATE: ME  
 ; COUNTRY: USA  
 ; ZIP: 03911  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/08/968,676  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Farrell, Kevin M  
 ; REGISTRATION NUMBER: 35,505  
 ; REFERENCE/DOCKET NUMBER: REH-9601  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (207) 363-0558  
 ; TELEFAX: (207) 363-0528  
 ; INFORMATION FOR SEQ ID NO: 24:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-968-676-24

Query Match 27.3%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9  
 |||  
 Db 4 KLP 6

RESULT 54  
 US-08-819-444-3  
 ; Sequence 3, Application US/08819444A  
 ; Patent No. 5968763  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FISCHETTI, Vincent A.  
 ; APPLICANT: PANCHOLI, Vijaykumar  
 ; TITLE OF INVENTION: ENZYME FOR CLEAVAGE OF THE ANCHOR REGION OF SURFACE  
 ; TITLE OF INVENTION: PROTEINS FROM GRAM POSITIVE BACTERIA  
 ; FILE REFERENCE: 016921-105  
 ; CURRENT APPLICATION NUMBER: US/08/819,444A  
 ; CURRENT FILING DATE: 1997-03-17  
 ; EARLIER APPLICATION NUMBER: US 08/319,540  
 ; EARLIER FILING DATE: 1994-10-07  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Enterococcus faecalis  
 ; US-08-819-444-3

Query Match 27.3%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 |||  
 Db 1 LPQ 3

RESULT 55  
 US-08-819-444-5  
 ; Sequence 5, Application US/08819444A  
 ; Patent No. 5968763  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FISCHETTI, Vincent A.  
 ; APPLICANT: PANCHOLI, Vijaykumar  
 ; TITLE OF INVENTION: ENZYME FOR CLEAVAGE OF THE ANCHOR REGION OF SURFACE  
 ; TITLE OF INVENTION: PROTEINS FROM GRAM POSITIVE BACTERIA  
 ; FILE REFERENCE: 016921-105  
 ; CURRENT APPLICATION NUMBER: US/08/819,444A  
 ; CURRENT FILING DATE: 1997-03-17  
 ; EARLIER APPLICATION NUMBER: US 08/319,540  
 ; EARLIER FILING DATE: 1994-10-07  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Enterococcus faecalis  
 ; US-08-819-444-5

Query Match 27.3%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 |||  
 Db 1 LPQ 3

RESULT 56  
 US-09-196-934-6  
 ; Sequence 6, Application US/09196934  
 ; Patent No. 6131256  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Li Ang  
 ; APPLICANT: Beutner, Joseph A.  
 ; APPLICANT: Carbonell, Ruben G.  
 ; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides

FILE REFERENCE: MSB-7251  
CURRENT APPLICATION NUMBER: US/09/196,934  
CURRENT FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-196-934-6

Query Match 27.3%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7  
Db 4 FYK 6

RESULT 57  
US-08-803-346-76  
Sequence 76, Application US/0803346  
Patent No. 6281346  
GENERAL INFORMATION:  
APPLICANT: HESS, JOHN W.  
APPLICANT: CASKEY, C. THOMAS  
APPLICANT: LIU, QINGYUN  
APPLICANT: PHILLIPS, MICHAEL SEAN  
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES  
TITLE OF INVENTION: ENCODING THEM  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,346  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: GIESSEY, JOANNE M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 19642Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3046  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-803-346-76

Query Match 27.3%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQ 3  
Db 1 MPQ 3

RESULT 58  
US-09-155-613A-36  
Sequence 36, Application US/09155613A  
Patent No. 6420120  
GENERAL INFORMATION:  
APPLICANT: Boulanger, Pierre  
APPLICANT: Bong, Saw See  
APPLICANT: Karayan, Lucie  
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
FILE REFERENCE: 032751-036  
CURRENT APPLICATION NUMBER: US/09/155,613A  
CURRENT FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: PCT/FR98/00184  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: FR 97/01005  
PRIOR FILING DATE: 1997-01-30  
PRIOR APPLICATION NUMBER: FR 97/11166  
PRIOR FILING DATE: 1997-09-09  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 36  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Phagotome  
US-09-155-613A-36

Query Match 27.3%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9  
Db 4 KLP 6

RESULT 59  
US-09-581-944A-30  
Sequence 30, Application US/09581944A  
Patent No. 644131  
GENERAL INFORMATION:  
APPLICANT: Ono Pharmaceutical Co., Ltd.  
TITLE OF INVENTION: PEPTIDES, METHOD FOR ASSAYING HUMAN PEPSINOGEN II OR HUMAN PEPSIN  
FILE REFERENCE: ASSAY KIT  
FILE REFERENCE: Q59565  
CURRENT APPLICATION NUMBER: US/09/581,944A  
CURRENT FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: P. Hei. 9-364796  
PRIOR FILING DATE: 1997-12-22  
PRIOR APPLICATION NUMBER: P. Hei. 10-213513  
PRIOR FILING DATE: 1998-07-13  
PRIOR APPLICATION NUMBER: PCT/JP98/05780  
PRIOR FILING DATE: 1998-12-21  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: substrate for human pepsin II or pepsinogen II  
NAME/KEY: MISC FEATURE  
LOCATION: (5)..(5)  
OTHER INFORMATION: 2-naphthyl Ala  
FEATURE:

NAME/KEY: MISC FEATURE  
 LOCATION: (6) (6)  
 OTHER INFORMATION: Ala which binds to p-nitroaniline  
 US-09-561-944A-30

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4  
 Db 1 PQN 3

RESULT 60  
 US-09-000-286A-2  
 Sequence 2, Application US/09000286A  
 Patent No. 6449562  
 GENERAL INFORMATION:  
 APPLICANT: Lumindex Corporation  
 APPLICANT: Chandler, Van S.  
 APPLICANT: Pulton, Jerrold R.  
 APPLICANT: Chandler, Mark B.  
 TITLE OF INVENTION: Multiplexed Analysis of Clinical Specimens Apparatus and Method  
 FILE REFERENCE: 112602560  
 CURRENT APPLICATION NUMBER: US/09/000,286A  
 CURRENT FILING DATE: 1996-08-18  
 PRIOR APPLICATION NUMBER: PCT/US96/16198  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: Patent in version 3.1  
 SEQ ID NO 2  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-000-286A-2

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 Db 4 LPQ 6

RESULT 61  
 US-08-469-260A-208  
 Sequence 208, Application US/08469260A  
 Patent No. 6451578  
 GENERAL INFORMATION:  
 APPLICANT: JOHN N. SIMONS  
 APPLICANT: TAMI J. PILOT-MATIAS  
 APPLICANT: GEORGE J. DAWSON  
 APPLICANT: GEORGE G. SCHLAUDER  
 APPLICANT: SURESH M. DESAI  
 APPLICANT: THOMAS P. LEARY  
 APPLICANT: ANTHONY SCOTT MUEHROFF  
 APPLICANT: JAMES C. ERKER  
 APPLICANT: SHERI L. BUIJK  
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
 NUMBER OF SEQUENCES: 716  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 STREET: 100 ABBOTT PARK ROAD  
 CITY: ABBOTT PARK  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/469,260A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FOREMBSKI, PRISCILLA E.

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/469,260A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FOREMBSKI, PRISCILLA E.  
 REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 5527.PC.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-6365  
 TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 208:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-469-260A-208

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 Db 4 LPQ 6

RESULT 62  
 US-08-469-260A-335  
 Sequence 335, Application US/08469260A  
 Patent No. 6451578  
 GENERAL INFORMATION:  
 APPLICANT: JOHN N. SIMONS  
 APPLICANT: TAMI J. PILOT-MATIAS  
 APPLICANT: GEORGE J. DAWSON  
 APPLICANT: GEORGE G. SCHLAUDER  
 APPLICANT: SURESH M. DESAI  
 APPLICANT: THOMAS P. LEARY  
 APPLICANT: ANTHONY SCOTT MUEHROFF  
 APPLICANT: JAMES C. ERKER  
 APPLICANT: SHERI L. BUIJK  
 APPLICANT: ISA K. MUSHAWAR  
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
 NUMBER OF SEQUENCES: 716  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 STREET: 100 ABBOTT PARK ROAD  
 CITY: ABBOTT PARK  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/469,260A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FOREMBSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 5527.PC.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-6365  
 TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 335:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-469-260A-335

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 DB 3 LPQ 5

RESULT 63  
 US-09-492-766-1  
 Sequence 1, Application US/09492766  
 Patent No. 6506732  
 GENERAL INFORMATION:  
 APPLICANT: AMIOT, Jean  
 TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS  
 FILE REFERENCE: 6013-57"US"  
 CURRENT APPLICATION NUMBER: US/09/492,766  
 CURRENT FILING DATE: 2000-01-27  
 EARLIER APPLICATION NUMBER: 60/117,661  
 EARLIER FILING DATE: 1999-01-28  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 1  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk  
 OTHER INFORMATION: proteins  
 US-09-492-766-1

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 DB 2 LPQ 4

RESULT 64  
 US-08-900-241-38  
 Sequence 38, Application US/08900241A  
 Patent No. 6518397  
 GENERAL INFORMATION:  
 APPLICANT: DEDHAR, Shoukat  
 TITLE OF INVENTION: PHARMACEUTICALS FOR MODULATING HORMONE RESPONSIVENESS  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Burns, Doane, Swecker & Mathis  
 STREET: P. O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/900,241A  
 FILING DATE: 24-Jul-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/377,432  
 FILING DATE: 24-JAN-1995  
 APPLICATION NUMBER: PCT/CA95/00664  
 FILING DATE: 23-NOV-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mooi, Leslie A.  
 REGISTRATION NUMBER: 37,047  
 REFERENCE/DOCKET NUMBER: 007315-015  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650)622-2300  
 TELEFAX: (650)622-2499  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
 US-08-900-241-38

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7  
 DB 3 FYK 5

RESULT 65  
 US-09-209-676-40  
 Sequence 40, Application US/09209676  
 Patent No. 6524856  
 GENERAL INFORMATION:  
 APPLICANT: Pangene Corporation  
 TITLE OF INVENTION: The Use of Consensus Sequences for Targeted Homologous  
 RECOMBINATION and Recombination in Gene Families  
 FILE REFERENCE: A-65878-1/AF7/NBC  
 CURRENT APPLICATION NUMBER: US/09/209,676  
 CURRENT FILING DATE: 2002-06-18  
 PRIOR APPLICATION NUMBER: US 60/070,734  
 PRIOR FILING DATE: 1997-12-11  
 NUMBER OF SEQ ID NOS: 95  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 40  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: consensus  
 OTHER INFORMATION: sequence  
 US-09-209-676-40

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4  
 DB 2 PQN 4

RESULT 66  
 US-09-555-352-26  
 Sequence 26, Application US/09555352

Patent No. 6544779  
 GENERAL INFORMATION:  
 APPLICANT: Cichutek, Klaus  
 TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH  
 MODIFIABLE SURFACE CAPSID PROTEINS  
 FILE REFERENCE: 11692-005001  
 CURRENT APPLICATION NUMBER: US/09/555,352  
 PRIORITY FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: PCT/DE98/03542  
 PRIOR FILING DATE: 1998-11-27  
 PRIOR APPLICATION NUMBER: DE 197 52 855.4  
 PRIOR FILING DATE: 1997-11-28  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 26  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Murine leukemia virus  
 US-09-555-352-26

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPQ 3  
 |||  
 Db 1 MPQ 3

RESULT 67  
 US-08-488-446-208  
 Sequence 208, Application US/08488446  
 Patent No. 6558898  
 GENERAL INFORMATION:  
 APPLICANT: JOHN N. SIMONS  
 APPLICANT: TAMI J. PILOT-MATIAS  
 APPLICANT: GEORGE J. DAWSON  
 APPLICANT: GEORGE G. SCHLAUDER  
 APPLICANT: SURESH M. DESAI  
 APPLICANT: THOMAS P. LEARY  
 APPLICANT: ANTHONY SCOTT MUEHRHOFF  
 APPLICANT: JAMES C. ERKER  
 APPLICANT: SHERI L. BUIJK  
 APPLICANT: ISA K. MUSHAWAR  
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
 NUMBER OF SEQUENCES: 716  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 STREET: 100 ABBOTT PARK ROAD  
 CITY: ABBOTT PARK  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,446  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FOREMSKI, PRISCILLA E.  
 REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 5527.PC.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-6365  
 TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 335:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-488-446-335

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 208:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-488-446-208

Query Match 27.3%; Score 3; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10  
 |||  
 Db 4 LPQ 6

RESULT 68  
 US-08-488-446-335  
 Sequence 335, Application US/08488446  
 Patent No. 6558898  
 GENERAL INFORMATION:  
 APPLICANT: JOHN N. SIMONS  
 APPLICANT: TAMI J. PILOT-MATIAS  
 APPLICANT: GEORGE J. DAWSON  
 APPLICANT: GEORGE G. SCHLAUDER  
 APPLICANT: SURESH M. DESAI  
 APPLICANT: THOMAS P. LEARY  
 APPLICANT: ANTHONY SCOTT MUEHRHOFF  
 APPLICANT: JAMES C. ERKER  
 APPLICANT: SHERI L. BUIJK  
 APPLICANT: ISA K. MUSHAWAR  
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
 NUMBER OF SEQUENCES: 716  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 STREET: 100 ABBOTT PARK ROAD  
 CITY: ABBOTT PARK  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,446  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FOREMSKI, PRISCILLA E.  
 REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 5527.PC.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-6365  
 TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 335:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-488-446-335

QY 8 LPQ 10  
Db 3 LPQ 5

RESULT 69  
US-08-467-344A-208  
; Sequence 208, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; TAMI J. PILOT-MATIAS  
; GEORGE J. DAWSON  
; GEORGE G. SCHLAUDER  
; SURESH M. DESAI  
; THOMAS P. LEARY  
; ANTHONY SCOTT MUEHROFF  
; JAMES C. ERKER  
; SHERI L. BUIJK  
; ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 208:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:  
US-08-467-344A-208  
Query Match 27.3%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
Db 4 LPQ 6

RESULT 70  
US-08-467-344A-335  
; Sequence 335, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; TAMI J. PILOT-MATIAS  
; GEORGE J. DAWSON  
; GEORGE G. SCHLAUDER  
; SURESH M. DESAI  
; THOMAS P. LEARY  
; ANTHONY SCOTT MUEHROFF  
; JAMES C. ERKER  
; SHERI L. BUIJK  
; ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 208:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:  
US-08-467-344A-208  
Query Match 27.3%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
Db 3 LPQ 5

RESULT 71  
PCT-US93-01669-26  
; Sequence 26, Application PC/TUS9301669  
; GENERAL INFORMATION:  
; APPLICANT: Trowbridge, Ian S.  
; APPLICANT: Collant, Jr., James P.  
; APPLICANT: Tainer, John A.  
; APPLICANT: Kuhn, Leslie A.  
; TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA

; ZIP: 90067  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/01669  
 ; FILING DATE: 01-MAR-1993  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/844,852  
 ; FILING DATE: 03-MAR-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wetherell, Jr. Ph.D., John R.  
 ; REGISTRATION NUMBER: 31,678  
 ; REFERENCE/DOCKET NUMBER: PD-1636  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 455-5100  
 ; TELEFAX: (619) 455-5110  
 ; INFORMATION FOR SEQ ID NO: 26:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: Peptide  
 ; PCT-US93-01669-26

Query Match 27.3%; Score 3; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6  
 ||||  
 Db 1 NFY 3

RESULT 72  
 US-08-127-499A-10  
 ; Sequence 10, Application US/08127499A  
 ; Patent No. 5510264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/127,499A  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids

; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-08-127-499A-10  
 ; Query Match 27.3%; Score 3; DB 1; Length 7;  
 ; Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 ; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 ||||  
 Db 1 LPQ 3

RESULT 73  
 US-08-482-847-10  
 ; Sequence 10, Application US/08482847  
 ; Patent No. 5556757  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/482,847  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/127,499  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/104/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-08-482-847-10

Query Match 27.3%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10  
 ||||  
 Db 1 LPQ 3

RESULT 74  
 US-08-537-069-14  
 ; Sequence 14, Application US/08537069  
 ; Patent No. 5688912

```

; GENERAL INFORMATION:
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Peptide Ligands Which Bind to
; TITLE OF INVENTION: von Willebrand Factor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,069
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gublin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-537-069-14

```

```

Query Match          27.3%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 5 FYK 7
Db 5 FYK 7

```

```

RESULT 75
US-08-177-109A-5
; Sequence 5, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-5

```

```

Query Match          27.3%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 PQN 4
Db 1 PQN 3

```

```

Search completed: November 25, 2003, 20:16:02
Job time : 12.9947 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 13.8032 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-7  
Perfect score: 15  
Sequence: 1 VLEMKFPPTQETVT 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	26.7	7	2 S71299	IC12 protein - Par
2	4	26.7	9	2 S66607	quinoxaline 2-oxid
3	4	26.7	10	2 A36454	trypsin-modulating
4	4	26.7	13	2 D39690	neural cell adhesi
5	4	26.7	14	2 C33098	223K exoantigen -
6	4	26.7	15	2 PT0037	light harvesting c
7	4	26.7	17	2 S57991	hydroxyproline-ric
8	4	26.7	17	2 S59481	hydroxyproline-ric
9	3	20.0	9	2 PT0272	Ig heavy chain CRD
10	3	20.0	9	2 A60427	macrophage cytotox
11	3	20.0	9	2 B30572	T-cell receptor be
12	3	20.0	10	2 S63478	dihydrolipoamide d
13	3	20.0	10	2 S70721	heat shock protein
14	3	20.0	10	2 B59272	peptide-N4-(N-acet
15	3	20.0	10	2 A61354	carnitine medium/1
16	3	20.0	10	2 C30572	T-cell receptor be
17	3	20.0	10	2 PH0923	T-cell receptor be
18	3	20.0	11	2 PC4267	ribosomal protein
19	3	20.0	11	2 B60769	Ig H2 chain - Paci
20	3	20.0	11	2 D45900	complement C3b rec
21	3	20.0	11	2 PH0804	T-cell receptor be
22	3	20.0	12	2 C35109	hypothetical 1.2K
23	3	20.0	12	2 FN0663	gustrophin-associ
24	3	20.0	12	2 B39690	neural cell adhesi
25	3	20.0	12	2 S69095	ubiquinol-cytochro
26	3	20.0	13	2 S21152	tryptophyl-in-rela
27	3	20.0	13	2 A05174	tryptophyl-in-13
28	3	20.0	13	2 S09716	2S albumin large c
29	3	20.0	13	2 PN0048	unidentified QM002

30	3	20.0	13	2 S01904	Ha-transporting tw
31	3	20.0	14	2 P80252	16K protein S404 -
32	3	20.0	14	2 S12904	protein kinase 18C
33	3	20.0	14	2 S03530	Ig heavy chain J r
34	3	20.0	14	2 B20872	alpha-2-macroglobu
35	3	20.0	14	2 S11129	phosphoprotein, bo
36	3	20.0	15	2 S26997	unspecific monocoy
37	3	20.0	15	2 PN0629	integration host f
38	3	20.0	15	2 PA0036	glycine cleavage s
39	3	20.0	15	2 PA0014	seed storage prote
40	3	20.0	15	2 PN0173	Ig heavy chain J r
41	3	20.0	15	2 S10388	Ig heavy chain J r
42	3	20.0	15	2 S10386	7.5k surfactant-as
43	3	20.0	15	2 A61522	T-cell receptor be
44	3	20.0	15	2 D28587	T-cell receptor be
45	3	20.0	15	2 P28587	T-cell receptor be
46	3	20.0	15	2 S53284	voltage-dependent
47	3	20.0	15	2 S146909	epoxypropan isomer
48	3	20.0	15	2 S72432	Ig heavy chain J r
49	3	20.0	16	2 S03532	Ig heavy chain J r
50	3	20.0	16	2 D49021	insulin-like growt
51	3	20.0	16	2 JH0517	T-cell receptor be
52	3	20.0	16	2 PH0763	T-cell receptor be
53	3	20.0	16	2 PH0759	Ig heavy chain J5
54	3	20.0	17	2 S03531	Ig heavy chain J r
55	3	20.0	17	2 S24570	Ig heavy chain J r
56	3	20.0	17	2 S26744	Ig heavy chain J r
57	3	20.0	17	2 A34572	osteonectin - rat
58	3	20.0	17	2 B53113	gingipain, 44K - P
59	3	20.0	17	2 B28027	protein P4 - curle
60	3	20.0	17	2 S24687	T-cell receptor be
61	3	20.0	17	2 G85956	hypothetical prote
62	3	20.0	17	2 FC2319	proteasome endopep
63	3	20.0	18	2 S03528	Ig heavy chain J1
64	3	20.0	18	2 PC2280	prolylendopeptidas
65	3	20.0	18	2 B44995	alkanal monooxygen
66	3	20.0	18	2 S10452	hypothetical prote
67	3	20.0	18	2 T13132	protein gp45.1 - p
68	3	20.0	18	2 A50195	Na+/K+-exchanging
69	3	20.0	19	2 S04186	superoxide dismuta
70	3	20.0	19	2 P20467	nitrogenase 18C.1
71	3	20.0	19	2 B26930	ermG leader peptid
72	3	20.0	19	2 S31613	beta-1,3-glucanase
73	3	20.0	19	2 A49780	promoter P8 hypoph
74	3	20.0	19	2 G56819	PS I complex subun
75	3	20.0	19	2 S0329	wd-repeat protein
76	3	20.0	19	2 PH1352	Ig heavy chain DJ
77	3	20.0	19	2 A39504	octamer-binding pr
78	3	20.0	19	2 S25715	hypothetical prote
79	3	20.0	19	2 A60459	aminopeptidase, 30
80	3	20.0	20	2 S04961	malate dehydrogena
81	3	20.0	20	2 S04958	malate dehydrogena
82	3	20.0	20	2 A33878	myosin light chain
83	3	20.0	20	2 A45806	T-cell receptor be
84	3	20.0	20	2 A05313	apolipoprotein A-I
85	3	20.0	20	2 JN0252	water-soluble 35K
86	3	20.0	20	2 I64036	hypothetical prote
87	3	20.0	20	2 B44835	drpoglucose 4,6-de
88	3	20.0	20	2 S46479	retinoid-X-recepto
89	3	20.0	20	2 S50203	zona pellucida gly
90	3	20.0	20	2 A41437	alpha-1-antitrypsi
91	3	20.0	20	2 A61506	alpha-1-antitrypsi
92	3	20.0	20	2 A42367	J-kappa recombina
93	3	20.0	20	2 A31516	lectin, galactose/
94	3	20.0	20	2 A45644	temperature-labile
95	3	13.3	3	3 A33802	thyrotropin-releas
96	2	13.3	3	3 S13894	histidinol dehydro
97	2	13.3	4	2 B43848	cell surface adhes
98	2	13.3	4	2 I40870	phospholipase C (E
99	2	13.3	4	2 I40804	endoglucanase F -
100	2	13.3	4	2 T46627	hypothetical prote

## ALIGNMENTS

## RESULT 1

ICL2 protein - Paramacium tetraurelia (fragment)  
 S71299  
 C:Species: Paramacium tetraurelia  
 C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
 C:Accession: S71299  
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
 Eur. J. Biochem. 238, 121-128, 1996  
 A>Title: Characterization of centrin genes in Paramacium.  
 A:Reference number: S71298; PMID:96248429; PMID:8665928  
 A:Accession: S71299  
 A:Molecule type: protein  
 A:Residues: 1-7 <MAD>  
 A:Experimental source: strain d4-2  
 C:Genetics:  
 A:Genetic code: SGCS

Query Match 26.7%; Score 4; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11  
 ||||  
 Db 3 PPPQ 6

## RESULT 2

quinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)  
 S6607  
 C:Species: Comamonas testosteroni  
 C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C:Accession: S6607  
 R:Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.  
 Eur. J. Biochem. 232, 536-544, 1995  
 A>Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from  
 A:Reference number: S66606; PMID:96035889; PMID:7556204  
 A:Accession: S6607  
 A:Molecule type: protein  
 A:Residues: 1-9 <SCH>  
 A:Experimental source: strain 63

Query Match 26.7%; Score 4; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFP 7  
 ||||  
 Db 1 MKFP 4

## RESULT 3

A36454  
 trypsin-modulating oostatic factor - yellow fever mosquito  
 C:Species: Aedes aegypti (yellow fever mosquito)  
 C>Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 24-May-1996  
 C:Accession: A36454; A61630  
 R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
 FASEB J. 4, 3015-3020, 1990  
 A>Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi  
 A:Reference number: A36454; PMID:90367888; PMID:2394318  
 A:Accession: A36454  
 A:Molecule type: protein  
 A:Residues: 1-10 <BOR>  
 R:Borovsky, D.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
 Insect Biochem. Mol. Biol. 23, 703-712, 1993  
 A>Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost  
 A:Reference number: A61630; PMID:93357794; PMID:8353526  
 A:Accession: A61630  
 A:Molecule type: protein  
 A:Residues: 1-10 <BO2>

A>Note: none of the amino acids is modified

C:Function:  
 A:Description: Inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep  
 C:Keywords: hormone

Query Match 26.7%; Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
 ||||  
 Db 5 PPPP 8

## RESULT 4

D39690  
 neural cell adhesion molecule, cardiac splice form +,-,+ - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C:Accession: D39690  
 R:Reyes, A.A.; Small, S.J.; Akeson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR  
 A:Reference number: A39690; PMID:9141516; PMID:1996115  
 A:Accession: D39690  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-13 <REY>  
 A:Cross-references: GB:M63970  
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 26.7%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11  
 ||||  
 Db 6 PPPQ 9

## RESULT 5

C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: C33098  
 R:Nichols, J.H.; Hager, L.P.  
 Submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: C33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <NIC>

Query Match 26.7%; Score 4; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQE 12  
 ||||  
 Db 3 PPQE 6

## RESULT 6

PT0037  
 light harvesting complex chain III/b, photosystem I - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
 C:Accession: PT0037; PS0205  
 R:Uchiyama, Y.; Tsugita, A.  
 submitted to JIPID, June 1991  
 A:Reference number: PS0189

A;Accession: PT0037  
A;Molecule type: protein  
A;Residues: 1-15 <UCH>

Query Match 26.7%; Score 4; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 PPPP 10  
|  
|  
|  
|  
Db 8 PPPP 11

## RESULT 7

S57991 hydroxyproline-rich protein - Sesbania rostrata (fragment)

C;Species: Sesbania rostrata  
C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 11-Jan-2000  
C;Accession: S57991

R;Goornachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.  
Submitted to the EMBL Data Library, March 1995  
A;Description: Use of differential display to identify novel Sesbania rostrata genes and  
A;Reference number: S57991

A;Accession: S57991  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-17 <G00>  
A;Cross-references: EMBL:Z48673; NID:G899484; PID:G899485  
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 PPPP 10  
|  
|  
|  
|  
Db 10 PPPP 13

## RESULT 8

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A;Title: Specificity in the immobilisation of cell wall proteins in response to different  
A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481  
A;Molecule type: protein  
A;Residues: 1-17 <WQJ>  
C;Keywords: glycoprotein; hydroxyproline  
F;6,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 PPPP 10  
|  
|  
|  
|  
Db 8 PPPP 11

## RESULT 9

PT0272

Ig heavy chain CRD3 region (clone 3-103B) - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0272  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0272

A;Molecule type: DNA

A;Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 EMK 5  
|  
|  
|  
|  
Db 6 EMK 8

## RESULT 10

A60427

macrophage cytotoxicity-inducing factor, 29K - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1993  
C;Accession: A60427  
R;Jones, C.M.; Prince, C.A.; Williams, J.S.  
Exp. Hematol. 19, 704-709, 1991

A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducing  
A;Reference number: A60427; MUID:91372335; PMID:1909970

A;Accession: A60427

A;Molecule type: protein

A;Residues: 1-9 <YON>

A;Note: the sequence from the text on page 706 is inconsistent with that from page 708 in

C;Keywords: cytokine

Query Match 20.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VLE 3  
|  
|  
|  
|  
Db 4 VLE 6

## RESULT 11

B30572

T-cell receptor beta chain C region (CRTB29) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997  
C;Accession: B30572

R;Williams, C.B.; Guttman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz.

A;Reference number: A30563; MUID:89110038; PMID:2563271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 <WIL>

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 13 TWT 15  
|  
|  
|  
|  
Db 5 TWT 7

## RESULT 12

S63478

dihydrolipoamide dehydrogenase (EC 1.8.1.4) beta chain E1 - Pseudomonas aeruginosa (frag

N;Alternate names: branched-chain-oxoacid dehydrogenase chain E1

C;Species: Pseudomonas aeruginosa

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S63478

R;Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.

Eur. J. Biochem. 233: 828-836, 1995

A;Title: Purification of active EL-alpha(2)-beta(2) of Pseudomonas putida branched-chain

A;Reference number: S63475; MUID:96085147; PMID:8521848

A;Accession: S63478

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HES>

C;Keywords: FAD; Flavoprotein; lipoamide; NAD; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTV 15

Db 6 TTV 8

RESULT 13

heat shock protein C62.5 homolog - Salmonella typhimurium (fragment)

N;Alternate names: high temperature protein G

C;Species: Salmonella typhimurium

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C;Accession: S70721

R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

Mol. Microbiol. 17: 523-531, 1995

A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophils

A;Reference number: S70719; MUID:96100451; PMID:8559071

A;Accession: S70721

A;Molecule type: protein

A;Residues: 1-10 <QIS>

A;Experimental source: strain S11344

C;Keywords: ATP binding; heat shock; molecular chaperone

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13

Db 4 QET 6

RESULT 14

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain

N;Alternate names: peptidase N-glycosidase

C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000

C;Accession: B59272

R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252: 118-123, 1998

A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A

A;Reference number: A59272; MUID:98181894; PMID:9523720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

C;Keywords: hydrolase

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPP 8

Db 8 FPP 10

RESULT 15

A61354

carnitine medium/long chain acyltransferase (EC 2.3.1.1-) - rat (fragment)

N;Alternate names: endoplasmic reticulum protein ERP61; glucose regulated protein GRP58;

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999

C;Accession: A61354

R;Murthy, M.S.R.; Pande, S.V.

Mol. Cell. Biochem. 122, 133-138, 1993

A;Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previa

A;Reference number: A61354; MUID:94049728; PMID:8232244

A;Accession: A61354

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <MUR>

C;Keywords: acyltransferase

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

Db 3 VLE 5

RESULT 16

T-cell receptor beta chain C region (CRTB49) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997

C;Accession: C30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz

A;Reference number: A30563; MUID:89110038; PMID:2563271

A;Accession: C30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-10 <WIL>

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTV 15

Db 5 TTV 7

RESULT 17

PH0923

T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0923

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0923

A;Molecule type: mRNA

A;Residues: 1-10 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13

Db 8 QET 10

## RESULT 18

PC4267  
ribosomal protein L12.1 - rice (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
C:Accession: PC4267  
R:Kawakami, T.; Kano, M.; Chen, M.C.; Tsugita, A.  
submitted to JIPID, April 1997  
A:Reference number: PC4267  
A:Accession: PC4267  
A:Molecule type: protein  
A:Residues: 1-11 <KAW>  
A:Experimental source: strain Japonica Nihonbare

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
DB 9 VLE 11

## RESULT 19

BE0769  
Ig H2 chain - Pacific hagfish (fragment)  
C:Species: Eptatretus stouti (Pacific hagfish)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 03-Jun-1993  
C:Accession: BE0769  
R:Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.  
J. Immunol. 145, 3823-3828, 1990  
A:Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.  
A:Reference number: AE0769; PMID:91060965; PMID:2123225  
A:Accession: BE0769  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <HAN>

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13  
|||  
DB 9 QET 11

## RESULT 20

D45900  
complement C3b receptor type 2 - mouse (clone 12) (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: D45900  
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.  
J. Immunol. 144, 3581-3591, 1990  
A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene.  
A:Reference number: A45900; PMID:90229754; PMID:2139460  
A:Accession: D45900  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-11 <KUR>

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9  
|||  
DB 9 PPP 11

## RESULT 21

## PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0904  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A:Reference number: PH0891; PMID:92078857; PMID:1836012  
A:Accession: PH0904  
A:Molecule type: mRNA  
A:Residues: 1-11 <GOL>  
A:Experimental source: myelin basic protein-immunized T-cell  
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13  
|||  
DB 8 QET 10

## RESULT 22

C39109  
hypothetical 1.2K protein - hepatitis C virus  
N:Alternate names: hypothetical protein 3  
C:Species: hepatitis C virus  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
C:Accession: C39109; J01586  
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
A:Reference number: A39109; PMID:91156678; PMID:1705704  
A:Accession: C39109  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-12 <HAN>

Query Match 20.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11  
|||  
DB 8 PPQ 10

## RESULT 23

PN0663  
dyotrophin-associated glycoprotein A3a-II - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
C:Accession: PN0663  
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.  
J. Biochem. 114, 634-639, 1993  
A:Title: A dyotrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A:Reference number: PN0662; PMID:94156881; PMID:8113213  
A:Accession: PN0663  
A:Molecule type: protein  
A:Residues: 1-12 <YOS>  
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
C:Keywords: glycoprotein; skeletal muscle

```

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      5 PPP 7

RESULT 24
B39690
neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: B39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: B39690
A>Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-12 <REI>
A:Cross-references: GB:M33970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      6 PPP 8

RESULT 25
S69095
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - Sulfolobus acidocal
N;Alternate names: Rieske iron-sulfur protein
C:Species: Sulfolobus acidocaldarius
C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 03-Jun-2002
C:Accession: S69095
R;Schmidt, C.L.; Anemuller, S.; Teixeira, M.; Schaefer, G.
FEBS Lett. 359, 239-243, 1995
A>Title: Purification and characterization of the Rieske iron-sulfur protein from the th
A:Reference number: S69095; MUID:95172243; PMID:7867807
A:Accession: S69095
A:Molecule type: protein
A:Residues: 1-12 <SCH>
C:Keywords: oxidoreductase

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
      |||
Db      8 TVT 10

RESULT 26
S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A>Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein

A;Residues: 1-13 <MIG>
A;Experimental source: skin
C;Superfamily: unassigned animal peptides

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      7 PPP 9

RESULT 27
A05174
tryptophyllin-13 - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C:Accession: A05174
R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A:Reference number: A05174
A:Accession: A05174
A:Molecule type: protein
A:Residues: 1-13 <MON>
C;Superfamily: unassigned animal peptides
C;Keywords: pyrrolutamic acid; skin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      7 PPP 9

RESULT 28
S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N;Alternate names: 2S albumin large chain nIII
C;Species: Brassica napus (rape)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R;Monsalve, R.L.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A>Title: beta-turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:9042374; PMID:2185951
A:Accession: S09716
A:Molecule type: protein
A;Residues: 1-9;10-13 <MON>
A;Experimental source: seed
A;Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A;Residues: 1-9;10-13 <MO2>
A;Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A;Residues: 1-9;10-13 <MO3>
A;Experimental source: seed

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      8 PPP 10

RESULT 29

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PN0048  
 unidentified QM0023 protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998  
 C:Accession: PN0048  
 R:Kato, H.  
 Kawasaki Igakkaishi 22, 245-259, 1996  
 A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro  
 A:Reference number: PN0041  
 A:Accession: PN0048  
 A:Molecule type: protein  
 A:Residues: 1-13 <XAP>  
 A:Experimental source: neuroblastoma cell  
 C:Comment: The molecular mass is 30,500 and the pI is 6.19.  
 C:Keywords: brain

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15  
 Db 11 TVT 13

RESULT 30  
 S01904  
 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro  
 C:Species: chloroplast Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 03-Jun-2002  
 C:Accession: S01904  
 R:Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.  
 Nucleic Acids Res. 16, 10372, 1988  
 A:Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon-subunit and elongator TRN  
 A:Reference number: S01903; MUID:89057486; PMID:29041134  
 A:Accession: S01904  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-13 <CHE>  
 A:Cross-references: EMBL:X12889; NID:gl1332; PIDN:CAA31380.1; PID:g829297  
 C:Genetics:  
 A:Gene: atpB  
 A:Genome: chloroplast  
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEM 4  
 Db 5 LEM 7

RESULT 31  
 PS0252  
 16k protein 5404 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Apr-1995  
 C:Accession: PS0252  
 R:Tsubota, A.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0206  
 A:Accession: PS0252  
 A:Molecule type: protein  
 A:Residues: 1-14 <TSU>  
 A:Experimental source: strain Nihonbare  
 C:Comment: Molecular weight 16k, pI 4.9.

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15  
 Db 11 TVT 13

RESULT 32  
 S12904  
 protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
 C:Species: Pisaster ochraceus  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
 C:Accession: S12904  
 R:Sanheta, J.S.; Ahersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
 PNAS Lett. 273, 223-226, 1990  
 A:Title: Identification of the sites in myelin basic protein that are phosphorylated by  
 A:Reference number: S12904; MUID:91032166; PMID:1699809  
 A:Accession: S12904  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <SAN>  
 C:Keywords: phosphotransferase

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9  
 Db 8 PPP 10

RESULT 33  
 S03530  
 Ig heavy chain J region (JH-4) - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 21-Jul-2000  
 C:Accession: S03530  
 R:Schwager, J.; Grossberger, D.; du Pasquier, L.  
 EMBO J. 7, 2409-2415, 1988  
 A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenop  
 A:Reference number: S01158; MUID:89052653; PMID:2903824  
 A:Accession: S03530  
 A:Molecule type: DNA  
 A:Residues: 1-14 <SCH>  
 A:Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33043.1; PID:gl1334657

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15  
 Db 11 TVT 13

RESULT 34  
 B20872  
 alpha-2-macroglobulin - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
 C:Accession: B20872  
 R:Nagase, H.; Harris Jr., E.D.; Woessner Jr., J.F.; Brew, K.  
 J. Biol. Chem. 258, 7481-7489, 1983  
 A:Title: Ovosatin: a novel proteinase inhibitor from chicken egg white. I. Purification  
 A:Reference number: A92427; MUID:83238315; PMID:6408074  
 A:Accession: B20872  
 A:Molecule type: protein  
 A:Residues: 1-14 <NAG>

Query Match 20.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15

Db 2 TWT 4  
|||

RESULT 35  
S11129  
phosphoprotein, bone - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 25-Oct-1996  
C:Accession: S11129  
R:MiKuni-Takagaki, Y.; Glincher, M.J.  
Biochem. J. 268, 565-591, 1990  
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification of  
A:Reference number: S11127; PMID:90303246; PMID:2363696  
A:Accession: S11129  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <MIK>  
C:Keywords: phosphoprotein

Query Match 20.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9  
|||

Db 5 PPP 7  
|||

RESULT 36  
B26997  
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2A1, hepatic - rat (fragment)  
N:Alternate names: cytochrome P450a  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 05-Mar-1999  
C:Accession: B26997  
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.  
Biochemistry 26, 3887-3894, 1987  
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca  
A:Reference number: A26997; PMID:8800604; PMID:3651420  
A:Accession: B26997  
A:Molecule type: protein  
A:Residues: 1-15 <GRA>  
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homolog  
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||

Db 8 VLE 10  
|||

RESULT 37  
PN0629  
integration host factor-like protein beta chain - Pseudomonas aeruginosa (fragment)  
C:Species: Pseudomonas aeruginosa  
C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: PN0629  
R:Toussaint, B.; Delic-Attrée, I.; Vignais, P.M.  
Biochem. Biophys. Res. Commun. 196, 416-421, 1993  
A:Title: Pseudomonas aeruginosa contains an IHF-like protein that binds to the algD prom  
A:Reference number: PN0628; PMID:94030028; PMID:8216322  
A:Accession: PN0629  
A:Molecule type: protein  
A:Residues: 1-15 <TOU>  
C:Comment: This protein forms a stable complex with the algD promoter in vitro, indicati

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TWT 15  
|||

Db 10 TWT 12  
|||

RESULT 38  
PA0036  
glycine cleavage system protein H1 and H2 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C:Accession: PA0036  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona  
A:Reference number: PA0001  
A:Accession: PA0036  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
A:Experimental source: stem

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||

Db 3 VLE 5  
|||

RESULT 39  
PA0014  
seed storage protein 12S 3 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C:Accession: PA0014  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona  
A:Reference number: PA0001  
A:Accession: PA0014  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
A:Experimental source: seed  
C:Keywords: seed; storage protein

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11  
|||

Db 7 PPQ 9  
|||

RESULT 40  
PN0173  
seed storage protein 12S4 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 22-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Mar-2001  
C:Accession: PN0173  
R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995  
A:Description: Two dimensional electrophoresis of plant proteins and standardization of  
A:Reference number: PN0173  
A:Accession: PN0173  
A:Molecule type: protein  
A:Residues: 1-15 <TSU>  
A:Experimental source: seeds

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 9 PPQ 11  
|||  
Db 7 PPQ 9

## RESULT 41

S10388  
Ig heavy chain J region (clone Rel02) - little skate (fragment)  
C:Species: Raja erinacea (little skate)  
C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 21-Jul-2000  
C:Accession: S10388  
R:Harding, F.A.; Cohen, N.; Litman, G.W.  
Nucleic Acids Res. 18, 1015-1020, 1990  
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja  
A:Reference number: S08462; MUID:90192082; PMID:2107524  
A:Accession: S10388  
A:Molecule type: DNA  
A:Residues: 1-15 <HAR>  
A:Cross-references: EMBL:X16146; NID:G64284; PIDN:CAA34271.1; PID:gl334773  
C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15  
|||  
Db 12 TVT 14

## RESULT 42

S10386  
Ig heavy chain J region (clone Rel07) - little skate (fragment)  
C:Species: Raja erinacea (little skate)  
C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Aug-1996  
C:Accession: S10386  
R:Harding, F.A.; Cohen, N.; Litman, G.W.  
Nucleic Acids Res. 18, 1015-1020, 1990  
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja  
A:Reference number: S08462; MUID:90192082; PMID:2107524  
A:Accession: S10386  
A:Molecule type: DNA  
A:Residues: 1-15 <HAR>  
A:Cross-references: EMBL:X15124  
C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15  
|||  
Db 12 TVT 14

## RESULT 43

A61522  
7.5k surfactant-associated protein - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 15-Oct-1994  
C:Accession: A61522  
R:Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.; Wong-Chong, M.L.; Gottron, S.A.  
Exp. Lung Res. 17, 559-567, 1991  
A:Title: Identification, isolation, and partial characterization of a 7.5-kDa surfactant  
A:Reference number: A61522; MUID:91317170; PMID:1860454  
A:Accession: A61522  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <SIN>

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VLE 3  
|||  
Db 6 VLE 8

## RESULT 44

D28587  
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C:Accession: D28587  
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A:Title: Organization and sequences of the diversity, joining, and constant region genes  
A:Reference number: A94081; MUID:86094276; PMID:3866244  
A:Accession: D28587  
A:Molecule type: DNA  
A:Residues: 1-15 <TOY>  
A:Cross-references: GB:M14159; NID:G338852; PIDN:AAA60679.1; PID:gs53690  
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QET 13  
|||  
Db 1 QET 3

## RESULT 45

F28587  
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C:Accession: F28587  
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A:Title: Organization and sequences of the diversity, joining, and constant region genes  
A:Reference number: A94081; MUID:86094276; PMID:3866244  
A:Accession: F28587  
A:Molecule type: DNA  
A:Residues: 1-15 <TOY>  
A:Cross-references: GB:M14159; NID:G338852; PIDN:AAA60681.1; PID:gs53692  
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15  
|||  
Db 13 TVT 15

## RESULT 46

I53284  
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: I53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.O.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and j  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: I53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <HAR>  
A:Cross-references: GB:S60737; NID:Q233916; PIDN:AA19525.1; PID:q233925  
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60747)

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
DB 13 TVT 15

RESULT 47

I46909  
voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kDa isoform  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999  
C;Accession: I46909  
R;Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.  
Neuron 8, 899-906, 1992  
A;Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.  
A;Reference number: I46909; PMID:92265303; PMID:1316766  
A;Accession: I46909  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-15 <MAL>  
A;Cross-references: GB:S36895; NID:G249481; PIDN:AA822180.1; PID:G249482

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4  
DB 13 LEM 15

RESULT 48

S72432  
epoxypropan isomerase component B - Xanthobacter sp. (strain Py2) (fragment)  
C;Species: Xanthobacter sp.  
A;Variety: strain Py2  
C;Date: 14-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 07-May-1999  
C;Accession: S72432  
R;Chan Kwo Chion, C.K.N.; Leak, D.J.  
Biochem. J. 319, 499-506, 1996  
A;Title: Purification and characterization of two components of epoxypropane isomerase/  
A;Reference number: S72431; PMID:97069704; PMID:8912687  
A;Accession: S72432  
A;Molecule type: protein  
A;Residues: 1-15 <CHA>  
A;Note: 3-Met and 13-Leu were also found  
C;Complex: homodimer  
C;Function:  
A;Description: NADP-dependent lipamide reductase  
A;Pathway: epoxypropane degradation  
A;Note: sensitive to N-ethyl-maleimide and p-chloromercuribenzoate  
C;Keywords: PAD

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKF 6  
DB 1 MKF 3

RESULT 49

S03532  
Ig heavy chain J region (JH-7) - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 20-Jun-2000  
C;Accession: S03532

R;Schwager, J.; Grossberger, D.; du Pasquier, L.  
EMBO J. 7, 2409-2415, 1988

A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus  
A;Reference number: S01158; PMID:89052653; PMID:2903824

A;Accession: S03532  
A;Molecule type: DNA  
A;Residues: 1-16 <SCH>

A;Cross-references: EMBL:X14918; NID:G64805; PIDN:CAA33046.1; PID:gl334660

A;Note: the authors translated the codon AAC for residue 1 as Asp  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
DB 13 TVT 15

RESULT 50

D49021  
Ig heavy chain J7 region - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C;Accession: D49021  
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.  
J. Exp. Med. 171, 1721-1737, 1990

A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation  
A;Reference number: A47824; PMID:90237760; PMID:2110243  
A;Accession: D49021

A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA

A;Residues: 1-16 <HAI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
DB 13 TVT 15

RESULT 51

JH0517  
insulin-like growth factor-binding protein 4 - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 23-Mar-1995  
C;Accession: JH0517  
R;Coleman, M.E.; Pan, Y.C.E.; Ehterton, T.D.  
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991  
A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth  
A;Reference number: JH0515; PMID:92109718; PMID:1722398  
A;Accession: JH0517  
A;Molecule type: protein  
A;Residues: 1-16 <COL>

A;Experimental source: serum

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9  
DB 7 PPP 9

RESULT 52

PH0763  
T-cell receptor beta chain (F15) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C;Accession: PH0763  
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-homologous genes: allelic exclusion and antigen-specific repertoire.  
 A;Reference number: PH0746; MUID:92078846; PMID:1836010  
 A;Accession: PH0763  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <AS>  
 A;Cross-references: EMBL:X60857; NID:g50933; PIDN:CAA43247.1; PID:g50934  
 A;Experimental source: T lymphocyte  
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11  
 |||  
 Db 5 PPQ 7

RESULT 53  
 PH0759  
 T-cell receptor beta chain (QB7.3.2) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C;Accession: PH0759  
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-homologous genes: allelic exclusion and antigen-specific repertoire.  
 A;Reference number: PH0746; MUID:92078846; PMID:1836010  
 A;Accession: PH0759  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <AS>  
 A;Cross-references: EMBL:X60854; NID:g53878; PIDN:CAA43244.1; PID:g53879  
 A;Experimental source: T lymphocyte  
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11  
 |||  
 Db 5 PPQ 7

RESULT 54  
 S03531  
 Ig heavy chain J5 region - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 20-Jun-2000  
 C;Accession: S03531; C43021  
 R;Schwager, J.; Grossberger, D.; du Pasquier, L.  
 EMBO J. 7, 2409-2415, 1988  
 A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis.  
 A;Reference number: S01158; MUID:89052653; PMID:2903824  
 A;Accession: S03531  
 A;Molecule type: DNA  
 A;Residues: 1-17 <SCH>  
 A;Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33044.1; PID:g1334658  
 R;Hairston, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.  
 J. Exp. Med. 171, 1721-1737, 1990  
 A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation in the V-H region of the immunoglobulin heavy chain.  
 A;Reference number: A47624; MUID:90237760; PMID:2110243  
 A;Accession: C43021  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 3-17 <HA1>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
 |||  
 Db 14 TVT 16

RESULT 55  
 S24570  
 Ig heavy chain J region - channel catfish  
 C;Species: Ictalurus punctatus (channel catfish)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C;Accession: S24570  
 R;Wilson, M.R.  
 Submitted to the EMBL Data Library, March 1992  
 A;Reference number: S24570  
 A;Accession: S24570  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-17 <WIL>  
 A;Cross-references: EMBL:X65182; NID:g64015; PIDN:CAA46293.1; PID:g64016  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
 |||  
 Db 14 TVT 16

RESULT 56  
 S26744  
 Ig heavy chain J region JH1 - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 25-Feb-1994 #sequence\_revision 24-Oct-1998 #text\_change 17-Mar-1999  
 C;Accession: S26744  
 R;Solari, M.L.; Kaartinen, M.  
 Immunogenetics 36, 306-313, 1992  
 A;Title: Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy chain.  
 A;Reference number: S26744; MUID:92355114; PMID:1644448  
 A;Accession: S26744  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-17 <SOL>  
 A;Cross-references: EMBL:X63164  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
 |||  
 Db 12 TVT 14

RESULT 57  
 A34572  
 osteonectin - rat (fragment)  
 N;Alternate names: BM-40; SPARC  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 17-Nov-2000  
 C;Accession: A34572  
 R;Cheng, C.Y.

Biochem. Biophys. Res. Commun. 167, 1393-1399, 1990  
 A>Title: Purification of a calcium binding protein (rat SPARC) from primary Sertoli cell  
 A;Reference number: A34572; MUID:90211328; PMID:232281  
 A;Accession: A34572  
 A;Molecule type: Protein  
 A;Residues: 1-17 <HE>  
 A;Superfamily: osteonectin; calmodulin repeat homology; Kazal proteinase inhibitor homol  
 C;Keywords: calcium binding; collagen binding; disulfide bond; EF hand; extracellular ma

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
 |||  
 Db 14 ETV 16

## RESULT 58

E53113  
 gingipain, 44K - Porphyromonas gingivalis (fragment)  
 N;Alternate names: arginine-specific cysteine proteinase, 44K  
 C;Species: Porphyromonas gingivalis  
 C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Apr-1995  
 C;Accession: E53113  
 R;Pike, R.; McGraw, W.; Potempa, J.; Travis, J.  
 J. Biol. Chem. 269, 406-411, 1994  
 A>Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolab  
 A;Reference number: A53113; MUID:94103245; PMID:8276827  
 A;Accession: E53113  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-17 <PIK>  
 A;Experimental source: H66  
 A;Note: sequence extracted from NCBI backbone (NCBIP:141695)

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
 |||  
 Db 7 VLE 9

## RESULT 59

B28027  
 protein P4 - curled-leaved tobacco (fragment)  
 C;Species: Nicotiana glauca (curled-leaved tobacco)  
 C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993  
 C;Accession: B28027  
 R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987  
 A>Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-  
 A;Reference number: A94167  
 A;Accession: B28027  
 A;Molecule type: protein  
 A;Residues: 1-17 <BAU>

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
 |||  
 Db 4 ETV 6

## RESULT 60

I24687  
 T-cell receptor beta-1 chain J-B1.6 segment - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999

C;Accession: I24687  
 R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A>Title: Organization and sequences of the diversity, joining, and constant region genes  
 A;Reference number: A94081; MUID:86094276; PMID:3866244  
 A;Accession: I24687  
 A;Molecule type: DNA  
 A;Residues: 1-17 <TOY>  
 A;Cross-references: GB:M14158; NID:g338844; PIDN:AAA60673.1; PID:g553685  
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15  
 |||  
 Db 15 TVT 17

## RESULT 61

G85956  
 hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL9  
 C;Species: Escherichia coli  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C;Accession: G85956  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: G85956  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-17 <STO>  
 A;Cross-references: GB:AF005174; NID:g12517539; PIDN:AGS9115.1; GSPDB:GN00145; UMG:P.Z43  
 C;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: Z4331

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
 |||  
 Db 2 ETV 4

## RESULT 62

PC2319  
 proteasome endopeptidase complex (EC 3.4.25.1), 2 chain - human (fragment)  
 N;Alternate names: protein  
 C;Species: Homo sapiens (man)  
 C;Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 17-Feb-2003  
 C;Accession: PC2319  
 R;Kristensen, P.; Johnsen, A.H.; Uerkvitz, W.; Tanaka, K.; Hendil, K.B.  
 Biochem. Biophys. Res. Commun. 205, 1785-1789, 1994  
 A>Title: Human proteasome subunits from 2-dimensional gels identified by partial sequenc  
 A;Reference number: PC2315; MUID:95110324; PMID:7811265  
 A;Accession: PC2319  
 A;Molecule type: protein  
 A;Residues: 1-17 <KKI>  
 A;Experimental source: placenta  
 C;Comment: The proteasome consists of subunits of 21K-30K arranged in 4 stacked rings.  
 C;Keywords: hydrolase; proteinase

Query Match 20.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
 |||

Db 8 VLE 10

# RESULT 63

S03528  
Ig heavy chain J1 region - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 20-Jun-2000  
C:Accession: S03528; G49021  
R:Schwager, J.; Groseberger, D.; du Pasquier, L.  
EMBO J. 7, 2403-2415, 1988  
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis  
A:Reference number: S01159; MUID:89052653; PMID:2903824  
A:Accession: S03528  
A:Molecule type: DNA  
A:Residues: 1-18 <SCH>  
A:Cross-references: EMBL:X14917; NID:G64802; PIDN:CAA33041.1; PID:g1334655  
R:Haide, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.  
J. Exp. Med. 171, 1721-1737, 1990  
A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation  
A:Reference number: A47624; MUID:90237760; PMID:2110243  
A:Accession: G49021  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 2-18 <HAI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 13 TVT 15  
Db 13 TVT 15

# RESULT 64

PC2280  
Prolylendopeptidase-inhibiting peptide - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997  
C:Accession: PC2280  
R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.  
Biochem. Biophys. Res. Commun. 202, 809-815, 1994  
A:Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.  
A:Reference number: PC2280; MUID:94324971; PMID:8048952  
A:Accession: PC2280  
A:Molecule type: protein  
A:Residues: 1-18 <OHM>  
A:Experimental source: brain  
C:Superfamily: cytoskeletal keratin

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 PPP 9  
Db 2 PPP 4

# RESULT 65

B44995  
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - flashlight fish symbiont  
C:Species: flashlight fish symbiont bacterium  
C>Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 26-May-2000  
C:Accession: B44995  
R:Archgood, M.G.  
Arch Microbiol. 154, 496-503, 1990  
A:Title: Relationship of the luminous bacterial symbiont of the Caribbean flashlight fish  
A:Reference number: A44995; MUID:91076680; PMID:2256783

A:Accession: B44995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-18 <HAY>

A:Cross-references: GB:M36597; NID:G213345; PIDN:AAA91214.1; PID:g1204253

C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 MKF 6  
Db 1 MKF 3

# RESULT 66

S10452  
hypothetical protein (bpha 5' region) - Aspergillus niger  
C:Species: Aspergillus niger  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Sep-1997  
C:Accession: S10452  
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken  
submitted to the EMBL Data Library, March 1990  
A:Reference number: S10452  
A:Accession: S10452  
A:Molecule type: DNA  
A:Residues: 1-18 <VAN>  
A:Cross-references: EMBL:X52521; NID:G23336; PID:G23337

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 QET 13  
Db 9 QET 11

# RESULT 67

T13132  
protein GP45.1 - phage N15  
C:Species: phage N15  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 13-Aug-1999  
C:Accession: T13132  
R:Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.  
submitted to the EMBL Data Library, May 1998  
A:Reference number: Z17603  
A:Accession: T13132  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-18 <HEN>  
A:Cross-references: EMBL:AF064539; NID:G3192683; PID:G3192731; PIDN:AAC19084.1  
C:Genetics:  
A:Note: gene 45.1

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 QET 13  
Db 15 QET 17

# RESULT 68

A54195  
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)  
C:Species: Squalus acanthias (spiny dogfish)  
C>Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 19-Apr-2002  
C:Accession: A54195  
R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.  
Biochemistry 33, 8044-8050, 1994

A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase  
 A:Reference number: A54195; MUID:94297020; PMID:8025109

A:Accession: A54195  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-18 <ESM>  
 A:Experimental source: rectal gland  
 A>Note: sequence extracted from NCBI backbone (NCBIP:149363)  
 C:Keywords: hydrolase

Query Match 20.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9  
 |||  
 Db 8 PPP 10

## RESULT 69

PS0186  
 Superoxide dismutase (EC 1.15.1.1) (Mn) - rice (fragment)

C:Species: Oryza sativa (rice)  
 C>Date: 05-Mar-1993 #sequence\_revision 05-Mar-1993 #text\_change 05-Mar-1999  
 C:Accession: PS0186  
 R:Kamo, M.; Tsugita, A.  
 submitted to JIPID, June 1991

A:Reference number: PS0184  
 A:Accession: PS0186  
 A:Molecule type: protein  
 A:Residues: 1-19 <RAM>  
 A:Experimental source: callus

C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
 |||  
 Db 2 ETV 4

## RESULT 70

PN0467

Nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha chain - Azotobacter chroococcum

C:Species: Azotobacter chroococcum  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
 C:Accession: PN0467

R:Jones, R.; Woodley, P.; Birkmann-Zinoni, A.; Robson, R.L.  
 Gene 123, 145-146, 1993

A:Title: The nifH gene encoding the Fe protein Component of the molybdenum nitrogenase

A:Reference number: JN0516; MUID:93138425; PMID:8423000  
 A:Accession: PN0467

A:Molecule type: DNA

A:Residues: 1-19 <JON>

A:Cross-references: GB:M73020; NID:gl42326; PIDN:AAA22141.1; PID:G289238

C:Genetics:

A:Gene: nifD

C:Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain

C:Keywords: ATP; nitrogen fixation; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
 |||  
 Db 16 VLE 18

## RESULT 71

B26930

ermG leader peptide 2 - Bacillus sphaericus

C:Species: Bacillus sphaericus  
 C>Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 26-Aug-1999  
 C:Accession: B26930  
 R:Monod, M.; Mohan, S.; Dubnau, D.  
 J. Bacteriol. 169, 340-350, 1987

A:Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance gene from *Bacillus sphaericus*

A:Reference number: A51840; MUID:87083389; PMID:3025178

A:Accession: B26930

A:Molecule type: DNA

A:Residues: 1-19 <MON>

A:Cross-references: GB:M15332; NID:gl42881; PIDN:AAA22418.1; PID:gl42883

C:Superfamily: ermC leader peptide

Query Match 20.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
 |||  
 Db 10 ETV 12

## RESULT 72

S31613

Beta-1,3-glucanase homolog (clone A28) - rape (fragment)

C:Species: Brassica napus (rape)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Nov-2000

C:Accession: S31613

R:Hird, D.; Morrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.

submitted to the EMBL Data Library, December 1992

A:Description: The anther-specific protein encoded by the Brassica napus and Arabidopsis

A:Reference number: S31612

A:Accession: S31613

A:Molecule type: mRNA

A:Residues: 1-19 <HIR>

A:Cross-references: EMBL:X69890; NID:gl7735; PID:gl7736

A:Experimental source: clone A28

C:Superfamily: beta-1,3-glucanase

Query Match 20.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFP 7  
 |||  
 Db 13 KFP 15

## RESULT 73

A49780

Promoter P8 hypothetical protein - Streptococcus thermophilus (strain A054) (fragment)

C:Species: Streptococcus thermophilus

C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999

C:Accession: A49780

R:Glos, P.; Bourquin, J.C.; Lemoine, Y.; Mercenier, A.

Appl. Environ. Microbiol. 57, 1333-1339, 1991

A:Title: Isolation and characterization of chromosomal promoters of Streptococcus salivarius

A:Reference number: A49780; MUID:91307302; PMID:1854195

A:Accession: A49780

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-19 <SLO>

A:Cross-references: GB:M69234

Query Match 20.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5

```

Db      2 EMK 4
      |||
RESULT 74
G56819
PS I complex subunit 6 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: G56819
R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A;Reference number: A56819; MUID:91355209; PMID:1883835
A;Accession: G56819
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <IWA>
A;Note: sequence extracted from NCBI backbone (NCBIP:58604)

Query Match      20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPP 9
      |||
Db      6 PPP 8

RESULT 75
T50329
wd-repeat protein popl. [imported] - fission yeast (Schizosaccharomyces pombe) (fragment
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50329
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25062
A;Accession: T50329
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <LYN>
A;Cross-references: EMBL:AL157874; PDB:1AB75991.1; GSPDB:GN00067; SPDB:SPBC1718.01
A;Experimental source: strain 972h(-); cosmid ci718
C;Genetics:
A;Gene: SPBC2G2.18; SPDB:SPBC1718.01
A;Map position: 2

Query Match      20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLE 3
      |||
Db     10 VLE 12

Search completed: November 25, 2003, 18:28:18
Job time : 14.8032 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 7.26064 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKPPPPQETWT 15

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	33.3	15	1 PRP_MYCBO	P80149 mycobacteri
2	4	26.7	10	1 Q20B_COMTE	P80465 comamonas t
3	4	26.7	10	1 TWF_AEDAE	P19425 asdes aegyp
4	3	20.0	9	1 FLA2_TREHY	P80159 treponema h
5	3	20.0	12	1 FIP1_SARBU	P83349 sarcophaga
6	3	20.0	13	1 IDHA_CANFA	P54836 canis fami
7	3	20.0	13	1 NO40_PEA	P55959 pisum sativ
8	3	20.0	13	1 TY13_PHYRO	P04096 phyllomedus
9	3	20.0	14	1 KLPS_SCARA	P58396 scaptocosa
10	3	20.0	16	1 AF2S_MALPA	P83142 malva parvi
11	3	20.0	16	1 IBP4_FIG	P24854 sus scrofa
12	3	20.0	17	1 LUXB_KRYAS	P81464 bombus pasc
13	3	20.0	18	1 APID_BOMPA	P18300 kryptophana
14	3	20.0	19	1 HI70_RAT	P21794 rattus norv
15	3	20.0	19	1 PSAE_CUCSA	P42047 cucumis sat
16	3	20.0	20	1 APAL_ERYPA	P18647 erythrocebu
17	3	20.0	20	1 CS21_STRTR	P81621 streptococ
18	3	20.0	20	1 DNAK_MYCAV	P80462 mycobacteri
19	3	20.0	20	1 MDH_KIBAR	P19978 kibelospor
20	3	20.0	20	1 MDH_MICGL	P19979 microtetras
21	3	20.0	20	1 RM01_YEAST	P36515 saccharomyc
22	3	20.0	20	1 E104_LITRU	P82100 litaria rub
23	3	20.0	20	1 PAP2_PARMA	P81864 pardachirus
24	3	20.0	20	1 ACPH_RABIT	P25154 oryctolagus
25	3	20.0	20	1 VP19_HSVIK	P23210 herpes simp
26	3	20.0	20	1 CCF1_ENTFA	P20104 enterococcu
27	3	20.0	20	1 TFYF_PACDA	P83455 pachymedusa
28	3	20.0	20	1 UF04_MOUSE	P38642 mus musculu
29	3	20.0	20	1 WWA1_ACHFU	P35919 achatina fu
30	3	20.0	20	1 WWA3_ACHFU	P35921 achatina fu
31	3	20.0	20	1 ALL5_CALVO	P41841 calliphora
32	3	20.0	20	1 CAD1_ENTFA	P13268 enterococcu
33	3	20.0	20	1 CLP_THICU	P80488 thiobacilli

#### ALIGNMENTS

RESULT 1

34	2	13.3	8	1	COW2_CONPU	P58785 conus purpu
35	2	13.3	8	1	NPB_BOVIN	P15507 bos taurus
36	2	13.3	8	1	PFK2_PIRAM	P82692 periplaneta
37	2	13.3	8	1	UH09_RAT	P56575 rattus norv
38	2	13.3	8	1	UPA1_HUMAN	P30087 homo sapien
39	2	13.3	8	1	AL10_CARMA	P81813 carinus ma
40	2	13.3	9	1	BS43_SBRPL	P83375 serrattia pl
41	2	13.3	9	1	FAR1_CALVO	P41856 calliphora
42	2	13.3	9	1	FIBB_ERYPA	P18346 erythrocebu
43	2	13.3	9	1	FIBB_PAPAN	P19344 papio anubi
44	2	13.3	9	1	FIBB_PAPHA	P19343 papio hamad
45	2	13.3	9	1	FIBB_THEGE	P19342 theriopthec
46	2	13.3	9	1	KNL3_BOWMA	P83058 bombina var
47	2	13.3	9	1	OXYT_RAJUL	P36884 staphylococ
48	2	13.3	9	1	LPCA_STAAU	P42994 raja clavav
49	2	13.3	9	1	SAMP_MUSCA	P19095 mustelus ca
50	2	13.3	9	1	SAP_STOVA	P24047 stomopneute
51	2	13.3	9	1	UHA2_HUMAN	P40929 homo sapien
52	2	13.3	9	1	ULAE_HUMAN	P31931 homo sapien
53	2	13.3	9	1	ULAH_HUMAN	P31934 homo sapien
54	2	13.3	9	1	UN19_CLOPA	P81355 clostridium
55	2	13.3	9	1	UPA3_HUMAN	P30089 homo sapien
56	2	13.3	9	1	YBFR_AZOVI	P25825 azotobacter
57	2	13.3	10	1	AH3_BRUSE	P29261 prunus sero
58	2	13.3	10	1	AKHX_LOCMI	P81626 locusta mig
59	2	13.3	10	1	BPP2_BOTIN	P30422 bothrops in
60	2	13.3	10	1	BPP2_BOTJA	P30422 bothrops ja
61	2	13.3	10	1	BPP8_BOTIN	P30426 bothrops in
62	2	13.3	10	1	BPP_VIPAS	P31351 vipera aspi
63	2	13.3	10	1	BRK_ONCMY	Q9PRZ1 oncorhynch
64	2	13.3	10	1	COXA_ONCMY	P80328 oncorhynch
65	2	13.3	10	1	ESL_LACCA	P81758 lactobacill
66	2	13.3	10	1	FARG_PANRE	P82660 panagrellus
67	2	13.3	10	1	GONI_PETMA	P84378 petromyzon
68	2	13.3	10	1	LABA_JATMU	P13270 jatropha mu
69	2	13.3	10	1	ODP2_BOVIN	P11180 bos taurus
70	2	13.3	10	1	PVK_LOCMI	P83382 locusta mig
71	2	13.3	10	1	SLAP_BACTG	P49325 bacillus th
72	2	13.3	10	1	TKL3_LOCMI	P30249 locusta mig
73	2	13.3	10	1	TKN1_SCYCA	P08608 scyllorhinu
74	2	13.3	10	1	TKS1_AEDAE	P42634 asdes aegyp
75	2	13.3	10	1	TKS2_AEDAE	P42635 asdes aegyp
76	2	13.3	10	1	UPA2_HUMAN	P30088 homo sapien
77	2	13.3	10	1	UPA5_HUMAN	P30091 homo sapien
78	2	13.3	10	1	URE3_MORMO	P17339 morganella
79	2	13.3	11	1	BPP3_BOTIN	P30423 bothrops in
80	2	13.3	11	1	BPP4_BOTIN	P30424 bothrops in
81	2	13.3	11	1	BPPB_AGKHA	P01021 agkistrodon
82	2	13.3	11	1	BPP_AGKHP	P04562 agkistrodon
83	2	13.3	11	1	BRK_MEGFL	P12797 megascolia
84	2	13.3	11	1	CEPI_ACHFU	P22790 achatina fu
85	2	13.3	11	1	COXA_CANFA	P99501 canis fami
86	2	13.3	11	1	EPG_CLOPA	P81350 clostridium
87	2	13.3	11	1	ESI_RAT	P56571 rattus norv
88	2	13.3	11	1	LADD_ONCMY	P80118 oncorhynch
89	2	13.3	11	1	MHBI_KLEPN	P80580 klebsiella
90	2	13.3	11	1	MLG_THETS	P41989 thermozon
91	2	13.3	11	1	MORN_HUMAN	P01163 homo sapien
92	2	13.3	11	1	NXSN_PSETE	P59072 pseudonaja
93	2	13.3	11	1	RANC_RANPI	P08952 rana pipien
94	2	13.3	11	1	RR2_CONAM	P42341 conopholis
95	2	13.3	11	1	TKNA_CHICK	P19850 gallus gall
96	2	13.3	11	1	TKNA_GADMO	P28498 gadus morhu
97	2	13.3	11	1	TKNA_HORSE	P01290 equus cabal
98	2	13.3	11	1	TKN_PHYFU	P08615 physalaema
99	2	13.3	12	1	FAR7_PENMO	P83322 peneaus mon
100	2	13.3	12	1	HCYE_MEGCR	Q10584 megathura c



```

PRP_MYCBO
ID PRP_MYCBO STANDARD; PRT; 15 AA.
AC P80149;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Proline-rich protein (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1785;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93281750; PubMed=8506381;
RA Romain F., Augier J., Pescher P., Marchal G.A.;
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
RT type hypersensitivity reactions only in guinea pigs immunized with
RT living mycobacteria."
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
CC REACTIONS IN GUINEA PIGS.
FT NON TER 15
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
DB 7 PPPPQ 11

RESULT 2
Q20B COMTE STANDARD; PRT; 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation."
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON TER 10
SQ SEQUENCE 10 AA; 1241 MW; C2B2C25DD9DC769 CRC64;

Query Match 26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MKFP 7
DB 1 MKFP 4

RESULT 3
ID TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19435;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating costatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito costatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut."
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=9357794; PubMed=835326;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating costatic factor (TMOF) and its analogs."
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
CC PIR; A36454; A36454.
KW Hormone.
DM DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD->DY [IN TMOF(B)].
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 5 PPPP 8

RESULT 4
ID FLA2_TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (fragment).
RN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,

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RA van der Zeijst B.A.M., Kusters J.G.;  
 RT "The periplasmic flagella of *Serpulina* (Treponema) hyodysenteriae are  
 RL composed of two sheath proteins and three core proteins.";  
 CC J. Gen. Microbiol. 138:2697-2706(1992).  
 CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLUM.  
 CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO  
 CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE  
 CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND  
 CC FLAB3 (32 kDa).  
 CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.  
 KW Flagella; Periplasmic.  
 FT UNSURE 2  
 FT UNSURE 8  
 FT NON-TER 9  
 SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 12 ETV 14  
 Db 1 ETV 3  
 RESULT 5  
 FIF\_SARBU STANDARD; PRT; 12 AA.  
 AC P83349;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neb-FIRamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Sarcophagidae; Sarcophaga.  
 CC NCBI\_TaxID=7385;  
 [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE-CNS.  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Neusen I., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;  
 RT "Identification in *Drosophila melanogaster* of the invertebrate G  
 RT protein-coupled FMRFamide receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
 CC junctions.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 PPO 11  
 Db 2 PPO 4  
 RESULT 6  
 IDHA CANFA STANDARD; PRT; 13 AA.  
 AC P54836;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial

DE (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD+-specific ICDH)  
 DE (fragment).  
 GN IDH3A.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 CC NCBI\_TaxID=9615;  
 [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J. Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) +  
 CC NADH.  
 CC -!- SUBUNIT: HETEROOLIGOMER OF SUBUNITS ALPHA, BETA, AND GAMMA IN THE  
 CC APPARENT RATIO OF 2:1:1 (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE  
 CC DEHYDROGENASES FAMILY.  
 CC HSC-2DPAGE; P54836; DOG.  
 DR InterPro; IPR001804; Isodh.  
 DR PROSITE; PS00470; IDH IMDH; PARTIAL.  
 KW Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.  
 FT NON-TER 13 13  
 SQ SEQUENCE 13 AA; 1356 MW; 9ABFBC2B2A34B2D1 CRC64;  
 Query Match 20.0%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 TVT 15  
 Db 6 TVT 8  
 RESULT 7  
 NC40\_PEA STANDARD; PRT; 13 AA.  
 AC P55959;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 13-DEC-1998 (Rel. 37, Last annotation update)  
 DE Early nodulin 40.  
 GN ENOD40.  
 OS Pisum sativum (Garden pea).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 CC NCBI\_TaxID=3888;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Sparkle; TISSUE=Root nodules;  
 RX MEDLINE=95036021; PubMed=7948896;  
 RA Matvienko M., van de Sande K., Yang W.C., van Kammen A., Bisseling T.,  
 RA Franssen H.J.;  
 RT "Comparison of soybean and pea ENOD40 cDNA clones representing genes  
 RT expressed during both early and late stages of nodule development.";  
 RL Plant Mol. Biol. 26:487-493(1994).  
 CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT  
 CC GROWTH REGULATOR THAT ALTERS PHYtohORMONE RESPONSES (BY  
 CC SIMILARITY).  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE  
 CC DEVELOPMENT.  
 -----  
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CC -----
CC EMBL: X81064; -, NOT_ANNOTATED_CDS.
CC -----
KW Modulation
SQ SEQUENCE 13 AA; 1565 MW; 3C695B66BD8A26C3 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKF 6
DB 1 MKF 3

RESULT 8
TY13 PHYRO
ID TY13 PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-13.
OS Phyllomedusa rhodei (Rhode's leaf frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
CC Phyllomedusinae; Phyllomedusa.
CC NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Ersamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rhodei."
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR: A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A21222773 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB 7 PPP 9

RESULT 9
KLPS SCARA
ID KLPS SCARA STANDARD; PRT; 14 AA.
AC P58396;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kinin-like peptide-S (Fragment).
OS Scaptocosa raptorix (Spider).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
CC Araneomorphae; Etelegynae; Lycosoidea; Lycosidae; Scaptocosa.
CC NCBI_TaxID=180440;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98267639; PubMed=9604280;
RA Ferreira L.A.F., Lucas S.M., Alves E.W., Hermann V.V., Reichl A.P.,
RA Habermehl G., Zingali R.B.;
RT "Isolation, characterization and biological properties of two
RT kinin-like peptides (peptide-S and peptide-R) from Scaptocosa
RT raptorix venom."
RL Toxicon 36:31-39(1998).
CC -!- FUNCTION: Has kinin-like biological properties. Causes contraction

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CC on the of mammalian ileum; relaxes the duodenum and increases the
CC capillary permeability.
CC Vasodilator.
KW NON_TER 14 14
SQ SEQUENCE 14 AA; 1510 MW; E811E2E5D2EE27CA CRC64;

Query Match 20.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 3 VLE 5

RESULT 10
AF2S MALPA
ID AF2S MALPA STANDARD; PRT; 16 AA.
AC P83142;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein-2, small subunit (CW-2) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
CC NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=1118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
RT parviflora)."
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
CC GO; GO:0003799; F:antifungal peptide activity; IDA.
DR Fungicide; Antibiotic.
KW NON_TER 16 16
FT SEQUENCE 16 AA; 2027 MW; 9998D9E8F8F7EE65 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
DB 9 PPQ 11

RESULT 11
IBP4 PIG
ID IBP4 PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Ehterton T.D.;

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RT Identification and NH2-terminal amino acid sequence of three
RL insulin-like growth factor-binding proteins in porcine serum."
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 IGF-BP domain.
CC -1- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR PIR: JH0517; JH0517.
DR InterPro: IPR000867; Insl_gro_fac_dr.
DR InterPro: IPR000716; Thyroglobulin_1.
DR PROSITE: PS00222; IGF BINDING; PARTIAL.
DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 4098884009655E2 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 12
APID_BOMPA STANDARD; PRT; 17 AA.
AC P11464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apidaecin.
OS Bombus pascuorum (Brown bumble bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=65598;
RN (1) SEQUENCE.
RC TISSUE=Hemolymph; PubMed=9219367;
EX MEDLINE=97362903;
EA Rees J.A., Moniatte M., Bulet P.;
ET "Novel antibacterial peptides isolated from a European bumblebee,
RL Bombus pascuorum (Hymenoptera, Apoidea).";
RL Insect Biochem. Mol. Biol. 27:413-422(1997).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -1- INDUCTION: By bacterial infection.
DR InterPro: IPR004828; Apidaecin.
DR Pfam: PF00807; Apidaecin; 1.
KW Insect immunity; Antibiotic; Hemolymph.
SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 8 PPP 10

RESULT 13
LUXB_KRYAS STANDARD; PRT; 18 AA.
AC P18300;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

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DE Alkanal monooxygenase beta chain (BC 1.14.14.3) (Bacterial luciferase
DE beta chain) (Fragment).
GN LUXB.
OS Kryptophanaron alfredi symbiont.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
CC Vibrionaceae; light emitting symbionts of fish.
OX NCBI_TaxID=28177;
RN (1) SEQUENCE FROM N.A.
EX MEDLINE=91076680; PubMed=2256783;
RA Haygood M.G.;
RT Relationship of the luminous bacterial symbiont of the Caribbean
RT flashlight fish, Kryptophanaron alfredi (family Anomalopidae) to
RT other luminous bacteria based on bacterial luciferase (luxA) genes.";
RL Arch. Microbiol. 154:496-503(1990).
CC -1- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE
CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY
CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: RCHO + FMNH(2) + O(2) = RCOOH + FMN + H(2)O +
CC light.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -----
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CC -----
DR EMBL: M36597; AAA91214.1;
DR InterPro: IPR002103; Bac_luciferase.
DR PROSITE: PS00494; BACTERIAL_LUCIFERASE; PARTIAL.
KW Photoprotein; luminescence; Oxidoreductase; Monooxygenase;
FW Flavoprotein; FMN.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKF 6
Db 1 MKF 3

RESULT 14
HI70_RAT STANDARD; PRT; 19 AA.
AC P21794;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Hormone-induced protein 70 kDa (HIP-70) (Fragment).
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10115;
RN (1) SEQUENCE.
EX MEDLINE=90208308; PubMed=2181662;
RA Mobbs C.V., Fink G., Pfaff D.W.;
RT "HIP-70: a protein induced by estrogen in the brain and LH-RH in the
RT pituitary.";
RL Science 247:1477-1479(1990).
CC -1- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN
CC HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH IN
CC PITUITARY.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2113 MW; F793A98720B68E3C CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;

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Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 VLE 3  
|||  
Db 2 VLE 4

## RESULT 15

PSAE\_CUCSA STANDARD; PRT; 19 AA.  
AC P42047;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 19.5 kDa protein) (PS I subunit 6) (Fragment).  
GN PSAB.  
OS Cucumis sativus (Cucumber).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
OX NCBI\_TaxID=3659;  
RN [1]  
RP SEQUENCE.

RC ISSUES=Cotyledon; PubMed=1893835;  
RA MEDLINE=91355209; Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;  
RA "Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing."  
RT Biochim. Biophys. Acta 1059:141-148(1991).  
CC -!- FUNCTION: Stabilizes the interaction between psaC and the PSI core, assists the docking of the ferredoxin to PSI and interacts with ferredoxin-NADP oxidoreductase (By similarity).  
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.  
CC -!- SIMILARITY: BELONGS TO THE PSAB FAMILY.  
RX PIR: G56819; G56819.  
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.  
FT NON TER 19 19  
SQ SEQUENCE 19 AA; 1810 MW; A93B8BDD089FB738 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 7 PPP 9  
|||  
Db 6 PPP 8

## RESULT 16

APAL\_ERYPA STANDARD; PRT; 20 AA.  
AC P18647;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apolipoprotein A-I (Apo-AI) (Fragment).  
GN APOA1.  
OS Erythrocybus patas (Red guenon) (Hussar).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Erythrocybus.  
OX NCBI\_TaxID=9538;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76184721; PubMed=178359;  
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;  
RT "Characterization of the plasma lipoproteins and apoproteins of the Erythrocybus patas monkey."  
RL Biochemistry 15:1928-1933(1976).  
CC -!- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN CHYLOMICRONS.  
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
DR PIR: A05313; A05313.  
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.  
FT NON TER 20 20  
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 3; Conservative 0; Indels 0; Gaps 0;

QY 9 PPQ 11  
|||  
Db 3 PPQ 5

## RESULT 17

CS21\_STETR STANDARD; PRT; 20 AA.  
AC P81621;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 21 kDa cold-shock induced protein (Fragment).  
OS Streptococcus thermophilus.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1308;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=99456673; PubMed=10525839;  
RA Perrin C., Guimont C., Braquart P., Gaillard J.L.;  
RA "Expression of a new cold shock protein of 21.5 kDa and of the major cold shock protein by Streptococcus thermophilus after cold shock."  
RL Curr. Microbiol. 39:342-347(1999).  
CC -!- INDUCTION: By cold shock.  
FT NON TER 20 20  
SQ SEQUENCE 20 AA; 2390 MW; 9C2CA57F266880AD CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 3; Conservative 0; Indels 0; Gaps 0;

QY 12 ETV 14  
|||  
Db 10 ETV 12

## RESULT 18

DNAB\_MYCAV STANDARD; PRT; 20 AA.  
AC P80462;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) (Fragment).  
GN DNAB.  
OS Mycobacterium avium.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1764;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97126793; PubMed=8971687;  
RA Ratnakar P., Rao S.P., Catanzaro A.;  
RA "Isolation and characterization of a 70 kDa protein from

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RT Mycobacterium avium.;
RL Microb. Pachos. 21:471-486(1996).
CC -1- INDUCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -1- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HAMAP; MF_00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70.1; PARTIAL.
DR PROSITE; PS00329; HSP70.2; PARTIAL.
DR PROSITE; PS01036; HSP70.3; PARTIAL.
KW Chaperone; ATP-binding; Heat shock.
FT VARIANT 17 17
FT NON_TER 20 20
FT SEQUENCE 20 AA; 1926 MW; 625A1CBBEP9ADC87 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 17 VLE 19

RESULT 19
MDH_KIBAR
ID MDH_KIBAR STANDARD; PRT; 20 AA.
AC P19978;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.
OS Kibdelosporangium aridum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Kibdelosporangium.
OX NCBI_TaxID=2030;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374824; PubMed=2775496;
RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
dehydrogenases from six actinomycetales strains and from
Phenyllobacterium immobile strain E."
RL Biol.Chem.Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20 20
FT SEQUENCE 20 AA; 1989 MW; 79587E5F58C00AC9 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 8 TVT 10

RESULT 20
MDH_MICGL
ID MDH_MICGL STANDARD; PRT; 20 AA.
AC P19979;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.

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OS Microtrasporea glauca.
OC Bacteria; Actinobacteridae; Actinobacteriales; Actinomycetales;
OC Streptosporangiaceae; Streptosporangiaceae; Microtrasporea.
OX NCBI_TaxID=1996;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374824; PubMed=2775496;
RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
dehydrogenases from six actinomycetales strains and from
Phenyllobacterium immobile strain E."
RL Biol.Chem.Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20 20
FT SEQUENCE 20 AA; 2065 MW; 740129BE59D01EBE CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 5 TVT 7

RESULT 21
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285105; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4
FT SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VT 15
DB 2 VT 3

RESULT 22
EI04_LITRU
ID EI04_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TV 14
DB 3 TV 4

RESULT 23
PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 4 FP 5

RESULT 24
ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
RN [1]_TaxID=5986;
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=5986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 25
VP19 HSV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Viron protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]_TaxID=10306;
RP SEQUENCE FROM N.A.
RX MEDLINE=91101267; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93765912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC -!- SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; G33245.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 3 EM 4

RESULT 30
WMA3 ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 3 EM 4

RESULT 31
ALI5 CALVO STANDARD; PRT; 8 AA.
AC P41841.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calliostatin 5 (Met-calliostatin 1) ([HYP3]Met-calliostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;

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RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Calliostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-calliostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION (20%).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PP 8
DB 2 PP 3

RESULT 32
CADI ENTFA STANDARD; PRT; 8 AA.
ID CADI_ENTFA
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CADI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Segakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CADI, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 33
CLP THICU STANDARD; PRT; 8 AA.
ID CLP_THICU
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemiluminophor-specific protein (Fragment).
OS Thioabacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]_SEQUENCE.
RP STRAIN=DSM 5494;
RC Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RA Submitted (SEP-1995) to the SWISS-PROT data bank.
RL -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOLUMINOGENICALLY.
CC NON TER
FT MOD_RES 8
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QE 12
Db 5 QE 6

RESULT 34
COW2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]_SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP STRAIN=Clipperton Island; TISSUE=Venom;
RC MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez B.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD_RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VL 2
Db 3 VL 4

RESULT 35
NFB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine";
PL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR, B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQ 11
Db 5 PQ 6

RESULT 36
PPK2_PERAM STANDARD; PRT; 8 AA.
ID _PPK2_PERAM
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-EK-2) (EXPRIL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Corpora cardiaca;
RC MEDLINE=9733923; PubMed=9210163;
RA Fredel R., Reilner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RC MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of EXPRILamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro, IPR001484; Pyrokinin.
DR PROSITE, PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 PP 8  
DB 2 PP 3

## RESULT 37

ID UH09 RAT STANDARD; PRT; 8 AA.  
AC P56575;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).  
OS Rattus norvegicus (Rat)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.

RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
RA Jungblut P.R.;  
RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 8.9, ITS MW IS: 42 KDa.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 1029 MW; 950775A6C4140B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 OE 12  
DB 1 QE 2

## RESULT 38

ID UPAL HUMAN STANDARD; PRT; 8 AA.  
AC P30087;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Faquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 4.9, ITS MW IS: 65 KDa.  
DR SWISS-2DPAGE; P30087; HUMAN.  
FT NON TER 1  
FT UNSURE 8  
FT NON TER 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 OE 12  
DB 2 QE 3

## RESULT 39

ID AL10 CARMA STANDARD; PRT; 9 AA.  
AC P81813;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 10.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas."  
Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 963 MW; 372D79CDB476C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQ 11  
DB 2 PQ 3

## RESULT 40

ID BS43 SERPL STANDARD; PRT; 9 AA.  
AC P83375;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bacteriocin serracin P 43 kDa subunit (Fragment).  
OC Serratia plymuthica.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OX NCBI\_TaxID=82996;  
RN [1]  
RP SEQUENCE, AND FUNCTION.

RC STRAIN=J7;  
RX MEDLINE=22293561; PubMed=12406768;  
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,  
RA Van Beeumen J., Thonart P.;  
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and  
its activity against *Erwinia amylovora*, the fire blight pathogen."  
Appl. Environ. Microbiol. 68:5704-5710(2002).  
CC -1- FUNCTION: Major component of a prophage tail sheath (Probable).  
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacterium  
*E. amylovora*.  
DR InterPro: IPR006498; Tail tube.  
DR Pfam: PF04985; Phage\_tube\_1.  
KW Antibiotic; Bacteriocin.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871E1FB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
8 VL 9

## RESULT 41

ID FARI CALVO STANDARD; PRT; 9 AA.  
AC P41856;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion; PubMed=1549595;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
CC SALIVARY GLAND OF CALLIPHORA.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR: A41978; A41978.  
KW Neuropeptide; Anidation.  
FT MOD\_RES 9 ANIDATION.  
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQ 11  
2 PQ 3

## RESULT 42

ID FIBB ERYPA STANDARD; PRT; 9 AA.  
AC P19346;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Erythrocybus patas (Red guenon) (Husar).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Erythrocybus.  
OX NCBI\_TaxID=9538;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=85289140; PubMed=3928610;  
RA Nakamura S., Takenaka O., Takahashi K.;  
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and  
RT patas monkey (Erythrocybus patas): their amino acid sequences,  
RT restricted mutations, and a molecular phylogeny for macaques,  
RT guenons, and baboons.";  
RL J. Biochem. 97:1487-1492(1985).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
CC PIR; D24180; D24180.  
DR InterPro; IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
4 VL 5

## RESULT 43

ID FIBB PAPAN STANDARD; PRT; 9 AA.  
AC P19344;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Papio.  
OX NCBI\_TaxID=9555;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84161822; PubMed=6423621;  
RA Nakamura S., Takenaka O., Takahashi K.;  
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,  
RT and Theropithecus gelada): their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the baboons.";  
RL J. Biochem. 94:1973-1978(1983).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
CC PIR; D28854; D28854.  
DR InterPro; IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1076 MW; DDP6409C7287B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QE 12  
2 QE 3

## RESULT 44

ID FIBB PAPA STANDARD; PRT; 9 AA.

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AC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecinae; Papio.
CC NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; E28854; E28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QE 12
DB 2 QE 3

RESULT 45
FIBB THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Theropithecus gelada (Gelada baboon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecinae; Theropithecus.
CC NCBI_TaxID=9565;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

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CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; E28854; E28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QE 12
DB 2 QE 3

RESULT 46
KNL3 BOMVA STANDARD; PRT; 9 AA.
ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
CC NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.P., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PP 8
DB 2 PP 3

RESULT 47
LPCA STAAU STANDARD; PRT; 9 AA.
ID LPCA_STAAU STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus agalactiae.
CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus; STRAIN=436; PLASMID=pSCS7;
RX MEDLINE=92027652; PubMed=1929326;

```

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RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus.";
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pSCS6;
RX MEDLINE=92388047; PubMed=1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus.";
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pUB112;
RX MEDLINE=86081739; PubMed=3865770;
RA Bruckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid PUB112.";
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.agalactiae; PLASMID=pIP501;
RX MEDLINE=91036867; PubMed=1461942;
RA Trieu-Cuot P., de Cespèdes G., Hovaud T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501.";
RL Plasmid 28:272-276(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
RN [6]
RX MEDLINE=588515; AAA26612.1; -
DR EMBL; M58516; AAA16528.1; -
DR EMBL; X02872; CAA26630.1; -
DR EMBL; X60827; CAA43217.1; -
DR EMBL; X65462; CAA46454.1; -
DR FIR; B24362; B24362.
DR FIR; S30494; S30494.
RX Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA, 1074 MW, 5D9CAB5AAB05B333 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MK 5
Db 1 MK 2

RESULT 48
OXYT_RAJCL STANDARD; PRT; 9 AA.
AC F42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glutitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualea; Pristiogalea; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]_TaxID=7781;
RP SEQUENCE.

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RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,
RT glutitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
RL the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -1- FUNCTION: ANTIDIURETIC HORMONE.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_borm.
DR Pfam; PF00230; hormone4.1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA, 984 MW, 17E9C76B455B04B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQ 11
Db 7 PQ 8

RESULT 49
SAMP MUSCA STANDARD; PRT; 9 AA.
AC F19055;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OX Mustelus.
OX NCBI_TaxID=7812;
RN [1]_TaxID=7812;
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma;
FT DOMAIN 1 >9
FT NON_TER 9 9
SQ SEQUENCE 9 AA, 965 MW, D05B5735B3386769 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 2 PP 3

RESULT 50
SAP_STOVA STANDARD; PRT; 9 AA.
ID SAP_STOVA
AC P24047;

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DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Sperm-activating peptide (SAP).  
 OS Stomopneustes variolaris (Sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Diadematacea; Phrynosomatoida; Stomechinidae;  
 OC Stomopneustes.  
 OX NCBI\_TaxID=7663;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BOND.  
 RC TISSUE=Egg jelly;  
 RX MEDLINE=92097763; PubMed=1756858;  
 RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;  
 RT "Determination of the amino acid sequence of an intramolecular  
 RT disulfide linkage-containing sperm-activating peptide by tandem mass  
 RT spectrometry.";  
 RL FEBS Lett. 294:179-182(1991).  
 CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY  
 CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF  
 CC CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT  
 CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF  
 CC GUANYLATE CYCLASE.  
 FT DISULFID 3  
 FT SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;  
 SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred.No.1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KF 6  
 DB 1 KF 2  
 RESULT 51  
 ULAE HUMAN  
 ID UHA2 HUMAN STANDARD; PRT; 9 AA.  
 AC P40929;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=95203287; PubMed=7895732;  
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
 RT "The human myocardial two-dimensional gel protein database: update  
 RT 1994.";  
 RL Electrophoresis 15:1459-1465(1994).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.  
 FT NON TER 9  
 FT SEQUENCE 9 AA; 1104 MW; 8874B1B5B5B01B2CA CRC64;  
 SQ SEQUENCE 9 AA; 1104 MW; 8874B1B5B5B01B2CA CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred.No.1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 VT 15  
 DB 3 VT 4  
 RESULT 52  
 ULAE HUMAN  
 ID ULAE HUMAN STANDARD; PRT; 9 AA.  
 AC P31931;

DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.  
 FT NON TER 9  
 FT SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;  
 SQ SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred.No.1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LE 3  
 DB 6 LE 7  
 RESULT 53  
 ULAE HUMAN  
 ID ULAE HUMAN STANDARD; PRT; 9 AA.  
 AC P31934;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spot 94) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.5, ITS MW IS: 12 kDa.  
 FT NON TER 1  
 FT SEQUENCE 3 3 A -> L.  
 FT VARIANT 3 3  
 FT NON TER 9  
 FT SEQUENCE 9 AA; 990 MW; F1CC7B172AB6DDCA CRC64;  
 SQ SEQUENCE 9 AA; 990 MW; F1CC7B172AB6DDCA CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred.No.1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LE 3  
 DB 6 LE 7  
 RESULT 54  
 UN19 CLOPA  
 ID UN19 CLOPA STANDARD; PRT; 9 AA.  
 AC P81355;

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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OK NCBI_TaxID=1501;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE
RC STRAIN=W5;
RX MEDLINE=96291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum WS.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -!- MISCELLANEOUS: 19:802-806(1998).
CC VARIANT 8 9 M -> D.
FT NON TER 9
SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5B19DA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EM 4
Db 7 EM 8

RESULT 55
UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OK NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RP TISSUE=Plasma;
RC MEDLINE=91092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FP 7
Db 4 FP 5

RESULT 56
YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25925;
DT 01-MAY-1992 (Rel. 22, Created)

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DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azorobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OK NCBI_TaxID=354;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE
RX MEDLINE=92196129; PubMed=1549605;
RA Groisman W.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Siedel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M83692; AAA22122.1; -
DR PIR; B41983; B41983.
KW Hypothetical Protein.
FT NON TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8
Db 3 PP 4

RESULT 57
AH3_PRUSE STANDARD; PRT; 10 AA.
AC F29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OK NCBI_TaxID=23207;
RN [1]_SEQUENCE.
RP TISSUE=Seed;
RC Li C.P., Swain E., Poulton J.E.;
RT "Prunus", serotina, amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
OK Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      7 PP 8
Db      3 PP 4

RESULT 58
AKHX LOOMI
ID AKHX LOOMI STANDARD; PRT; 10 AA.
AC P81626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peptide hormone.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC Tissue=Corpora cardiaca;
RA Siebert K.J.;
RL Submitted (DEC-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
CC -!- INTERMEDIARY METABOLISM. BEHAVIOR AND/OR DEVELOPMENT.
CC -!- SIMILARITY. BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR InterPro: IPR0020477, AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 VT 15
Db      2 VT 3

RESULT 59
BPP2 BOTIN
ID BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC Tissue=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC it acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 VT 15
Db      2 VT 3

RESULT 59
BPP2 BOTIN
ID BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC Tissue=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC it acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PP 8
Db      9 PP 10

RESULT 60
BPP2 BOTIN
ID BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC Tissue=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocoy O.;
RT Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PP 8
Db      9 PP 10

RESULT 61
BPP8 BOTIN
ID BPP8 BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC Tissue=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).

```

CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.

DR PIR: H37196; H37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8

Db 9 PP 10

# RESULT 62

ID\_BPP\_VIPAS STANDARD; PRT; 10 AA.

AC P31351;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide (Angiotensin-converting

DE enzyme inhibitor).

OS Vipera aspis (Aspic viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;

OC Viperidae; Viperinae; Vipera.

OX NCBI\_TaxID=8706;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90382616; PubMed=2169439;

RA Komori Y., Sugihara H.;

RT "Characterization of a new inhibitor for angiotensin converting

RT enzyme from the venom of Vipera aspis aspis.";

RL Int. J. Biochem. 22:767-771(1990).

CC -1- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

CC PIR: A60377; XASNPC.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8

Db 9 PP 10

# RESULT 63

ID\_BKK\_ONCMY STANDARD; PRT; 10 AA.

AC Q9PZL1.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lysyl-bradykinin-like.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_TaxID=8022;

RN [1]

RP SEQUENCE.

RX MEDLINE=94039817; PubMed=8224232;

RA Conlon J.M., Olson K.R.;

RT "Purification of a vasoactive peptide related to lysyl-bradykinin from

RT trout plasma.";

RL FEBS Lett. 334:75-78(1993).

CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR

CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

DR PIR: S39030; S39030.

KW Bradykinin; Vasodilator.

SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8

Db 3 PP 4

# RESULT 64

ID\_COXA\_ONCMY STANDARD; PRT; 10 AA.

AC P80328;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_TaxID=8022;

RN [1]

RP SEQUENCE.

RX TISSUE=Liver;

RC MEDLINE=94237150; PubMed=8181469;

RA Freund R., Kadenbach B.;

RT "Identification of tissue-specific isoforms for subunits Vb and Vlla

RT of cytochrome c oxidase isolated from rainbow trout.";

RL Eur. J. Biochem. 221:1111-1116(1994).

CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C

CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.

DR PIR: S43625; S43625.

KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ET 13

Db 6 ET 7

# RESULT 65

ID\_ESL\_LACCA STANDARD; PRT; 10 AA.

AC P81758;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).

OS Lactobacillus casei.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1592;  
 RN [1] \_SEQUENCE  
 RP STRAIN=IPPL731;  
 RC Lopez de Felipe F.;  
 RA Submitted (MAR-1999) to the SWISS-PROT data bank.  
 RL Hydrolase; Serine esterase.  
 KW NON\_TER 10  
 PT SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;  
 SQ

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
 ||  
 Db 6 VL 7

## RESULT 66

FAR6\_PANRE  
 ID FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82620;  
 DT 18-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE FMRamide-like neuropeptide PF6 (NGAPQFVRP-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1] \_SEQUENCE, FUNCTION, AND AMIDATION.  
 RP Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of FMRamide-related  
 RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 10 10  
 FT SEQUENCE 10 AA; 1132 MW; CH1384C9D776C76D CRC64;  
 SQ

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQ 11  
 ||  
 Db 4 PQ 5

## RESULT 67

GON1\_PETWA  
 ID GON1\_PETWA STANDARD; PRT; 10 AA.  
 AC P04378;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (gonadotropin-releasing hormone I) (GNRH-I)  
 DE (Luliberin I).  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 OX NCBI\_TaxID=7757;  
 RN [1] \_SEQUENCE.  
 RP TISSUE=Brain;  
 RC MEDLINE=86158192; PubMed=3514603;  
 RX

RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;  
 RT "Primary structure of gonadotropin-releasing hormone from lamprey  
 RT brain."  
 RN J. Biol. Chem. 261:4812-4819(1986).  
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
 CC the secretion of both luteinizing and follicle-stimulating  
 CC hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the GNRH family.

DR PIR: A01412; ERLWGS.  
 DR InterPro: IPR002012; GNRH.  
 DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.  
 DR MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3  
 ||  
 Db 5 LE 6

## RESULT 68

LABA\_JATMU  
 ID LABA\_JATMU STANDARD; PRT; 10 AA.  
 AC P13270;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Labaditin.  
 OS Jatropha multifida (Physic nut).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Euphorbiaceae; Jatropha.  
 OX NCBI\_TaxID=3996;  
 RN [1] \_SEQUENCE

RP TISSUE=Latex;

RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;  
 RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha  
 RT multifida L. (Euphorbiaceae): Isolation and sequence determination  
 RT by means of two-dimensional NMR."  
 RL FEBS Lett. 256:91-96(1989).

CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE  
 CC CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY  
 CC SEEMS TO BE BASED ON AN INTERACTION WITH C1.

CC -!- PTM: This is a cyclic peptide.

CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR  
 CC TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.

SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TV 14  
 ||  
 Db 5 TV 6

## RESULT 69

ODP2\_BOVIN  
 ID ODP2\_BOVIN STANDARD; PRT; 10 AA.  
 AC P11180;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase

```

DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aicken A., James L.A., Yeaman S.J.;
RT "Primary structures around the lipote attachment site on the E2
RT component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
CC COPACITOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro: IPR003016; Lipoyl
DR PROSITE: PS00189; LIPOYL, PARTIAL.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.
FT NON_TER 1 1
FT BINDING 5 5 LIPOYL.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BECDA33AB1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ET 13
DB 2 ET 3

RESULT 70
PVK_LOCOMI
ID PVK_LOCOMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal
RT perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 7 FP 8

RESULT 71
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE S-layer protein (Surface layer protein) (Fragment).
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. Galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RP STRAIN=NRRL 4045; PubMed=2592346;
RX MEDLINE=90078111;
RA Luckeovich M.D., Beveridge T.O.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FP 7
DB 5 FP 6

RESULT 72
TKL3_LOCOMI
ID TKL3_LOCOMI STANDARD; PRT; 10 AA.
AC P30249;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin III (TK-III).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family.";
RL Regul. Pept. 31:199-212(1990).

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CC -I- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; A60073; ECLQ3M.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 10 PQ 11  
 DB 2 PQ 3  
 RESULT 73  
 ID TKN1 SCYCA STANDARD; PRT; 10 AA.  
 AC P08608;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Scyllorhinin I.  
 OS Scyllorhinus canicula (Spotted dogfish)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 CC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;  
 CC Scyllorhinidae; Scyllorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=86192829; PubMed=2422058;  
 RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;  
 RT "Scyllorhinin I and II: two novel tachykinins from dogfish gut.";  
 RL FEBS Lett. 200:111-116(1986).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 EX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;  
 RT "Primary structures and biological activities of substance-P-related  
 peptides from the brain of the dogfish, Scyllorhinus canicula.";  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; A24867; A24867.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 5 KF 6  
 DB 2 KF 3  
 RESULT 74  
 ID TKN1 AEDAE STANDARD; PRT; 10 AA.  
 AC P42634;  
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Sialokinin I.  
 OS Aedes aegypti (Yellowfever mosquito).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
 OX NCBI\_TaxID=7159;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Rockefeller; TISSUE=Salivary gland;  
 RX MEDLINE=94105119; PubMed=8278354;  
 RA Champagne D.E., Ribeiro J.M.C.;  
 RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever  
 mosquito Aedes aegypti.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).  
 CC -I- FUNCTION: VASODILATORY PEPTIDE. MAY ACTIVATE MACROPHAGES AT THE  
 CC SITE OF FEEDING.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; A49581; A49581.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1145 MW; 3DCFD6B59C33AA8 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 5 KF 6  
 DB 5 KF 6  
 RESULT 75  
 ID TKN2 AEDAE STANDARD; PRT; 10 AA.  
 AC P42635;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE Sialokinin II.  
 OS Aedes aegypti (Yellowfever mosquito).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
 OX NCBI\_TaxID=7159;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Rockefeller; TISSUE=Salivary gland;  
 RX MEDLINE=94105119; PubMed=8278354;  
 RA Champagne D.E., Ribeiro J.M.C.;  
 RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever  
 mosquito Aedes aegypti.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).  
 CC -I- FUNCTION: VASODILATORY PEPTIDE. MAY ACTIVATE MACROPHAGES AT THE  
 CC SITE OF FEEDING.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; B49581; B49581.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 5 KF 6  
 DB 5 KF 6

Search completed: November 25, 2003, 18:17:27  
Job time : 8.26064 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 36.1436 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKFPFPQETWT 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 810525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL\_23:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	26.7	12	4	Q9BZ49
2	4	26.7	15	6	Q9T814
3	4	26.7	15	10	P82439
4	4	26.7	17	6	Q9TR22
5	4	26.7	17	10	O49225
6	4	26.7	17	10	Q41400
7	4	26.7	18	4	Q9UCT9
8	4	26.7	20	11	O64619
9	3	20.0	7	2	Q54248
10	3	20.0	8	4	Q81UB8
11	3	20.0	9	4	Q9UCS8
12	3	20.0	9	4	Q9H4M8
13	3	20.0	9	5	O96417
14	3	20.0	9	10	P82429
15	3	20.0	10	4	Q9H121
16	3	20.0	10	4	Q9UMK9

17	3	20.0	10	4	Q9UCP3
18	3	20.0	10	8	Q94VG5
19	3	20.0	10	8	Q9TG95
20	3	20.0	10	10	P81898
21	3	20.0	10	12	Q9Q0W9
22	3	20.0	10	12	Q8JV70
23	3	20.0	10	12	Q9Q0W1
24	3	20.0	10	12	Q8JV68
25	3	20.0	10	12	Q9Q0V9
26	3	20.0	10	12	Q9Q0W7
27	3	20.0	10	12	Q8JV66
28	3	20.0	10	12	Q9Q0V7
29	3	20.0	10	12	Q8JV82
30	3	20.0	10	12	Q8JV76
31	3	20.0	10	12	Q8JV74
32	3	20.0	10	12	Q9Q0W5
33	3	20.0	10	12	Q9Q0X3
34	3	20.0	10	12	Q9Q0X5
35	3	20.0	10	12	Q9Q0W3
36	3	20.0	10	12	Q8JV80
37	3	20.0	10	12	Q9Q0X1
38	3	20.0	10	12	Q9Q0X9
39	3	20.0	10	12	Q8JV72
40	3	20.0	11	2	O44237
41	3	20.0	11	10	P82436
42	3	20.0	11	12	Q8S083
43	3	20.0	11	13	P83168
44	3	20.0	12	4	Q9UGS1
45	3	20.0	12	7	O77879
46	3	20.0	12	10	Q93X21
47	3	20.0	13	6	Q9BDQ8
48	3	20.0	13	15	Q98XM1
49	3	20.0	14	2	Q9ZB42
50	3	20.0	14	4	Q96KF9
51	3	20.0	14	5	P82216
52	3	20.0	14	10	Q94IT6
53	3	20.0	14	10	P82335
54	3	20.0	14	11	Q94JUS
55	3	20.0	14	12	Q9S0N0
56	3	20.0	14	12	Q9E0N1
57	3	20.0	14	12	Q995W2
58	3	20.0	15	2	Q9R533
59	3	20.0	15	3	Q96V23
60	3	20.0	15	4	Q15344
61	3	20.0	15	4	Q9UCJ8
62	3	20.0	15	5	Q9TWC7
63	3	20.0	15	6	Q28822
64	3	20.0	15	10	Q9S8Q8
65	3	20.0	15	10	Q9S8N8
66	3	20.0	15	11	Q9QVB6
67	3	20.0	15	11	Q9QVK9
68	3	20.0	15	11	Q9QWT2
69	3	20.0	15	11	Q9QVY3
70	3	20.0	15	11	Q9QVB7
71	3	20.0	15	13	Q9FTM6
72	3	20.0	15	13	Q9PS61
73	3	20.0	15	13	P83102
74	3	20.0	15	15	O85713
75	3	20.0	16	2	Q9R4D1
76	3	20.0	16	6	Q9BG68
77	3	20.0	16	6	Q9TQ27
78	3	20.0	16	6	Q9TRD1
79	3	20.0	16	8	O8SLF0
80	3	20.0	16	10	P82161
81	3	20.0	16	12	P83511
82	3	20.0	16	12	O89560
83	3	20.0	16	13	Q9PRU6
84	3	20.0	17	2	Q9R528
85	3	20.0	17	2	Q9R512
86	3	20.0	17	8	Q9ZYW0
87	3	20.0	17	8	Q8H8Z4
88	3	20.0	17	11	Q9QVK3
89	3	20.0	17	11	Q9Z0M0

Q9ucp3 homo sapien  
Q94vg5 varanus gri  
Q9tg95 annella ge  
P81898 prunus dulc  
Q9q0w9 polyomaviru  
Q8jv70 polyomaviru  
Q9q0w1 polyomaviru  
Q8jv68 polyomaviru  
Q9q0v9 polyomaviru  
Q9q0w7 polyomaviru  
Q8jv66 polyomaviru  
Q9q0v7 polyomaviru  
Q8jv82 polyomaviru  
Q8jv76 polyomaviru  
Q8jv74 polyomaviru  
Q9q0w5 polyomaviru  
Q9q0x3 polyomaviru  
Q9q0x5 polyomaviru  
Q9q0w3 polyomaviru  
Q8jv80 polyomaviru  
Q9q0x1 polyomaviru  
Q9q0x9 polyomaviru  
Q8jv72 polyomaviru  
Q42377 anabaena sp  
P82436 nicotiana t  
Q83083 leucania se  
P83168 struthio ca  
Q9ugs1 homo sapien  
O77879 oreochromis  
Q93x21 zea mays (m  
Q9bdq8 sus scrofa  
Q98ym1 human immun  
Q9zb42 streptococc  
Q96kf9 homo sapien  
P82216 bombyx mori  
Q94it6 fragaria ru  
P82335 pisum sativ  
Q9jjus mus musculu  
Q9e0n1 human herpe  
Q9e0n1 human herpe  
Q99bw2 human herpe  
Q9r533 pseudomonas  
Q96v23 cryptococcu  
Q15344 homo sapien  
Q9ucj8 homo sapien  
Q9tvc7 dirofilaria  
Q28822 eryctolagus  
Q9s8q8 ricinus com  
Q9s8n8 hordeum vul  
Q9gvb6 rattus sp.  
Q9gvx9 mus sp. nep  
Q9gw2 rattus norv  
Q9qv3 rattus sp.  
Q9vb7 rattus sp.  
Q9tne6 poephila gu  
Q9p6c1 galus gail  
P83012 scyllorhinu  
P83102 rous sarcom  
Q9r4d1 naemophilus  
Q9bgg8 sorax arane  
Q9tq27 bos taurus  
Q9trd1 sus scrofa  
Q8slf0 taraxacum (P  
P82161 spinacia ol  
P83511 delonix reg  
O89560 kaposi's sa  
Q9pru6 gallus gall  
Q9r512 porphyromon  
Q9zyw0 betyobraco  
Q8hrz4 sphenia sin  
Q9gvk3 rattus sp.  
Q9z0m0 rattus norv

90 Q9PRU7  
91 Q8X4A4  
92 Q96V21  
93 Q96V22  
94 Q01672  
95 Q9UCG7  
96 Q16173  
97 Q9UC58  
98 Q9NB54  
99 Q9TW64  
100 Q9TRD8

Q9PRU7 gallus gall  
Q8X4A4 escherichia  
Q96V21 cryptococcus  
Q96V22 cryptococcus  
Q01672 pneumocysti  
Q9UCG7 homo sapien  
Q16173 homo sapien  
Q9UC58 homo sapien  
Q9NB54 homo sapien  
Q9TW64 aplysia cal  
Q9TRD8 oryctolagus

## ALIGNMENTS

RESULT 1  
Q9BZ49 PRELIMINARY; PRT; 12 AA.

ID Q9BZ49  
AC Q9BZ49  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Glycophorin C (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,  
Zimmerman P.A.;  
RT "the association of the glycoprotein C exon 3 deletion with  
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New  
RT Guinea";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF342984; AAK01459.1; -;  
FT NON TER 1 1  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1361 MW; 2A070444DB8377378 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11  
DB 9 PPPQ 12

RESULT 2  
Q9TR14 PRELIMINARY; PRT; 15 AA.

ID Q9TR14  
AC Q9TR14  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide  
DE (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96187584; PubMed=8611748;  
RA Nakai Y., Nishimura T., Shimizu M., Arai S.;  
RT "Effects of freezing on the proteolysis of beef during storage at 4  
RT degrees C";  
RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).  
SQ SEQUENCE 15 AA; 1597 MW; C98A5B4A79E4777 CRC64;

Query Match 26.7%; Score 4; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 2 PPPP 5

RESULT 3  
P82439 PRELIMINARY; PRT; 15 AA.

ID P82439  
AC P82439  
DT 01-JUN-2000 (TREMBLrel. 14, Created)  
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE 200 kDa cell wall protein (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE.  
RC SPRAIN-cv. PETIT HAVANA;  
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
Wojtaszek P., Bolwell G.P.;  
RT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture";  
RL Planca 0:0-0(2000).  
CC -1- SUBCELLULAR LOCATION: CELL WALL.  
CC -1- TISSUE SPECIFICITY: XYLEM.  
KW Cell wall; Hydroxylation.  
FT MOD RES 6 6 HYDROXYLATION.  
FT NON TER 15 15  
SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 6 PPPP 9

RESULT 4  
Q9TR22 PRELIMINARY; PRT; 17 AA.

ID Q9TR22  
AC Q9TR22  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE NONAMELOGENIN glycoprotein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96126798; PubMed=8564801;  
RA Punzi J.S., Denbesten P.K.;  
RT "Purification of nonamelogenin proteins from bovine secretory  
RT enamel";  
RL Calif. Tissue Int. 57:379-384(1995).  
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match 26.7%; Score 4; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10



Db 8 PPPP 11  
||||

## RESULT 5

O49225 O49225 PRELIMINARY; PRT; 17 AA.  
AC O49225;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hydroxyproline-rich glycoprotein (Fragment).  
CN HRGP.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RX MEDLINE=94211912; PubMed=8159793;  
RA Hong J.C., Cheong Y.H., Nagao R.T., Baik J.D., Cho M.J., Key J.L.;  
RT "Isolation and characterization of three soybean extensin cDNAs.";  
RL Plant Physiol. 104:793-796(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RA Mahalingam R., Knap H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047052; AAC03558.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 PPPP 10  
||||  
Db 11 PPPP 14

## RESULT 6

O41400 O41400 PRELIMINARY; PRT; 17 AA.  
AC O41400;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Hydroxyproline-rich protein (Fragment).  
OS Sesbania rostrata.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.  
OX NCBI\_TaxID=3895;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sesbania rostrata;  
RC TISSUE=Bacterial infected stem located root primordia;  
RX MEDLINE=96113737; PubMed=8664492.  
RA Goormachtig S., Valerio-Lepiniec M., Szczylowski K., Van Montagu M.,  
RA Holsters M., De Bruijn F.;  
RT "Use of differential display to identify novel Sesbania rostrata genes  
RT enhanced by Azorhizobium caulinodans infection.";  
RL Mol. Plant Microbe Interact. 8:816-824(1995).  
DR EMBL; Z48673; CAA88592.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 PPPP 10  
||||  
Db 10 PPPP 13

## RESULT 7

OSUQT9 OSUQT9 PRELIMINARY; PRT; 18 AA.  
AC OSUQT9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE PRG=PROLINE-rich glycoprotein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91373355; PubMed=1894623;  
RA Gilless-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,  
RA Fisher S.J.;  
RT "Structure and bacterial receptor activity of a human salivary  
RT proline-rich glycoprotein.";  
RL J. Biol. Chem. 266:17358-17368(1991).  
RN [2]  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PPPQ 11  
||||  
Db 14 PPPQ 17

## RESULT 8

O64619 O64619 PRELIMINARY; PRT; 20 AA.  
AC O64619;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Polymerase-beta (EC 2.7.7.7) (Fragment).  
GN POLB.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=87257910; PubMed=3600656;  
RA Yamaguchi M., Hirose F., Hayashi Y., Nishimoto Y., Matsukage A.;  
RT "Murine DNA polymerase beta gene: Mapping of transcription initiation  
RT sites and the nucleotide sequence of the putative promoter region.";  
RL Mol. Cell. Biol. 7:2012-2018(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=88294046; PubMed=3042024;  
RA Date T., Yamaguchi M., Hirose F., Nishimoto Y., Tanihara K.,  
RA Matsukage A.;  
RT "Expression of active rat DNA polymerase beta in Escherichia coli.";  
RL Biochemistry 27:2983-2990(1988).  
DR EMBL; M19679; AAA41902.1; -.  
DR HSSP; P06766; 1BNO.  
KW Nucleotidyltransferase; Transferase.  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2190 MW; B7D8F9A3C5801825 CRC64;

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Query Match      26.7%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PQET 13
DB      7 PQET 10

RESULT 9
Q54248      PRELIMINARY;      PRT;      7 AA.
AC Q54248;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RplO protein (Fragment).
GN RPL0.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=N2-3-11;
RC MEDLINE=20011291; PubMed=10542330;
RA Poshling S., Siepersberg W., Wenmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
RT N2-3-11 and interaction of the sec Y protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
DB      2 TVT 4

RESULT 10
Q81UB8      PRELIMINARY;      PRT;      8 AA.
AC Q81UB8;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD95 antigen (Fragment).
GN CD95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kuth J., Pernik A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuipers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; AJ509178; CAD48928.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 846 MW; 34B724405DC2D1AB CRC64;

Query Match      20.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
DB      2 TVT 4

RESULT 11
Q9UCS8      PRELIMINARY;      PRT;      9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075698; PubMed=1742316;
RA Ehnholm C., Bozas S.E., Tenkanen H., Kirezbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I.";
RL Biochim. Biophys. Acta 1086:255-260(1991).
FT NON TER 1 1
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match      20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PPQ 11
DB      3 PPQ 5

RESULT 12
Q9H4M8      PRELIMINARY;      PRT;      9 AA.
AC Q9H4M8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PAR2 (Fragment).
GN NR112.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Periphereal blood;
RA Pentecost B.T., Ling G.;
RT "The human pregnane X receptor promoter complex provides
RT transcriptional starts for a number of PXR related transcripts.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007189; AAG23345.1; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 82F8B1F1B411B2D1 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
DB      2 TVT 4

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RESULT 13
O96417 ID O96417 PRELIMINARY; PRT; 9 AA.
AC O96417;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE SXL E1 form (Fragment).
GN SXL.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96337843; PubMed=9671597;
RX Erickson J.W., Cline T.W.;
RA "Key aspects of the primary sex determination mechanism are conserved
RT across the genus Drosophila.";
RL Development 125:3259-3268(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bell M., Cline T.W.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF046045; AAC97605.1; -.
DR FlyBase; FBgn0016470; Dvir\Xsl.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1089 MW; 9A8BD1AAA9C449CA CRC64;

Query Match 20.0%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
Db 7 TVT 9

RESULT 14
P82429 ID P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-JUN-2000 (TEMBLrel. 14, Created)
DT 01-JUN-2000 (TEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE 44 kDa cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RA STRAIN=cv. PETIT HAVANA;
RC Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000);
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 9
SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C77776 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
Db 9 PPQ 11

RESULT 15
O9H121 ID O9H121 PRELIMINARY; PRT; 10 AA.
AC O9H121;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE DJ309P20.1-2 (Isoform 2 of guanine nucleotide binding protein (G
DE protein), alpha stimulating activity polypeptide 1) (Fragment).
GN GNAS1 (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121917; CAC18783.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1095 MW; 7809E3D322C7244B CRC64;

Query Match 20.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
Db 1 VLE 3

RESULT 16
O9UMK9 ID O9UMK9 PRELIMINARY; PRT; 10 AA.
AC O9UMK9;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Dystrophin (Fragment).
GN DAG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Saad F.A., Moatacciulo M.L., Merlini L., Trevisan C., Tomelleri G.,
RA Angelini C., Danieli G.A.;
RT "Novel point mutations in the human dystrophin gene detected by double
RT strand conformation analysis.";
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; L41643; AAB59464.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1223 MW; 5D3C9185A2CAB6D7 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKF 6
Db 8 MKF 10

RESULT 17
O9UCP3 ID O9UCP3 PRELIMINARY; PRT; 10 AA.
AC O9UCP3;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE GMP-inhibited LOW K(M) cAMP phosphodiesterase PEAK 37, CGI-PDE  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92283180; PubMed=1317779;  
 RX LeBon T.R., Kasuya J., Paxton R.J., Belfrage P., Hockman S.,  
 RA Manganiello V.C., Fujita Yamaguchi Y.;  
 RT "Purification and characterization of guanosine 3',5'-monophosphate-  
 RT inhibited low K(M) adenosine 3',5'-monophosphate phosphodiesterase  
 RT from human placental cytosolic fractions.";  
 RL Endocrinology 130:3265-3274(1992).  
 FT NON\_TER 1 10  
 FT NON\_TER 1 10  
 SQ SEQUENCE 10 AA; 1272 MW; C80C440B549C046 CRC64;  
  
 Query Match 20.0%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 ENK 5  
 DB 8 ENK 10  
  
 RESULT 18  
 ID Q94VG5 PRELIMINARY; PRT; 10 AA.  
 AC Q94VG5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 DE COI.  
 GN Varanus griseus griseus.  
 OS Varanus griseus griseus.  
 OG Mitochondrion.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.  
 OK NCBI\_TaxID=169828;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ast J.C.;  
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
 RL Cladistics 17:0-0(2001).  
 DR ENBL; AF407503; AAL10063.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1219 MW; C97C0CB7336411B2 CRC64;  
  
 Query Match 20.0%; Score 3; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 13 TVT 15  
 DB 2 TVT 4  
  
 RESULT 19  
 ID Q9TG95 PRELIMINARY; PRT; 10 AA.  
 AC Q9TG95;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 DE COI.  
 GN Anniella geronimensis.  
 OS Anniella geronimensis.  
 OG Mitochondrion.

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Anguillidae;  
 CC Anniellinae; Anniella.  
 OK NCBI\_TaxID=52220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9343613; PubMed=10413621;  
 RX Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,  
 RA Papenfuss T.J.;  
 RT "Molecular phylogenetics, rRNA evolution, and historical biogeography  
 RT in anguilliforms and related taxonomic families.";  
 RL Mol. Phylogenet. Evol. 12:250-272(1999).  
 DR ENBL; AF085605; AAD51505.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1241 MW; DFEE80C7336411B2 CRC64;  
  
 Query Match 20.0%; Score 3; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 13 TVT 15  
 DB 2 TVT 4  
  
 RESULT 20  
 ID P81898 PRELIMINARY; PRT; 10 AA.  
 AC P81898;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, small  
 DE chain (Subunit B) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-  
 DE glycosidase) (N-glycanase) (Fragment).  
 OS Prunus dulcis (Almond) (Prunus amygdalus).  
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OK NCBI\_TaxID=3755;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RA PubMed=9523720;  
 RA Altmann F., Faschinger K., Dalik T., Vorauer K.;  
 RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine  
 RT amidase A and its N-glycans.";  
 RL Eur. J. Biochem. 252:118-123(1998).  
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-  
 CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-  
 CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A  
 CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE  
 CC CONTAINING AN ASPARTIC RESIDUE.  
 CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.  
 CC -1- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-  
 CC DEGLYCOSYLATION.  
 CC -1- MASS SPECTROMETRY: MW=21247; METHOD=MALDI.  
 KW Hydroxylase; Glycoprotein.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1149 MW; 863278CA1E73771 CRC64;  
  
 Query Match 20.0%; Score 3; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 FPP 8  
 DB 8 FPP 10  
  
 RESULT 21  
 ID Q9Q0W9 PRELIMINARY; PRT; 10 AA.

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AC Q9QW9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UMEA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119350; AAF24106.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db |||
  |||

RESULT 22
Q8JV70
ID Q8JV70 PRELIMINARY; PRT; 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 5;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db |||
  |||

RESULT 23
Q9QW1
ID Q9QW1 PRELIMINARY; PRT; 10 AA.
AC Q9QW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119354; AAF24114.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db |||
  |||

RESULT 24
Q8JV68
ID Q8JV68 PRELIMINARY; PRT; 10 AA.
AC Q8JV68;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db |||
  |||

RESULT 25
Q9QV9
ID Q9QV9 PRELIMINARY; PRT; 10 AA.
AC Q9QV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).

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DR EMBL; AF119355; AAF24116.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 26
Q9Q0W7 PRELIMINARY; PRT; 10 AA.
ID Q9Q0W7;
AC Q9Q0W7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 27
Q8JV66 PRELIMINARY; PRT; 10 AA.
ID Q8JV66;
AC Q8JV66;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAM97808.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 PPP 9
Db |||
7 PPP 9

RESULT 28
Q9Q0V7 PRELIMINARY; PRT; 10 AA.
ID Q9Q0V7;
AC Q9Q0V7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSFJ;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119356; AAF24118.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 29
Q8JV82 PRELIMINARY; PRT; 10 AA.
ID Q8JV82;
AC Q8JV82;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303944; AAM97792.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 30
Q8JV76 PRELIMINARY; PRT; 10 AA.
ID Q8JV76

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AC Q8JVV76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR ENBL; AF303947; AAM97798.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 31
Q8JVV74
ID Q8JVV74 PRELIMINARY; PRT; 10 AA.
AC Q8JVV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA3;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR ENBL; AF303948; AAM97800.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 32
Q9QOW5
ID Q9QOW5 PRELIMINARY; PRT; 10 AA.
AC Q9QOW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

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OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR ENBL; AF119352; AAF24110.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 33
Q9QOX3
ID Q9QOX3 PRELIMINARY; PRT; 10 AA.
AC Q9QOX3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN8;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR ENBL; AF119348; AAF24102.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 34
Q9QOX5
ID Q9QOX5 PRELIMINARY; PRT; 10 AA.
AC Q9QOX5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).

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DR EMBL; AF119347; AAF24100.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 35
Q9Q0W3 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W3 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PRETORIAL;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 36
Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=E2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Perinatal transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAW97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 37
Q9Q0X1 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X1 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 38
Q9Q0X9 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X9 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BCNU;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119345; AAF24096.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
Db |||
7 PPP 9

RESULT 39
Q8JV72 PRELIMINARY; PRT; 10 AA.
AC Q8JV72

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 4;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Boffill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304386; AAM97802.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;  
  
 Query Match 20.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 PPP 9  
 Db 7 PPP 9  
  
 RESULT 40  
 Q44237 PRELIMINARY; PRT; 11 AA.  
 AC Q44237;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Glutamine synthetase (fragment).  
 GN GLN.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7120;  
 RA Warner L.E., Ligon P.J., Stahl A.W., Curtis S.E.;  
 RT "The apcF gene of Anabaena sp. strain PCC 7120 is regulated by  
 RT nitrogen and the apcF and glnA promoters overlap.";  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7120;  
 RA Scappino L.A.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U21853; AAA5652.1; -;  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;  
  
 Query Match 20.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 10 PQE 12  
 Db 4 PQE 6  
  
 RESULT 41  
 P82436 PRELIMINARY; PRT; 11 AA.  
 AC P82436;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE 65 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco cultures.";  
 RL planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;  
  
 Query Match 20.0%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 PPP 9  
 Db 2 PPP 4  
  
 RESULT 42  
 Q83083 PRELIMINARY; PRT; 11 AA.  
 AC Q83083;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE P13 mini peptide.  
 OS Leucania separata nuclear polyhedrosis virus (LanPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=41714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96140622; PubMed=8572949;  
 RA Wang J.W., Qi Y.P., Huang Y.X., Li S.D.;  
 RT "Nucleotide sequence of a 1446 base pair SalI fragment and structure  
 RT of a novel early gene of Leucania separata nuclear polyhedrosis  
 RT virus.";  
 RL Arch. Virol. 140:2283-2291(1995).  
 DR EMBL; U30303; AAA99737.1; -;  
 SQ SEQUENCE 11 AA; 1339 MW; F7BDBE0BD40DC401 CRC64;  
  
 Query Match 20.0%; Score 3; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 VLE 3  
 Db 8 VLE 10  
  
 RESULT 43  
 P83168 PRELIMINARY; PRT; 11 AA.  
 AC P83168;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Alpha-2-antiplasmin (Alpha-2-plasmin inhibitor) (Alpha-2-Pi) (Alpha-2-  
 DE AP) (Fragment).  
 OS Struthio camelus (Ostrich).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;

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OC Struthio.
OX NCBI_TaxID=8801;
RN [1]_
RP SEQUENCE, AND FUNCTION.
RX MEDLINE=21328857; PubMed=11435135;
RA Thomas A.R., Naude R.J., Oelofsen W., Naganuma T., Muramoto K.;
RT "Purification and partial characterisation of alpha(2)-antiplasmin and
RL plasmin(ogen) from ostrich plasma.";
RL Comp. Biochem. Physiol. 129B:809-820(2001).
CC -1- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND
CC TRYPSIN. BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
KW Serpin; Serine protease inhibitor.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1261 MW; 950806B32C73B5A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 7 VLE 9

RESULT 44
Q9UGS1
ID Q9UGS1 PRELIMINARY; PRT; 12 AA.
AC Q9UGS1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE D0796117.4 (Novel protein similar to GS2) (Fragment).
GN D0796117.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035398; CAB63074.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69A46 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 3 LEM 5

RESULT 45
O77879
ID O77879 PRELIMINARY; PRT; 12 AA.
AC O77879;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 2 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]_
RP SEQUENCE FROM N.A.
RA MEDLINE=98315113; PubMed=9649539;
RX

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RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF049988; AAC41327.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1214 MW; 86535979D0B879CE CRC64;

Query Match 20.0%; Score 3; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 10 TVT 12

RESULT 46
Q93X21
ID Q93X21 PRELIMINARY; PRT; 12 AA.
AC Q93X21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polynibiquitin homolog (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]_
RP SEQUENCE FROM N.A.
RA STRAIN=cv. INRA 258; TISSUE=Leaf;
RX MEDLINE=96236829; PubMed=8680303;
RT Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;
RT "Heavy-metal-responsive genes in maize: identification and comparison
RT of their expression upon various forms of abiotic stress.";
RL Planta 199:1-8(1996).
DR EMBL; S82313; AAB47175.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB 2 PPP 4

RESULT 47
Q9BDQ8
ID Q9BDQ8 PRELIMINARY; PRT; 13 AA.
AC Q9BDQ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Cholesteryl ester transfer protein (Fragment).
GN CETP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_
RP SEQUENCE FROM N.A.
RA Shi X.W., Tuggle C.K.;
RT "Genetic linkage and physical mapping of porcine cholesteryl ester
RT transfer protein (CETP) gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333037; AAK16584.1; -.

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FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1551 MW; 779D9C94B9A742CB CRC64;

Query Match 20.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13
DB 2 QET 4

RESULT 48
Q98YM1 PRELIMINARY; PRT; 13 AA.
AC Q98YM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=991043;
RA Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E., Korn K.;
RT "Sequencing of HIV-1 pol gene sequences by direct sequencing of amplification products derived from plasma samples.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF347446; AAK32523.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1390 MW; 805408704623D1AA CRC64;

Query Match 20.0%; Score 3; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 8 VLE 10

RESULT 49
Q92B42 PRELIMINARY; PRT; 14 AA.
AC Q92B42;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Ssba (fragment).
GN SSBA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CS101;
RA Roddieski A., Wolschnik M., Leonard B.A.B., Schmidt K.H.;
RT "Characterization of nra, a global negative regulator gene in group A streptococci.";
RL Mol. Microbiol. 31:0-0(1999).
DR EMBL; U49397; AAC97153.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1618 MW; 47074E277A834F17 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLE 3
DB 6 VLE 8

RESULT 50
Q96KF9 PRELIMINARY; PRT; 14 AA.
AC Q96KF9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative magnesium transporter (fragment).
GN MRS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=21295035; PubMed=11401429;
RA Zsurka G., Gregan J., Schweyen R.J.;
RT "The human mitochondrial MRS2 protein functionally substitutes for its yeast homologue, a candidate magnesium transporter.";
RL Genomics 72:158-168(2001).
DR EMBL; AF293077; AAK38616.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1537 MW; C6344FF1E984AFB2 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 6 TVT 8

RESULT 51
P82216 PRELIMINARY; PRT; 14 AA.
AC P82216;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]_
RP SEQUENCE.
RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of silkworm.";
RL 1. Chuan Houeh Pao 28:217-224(2001).
CC 1.- SIMILARITY: TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1619 MW; 86C63995B983BC45 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
DB 10 ETV 12

```

## RESULT 52

Q94176 PRELIMINARY; PRT; 14 AA.  
 AC Q94176  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Regulator of anthocyanin biosynthesis pathway (fragment).  
 OS Fragaria nubicola.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
 OX NCBI\_TaxID=60188;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. FRA520;  
 RA Deng C., Davis T.;  
 RT "Molecular identification of the yellow fruit color (c) locus in  
 RT diploid strawberry: a candidate gene approach.";  
 RL Theor. Appl. Genet. 0:0-0(2001).  
 DR EMBL; AY017488; AAK33145.1; -.  
 FT NON TER 1  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1533 MW; C2862EA5812DC832 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

Db 7 VLE 9

## RESULT 53

P82335 PRELIMINARY; PRT; 14 AA.  
 ID P82335  
 AC P82335  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Unknown protein from 2D-page of thylakoid (SPOT119) (fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
 RA Adamska I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 RT targeting analysis of luminal and peripheral thylakoid proteins.";  
 RL Plant Cell 12:319-341(2000).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMAL SIDE OF THE THYLAKOID  
 CC MEMBRANE.  
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 29.9 KDA.  
 KW Chloroplast; Thylakoid membrane.  
 FT NON TER 14  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1477 MW; 9397654B0784A231 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14

Db 12 ETV 14

Db 12 ETV 14

## RESULT 54

Q94JUS PRELIMINARY; PRT; 14 AA.  
 ID Q94JUS  
 AC Q94JUS  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE B-Raf protein (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barnier J.V.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Barnier J.V., Papin C., Eyche A., Jacq O.;  
 RT "The mouse B-Raf gene encodes multiple protein isoforms with tissue-  
 RT specific expression.";  
 RL J. Biochem. 270:23381-23389(1995).  
 DR EMBL; AF276308; CAB81556.1; -.  
 FT NON TER 1  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFP 7

Db 3 KFP 5

## RESULT 55

Q9E0N0 PRELIMINARY; PRT; 14 AA.  
 ID Q9E0N0  
 AC Q9E0N0  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Immediate early protein ICP47 (fragment).  
 GN US12.  
 OS Human herpesvirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10298;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Maatzdorf J., Van der lelij A., Baarma G.S., Osterhaus A.D.M.E.,  
 RA Verjans G.M.G.M.;  
 RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following  
 RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission  
 RT of HSV-1.";  
 RL Ann. Neurol. 48:0-0(2000).  
 DR EMBL; AF290018; AAG33334.1; -.  
 FT NON TER 14  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4

Db 5 LEM 7

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RESULT 56
ID Q9E0N1 PRELIMINARY; PRT; 14 AA.
AC Q9E0N1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RA Maertzdorf J., Van der lელი A., Baarma G.S., Osterhaus A.D.M.E.,
RA Verjans G.M.G.M.;
RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
RT of HSV-1."
RL Ann. Neurol. 48:0-0(2000).
DR EMBL; AF290017; AAG39133.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 5 LEM 7

RESULT 57
ID Q99BW2 PRELIMINARY; PRT; 14 AA.
AC Q99BW2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RA Reweijer L., Maertzdorf J., Doornenbal P., Verjans G.M.G.M.,
RA Osterhaus A.D.M.E.;
RT "Herpes simplex virus type 1 transmission through corneal
RT transplantation."
RL Lancet 357:442-442(2001).
DR EMBL; AF324428; AAK12110.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 5 LEM 7

RESULT 58
ID Q9R533 PRELIMINARY; PRT; 15 AA.
AC Q9R533;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Integration host factor-like protein beta subunit (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE.
RA MEDLINE=94030028; PubMed=8216322;
RA Tousseint B., Delic-Attree I., Vignais P.M.;
RT "Pseudomonas aeruginosa contains an IHF-like protein that binds to the
RT alga promoter."
RL Biochem. Biophys. Res. Commun. 196:416-421(1993).
SQ SEQUENCE 15 AA; 1703 MW; 7315E3A63536EF32 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 10 TVT 12

RESULT 59
ID Q96V23 PRELIMINARY; PRT; 15 AA.
AC Q96V23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pheromone alpha (Fragment).
GN MFALPHA1A.
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUM 89-3369;
RX MEDLINE=21538945; PubMed=11682503;
RA Cogliati M., Esposito M.C., Clarke D.L., Wickes B.L., Viviani M.A.;
RT "Origin of Cryptococcus neoformans var. neoformans Diploid Strains."
RL J. Clin. Microbiol. 39:3889-3894(2001).
DR EMBL; AF376995; AAK5591.1; -.
FT NON_TER 1 15
SQ SEQUENCE 15 AA; 1563 MW; 9AE1F336ACF0E29B CRC64;

Query Match 20.0%; Score 3; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 11 TVT 13

RESULT 60
ID Q15344 PRELIMINARY; PRT; 15 AA.
AC Q15344;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Aml1 protein (Fragment).
GN AML1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=96226397; PubMed=8634147;
RX  Levanon D., Bernstein Y., Negreanu V., Ghozi M.C., Bar-Am I.,
RA  Aloya R., Goldenberg D., Lotem J., Groner Y.,
RT  "A large variety of alternatively spliced and differentially expressed
RL  mRNAs are encoded by the human acute myeloid leukemia gene AML1."
DR  DNA Cell Biol. 15:175-185(1996).
DL  EMBL; X90980; CAA62467.2; -.
FT  NON_TER 1
FT  SEQUENCE 15 AA; 1931 MW; 228A48BEE675423 CRC64;
SQ  SEQUENCE 15 AA; 1931 MW; 228A48BEE675423 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPP 8
Db 7 FPP 9

RESULT 61
O9UCJ8 PRELIMINARY; PRT; 15 AA.
AC Q9UCJ8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Type IV PROCOLLAGENASE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=93125366; PubMed=1480041;
RA Sterler-Stevenson W.G., Kruttsch H.C., Liotta L.A.;
RT "TMP-2: identification and characterization of a new member of the
RT metalloproteinase inhibitor family.";
RL Matrix Suppl. 1:299-306(1992).
SQ SEQUENCE 15 AA; 1537 MW; DSDA1AA9C32276C CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFP 7
Db 7 KFP 9

RESULT 62
O9TWC7 PRELIMINARY; PRT; 15 AA.
AC Q9TWC7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 20 kDa excretory-secretory protein (Fragment).
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE
RX MEDLINE=96258562; PubMed=8992320;
RA Frank G.R., Griewe R.B.;
RT "Purification and characterization of three larval excretory-secretory
RT proteins of Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 75:221-229(1996).
SQ SEQUENCE 15 AA; 1801 MW; F074BFEBE0E48CB CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
Db 8 ETV 10

RESULT 63
Q28622 PRELIMINARY; PRT; 15 AA.
AC Q28622
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Voltage-dependent dihydropyridine-sensitive calcium channel alpha 1
DE subunit 155 kDa isoform (fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92265303; PubMed=1316766;
RA Malouf N.N., McMahon D.K., Hainsworth C.N., Kay B.K.;
RT "A two-motif isoform of the major calcium channel subunit in skeletal
RT muscle.";
RL Neuron 8:899-906(1992).
DR EMBL; S36895; AAB22180.1; -.
FT NON_TER 1
FT SEQUENCE 15 AA; 1796 MW; 841B2DB08BF99DB CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
Db 13 LEM 15

RESULT 64
Q9S8Q8 PRELIMINARY; PRT; 15 AA.
AC Q9S8Q8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Phospholipase D IEC 3.1.4.4 (Fragment).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE
RX MEDLINE=94029022; PubMed=8215453;
RA Wang X., Dyer J.H., Zheng L.;
RT "Purification and immunological analysis of phospholipase D from
RT castor bean endosperm.";
RL Arch. Biochem. Biophys. 306:486-494(1993).
SQ SEQUENCE 15 AA; 1620 MW; 7C3849DA9B2F50C CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
Db 8 ETV 10

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## RESULT 65

Q9S8N8 PRELIMINARY; PRT; 15 AA.  
AC Q9S8N8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Protein E-22 (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=94170739; PubMed=8125056;  
RA Flengsrud R.;  
RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis.";  
RL Electrophoresis 14:1060-1066(1993).  
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPO 11  
|||

DB 5 PPO 7  
|||

## RESULT 66

Q9QVB6 PRELIMINARY; PRT; 15 AA.  
AC Q9QVB6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Plasma T-kinin isoform II (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=22348359; PubMed=1639765;  
RA Enyori K.; Kato H.;  
RT Purification and Characterization of two isoforms of T-kininogens from rat liver microsomes.";  
RL J. Biochem. 111:670-675(1992).  
SQ SEQUENCE 15 AA; 1717 MW; 82BE84AE486A0AAB CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
|||

DB 12 ETV 14  
|||

## RESULT 67

Q9QVK9 PRELIMINARY; PRT; 15 AA.  
AC Q9QVK9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;

## RN [1]

RP SEQUENCE.  
RX MEDLINE=91363409; PubMed=1888759;  
RA Flannery A.V.; Macadam G.C.; Beynon R.J.;  
RT "Immunological characterisation of different meprin species in mice.";  
RL Biochim. Biophys. Acta 1079:119-122(1991).  
FT NON\_TER 1  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1662 MW; FF7E0C2A04A388F2 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14  
|||

DB 2 ETV 4  
|||

## RESULT 68

Q9QWT2 PRELIMINARY; PRT; 15 AA.  
AC Q9QWT2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Nitric oxide synthase 1 (Fragment).  
GN NOS1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98368654; PubMed=9705156;  
RA Oberbauer I.; Moser D.; Bachmann S.;  
RT "Nitric oxide synthase 1 mRNA: Tissue-specific variants with new alternative first exons from rat.";  
RL Biol. Chem. 379:913-919(1998).  
DR EMBL; AJ005845; CAA06740.1; -.  
FT NON\_TER 1  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1560 MW; 42DE978DAF21ED38 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5  
|||

DB 6 EMK 8  
|||

## RESULT 69

Q9QUY3 PRELIMINARY; PRT; 15 AA.  
AC Q9QUY3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE L-glutamate/aspartate NEUROTRANSMITTER transporter (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96085162; PubMed=8521863;  
RA Schulte S.; Stoffel W.;  
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins.";  
RL Eur. J. Biochem. 233:947-953(1995).

SQ SEQUENCE 15 AA; 1724 MW; CBB53AD02748CA16 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5  
|||  
Db 13 EMK 15

RESULT 70

Q9QV7 PRELIMINARY; PRT; 15 AA.

AC Q9QV7;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DE Factor XA light CHAIN. VAPAM light CHAIN-23 kDa PARAMYXOVIRUS-  
activating endoprotease light chain (Fragment).  
OS Gallus gallus (Chicken)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae;  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92164779; PubMed=1537403;  
RA Gotoh B., Yamauchi F., Ogasawara T., Nagai Y.;  
RT "Isolation of factor Xa from chick embryo as the amniotic endoprotease  
responsible for paramyxovirus activation.";  
RL FEBS Lett. 296:274-278(1992).  
FT NON TER 1  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1766 MW; B84F5F7ED0E57533 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5  
|||  
Db 7 EMK 9

RESULT 73

P83012 PRELIMINARY; PRT; 15 AA.

AC P83012;  
DT 01-OCT-2001 (TremBLrel. 18, Created)  
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)  
DE Cytochrome C oxidase polypeptide VA, mitochondrial (EC 1.9.3.1)  
(Fragment).  
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcariniformes;  
OC Scyllorhinidae; Scyllorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC Tissue=Rectal gland;  
RA Schuurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bonga S.E.;  
RT "Phospholipase in the rectal gland of shark.";  
RL Submitted (JUN-2001) to the SWISS-PROT data bank.  
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4  
PERICYTOCHROME C.  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (BY  
SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
DB InterPro: IPR003204; Cyt\_c\_ox5a.  
DR Pfam: PF02284; COX5A; 1\_ox5a.  
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
FT NON TER 15  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1720 MW; 937518D7590B3C5 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
Db 2 VLE 4

SQ SEQUENCE 15 AA; 1724 MW; CBB53AD02748CA16 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5  
|||  
Db 13 EMK 15

RESULT 70

Q9QV7 PRELIMINARY; PRT; 15 AA.

AC Q9QV7;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DE Factor XA light CHAIN. VAPAM light CHAIN-23 kDa PARAMYXOVIRUS-  
activating endoprotease light chain (Fragment).  
OS Gallus gallus (Chicken)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae;  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92164779; PubMed=1537403;  
RA Gotoh B., Yamauchi F., Ogasawara T., Nagai Y.;  
RT "Isolation of factor Xa from chick embryo as the amniotic endoprotease  
responsible for paramyxovirus activation.";  
RL FEBS Lett. 296:274-278(1992).  
FT NON TER 1  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1766 MW; B84F5F7ED0E57533 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5  
|||  
Db 7 EMK 9

RESULT 73

P83012 PRELIMINARY; PRT; 15 AA.

AC P83012;  
DT 01-OCT-2001 (TremBLrel. 18, Created)  
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)  
DE Cytochrome C oxidase polypeptide VA, mitochondrial (EC 1.9.3.1)  
(Fragment).  
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcariniformes;  
OC Scyllorhinidae; Scyllorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC Tissue=Rectal gland;  
RA Schuurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bonga S.E.;  
RT "Phospholipase in the rectal gland of shark.";  
RL Submitted (JUN-2001) to the SWISS-PROT data bank.  
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4  
PERICYTOCHROME C.  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (BY  
SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
DB InterPro: IPR003204; Cyt\_c\_ox5a.  
DR Pfam: PF02284; COX5A; 1\_ox5a.  
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
FT NON TER 15  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1720 MW; 937518D7590B3C5 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
Db 2 VLE 4



QY 11 QET 13  
| | |  
Db 5 QET 7

## RESULT 74

Q85713  
ID Q85713 PRELIMINARY; PRT; 15 AA.  
AC Q85713  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 29 (RSV-29) src (Fragment).  
OS Rous sarcoma virus.  
OC Viruses; Retrovird viruses; Retroviridae; Alpharetrovirus.  
OX NCBI\_TaxID=11886;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85265036; PubMed=2991593;  
RA Dutta A., Wang L.-H., Hanafusa T., Hanafusa H.;  
RT "Partial nucleotide sequence of Rous sarcoma virus-29 provides  
RT evidence that the original rous sarcoma virus was replication  
RT defective.";  
RL J. Virol. 55:728-735(1985).  
DR EMBL: M11117; AAA42556.1; -.  
FT NON TER 1  
SQ SEQUENCE 15 AA; 1597 MW; DB53E0F31273C5C1 CRC64;

Query Match 20.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred.No. 8.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
| | |  
Db 10 VLE 12

## RESULT 75

Q9R4D1  
ID Q9R4D1 PRELIMINARY; PRT; 16 AA.  
AC Q9R4D1  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE 30 kDa IGA NEPHROPATHY-associated outer membrane antigen (Fragment).  
OS Haemophilus parainfluenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=729;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96215401; PubMed=8625525;  
RA Suzuki S., Nakatomi Y., Odani S., Sato H., Gejyo F., Arakawa M.;  
RT "Circulating IGA, IgG, and IGM class antibody against Haemophilus  
RT parainfluenzae antigens in patients with IGA nephropathy.";  
RL Clin. Exp. Immunol. 104:306-311(1996).  
SQ SEQUENCE 16 AA; 1645 MW; D19D462569AFF83D CRC64;

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred.No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQE 12  
| | |  
Db 2 PQE 4

Search completed: November 25, 2003, 18:25:23  
Job time : 38.1936 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 48.5904 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKFPFPPTVT 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03.\*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Colostrinin derive
2	15	100.0	15	22	Colostrinin peptid
3	15	100.0	15	22	Colostrinin peptid
4	15	100.0	15	22	Ewe colostrinin pe
5	15	100.0	15	22	Colostrinin consti
6	15	100.0	15	23	Colostrinin consti
7	15	100.0	15	23	Neural cell regula
8	15	100.0	16	22	Ewe colostrinin pe
9	6	40.0	10	11	Smooth muscle myos

10	5	33.3	5	19	AAW37157	EVH1 ligand motif.
11	5	33.3	5	20	AAW89423	Moraxella lactofer
12	5	33.3	5	22	AAW79177	Amino acid sequenc
13	5	33.3	5	22	AAU09140	Ena/VASP homology
14	5	33.3	5	23	AAO17762	Zyxine VASP bindin
15	5	33.3	6	19	AAO14441	Transcriptional ac
16	5	33.3	7	22	AAW72259	Colostrinin derive
17	5	33.3	7	22	AAW72512	Colostrinin peptid
18	5	33.3	7	22	AAW72544	Colostrinin peptid
19	5	33.3	7	22	AAW59315	Ewe colostrinin pe
20	5	33.3	7	23	AAE20241	Colostrinin consti
21	5	33.3	7	23	AAW51048	Colostrinin consti
22	5	33.3	7	23	AAO14590	Neural cell regula
23	5	33.3	9	21	AAW35516	S. cerevisiae RNA
24	5	33.3	9	21	AAW32219	Motif A of RNA tri
25	5	33.3	9	22	AAU09144	Ena/VASP homology
26	5	33.3	9	23	ABJ05692	Peptide motif of R
27	5	33.3	9	24	ABR27236	Human cancer-relat
28	5	33.3	9	24	ABR28248	Human cancer-relat
29	5	33.3	9	24	ABR28254	Human cancer-relat
30	5	33.3	9	24	ABR28437	Human cancer-relat
31	5	33.3	10	22	AAU09138	Ena/VASP homology
32	5	33.3	10	24	ABR27336	Human cancer-relat
33	5	33.3	10	24	ABR27737	Human cancer-relat
34	5	33.3	10	24	ABR27891	Human cancer-relat
35	5	33.3	10	24	ABR28332	Human cancer-relat
36	5	33.3	10	24	ABR28354	Human cancer-relat
37	5	33.3	10	24	ABR28537	Human cancer-relat
38	5	33.3	14	22	AAW79174	Peptide derived fr
39	5	33.3	14	22	AAW85935	2A11 seed storage
40	5	33.3	15	14	AAW32641	N-terminal sequenc
41	5	33.3	15	18	AAW39038	Peptide resembling
42	5	33.3	15	18	AAW39006	Peptide resembling
43	5	33.3	15	18	AAW38970	Peptide resembling
44	5	33.3	15	18	AAW38976	Peptide resembling
45	5	33.3	15	18	AAW38942	Peptide resembling
46	5	33.3	15	18	AAW38952	Peptide resembling
47	5	33.3	15	21	AAW93014	Transforming growt
48	5	33.3	15	21	AAW93015	Transforming growt
49	5	33.3	15	22	AAW79166	Synthetic antigeni
50	5	33.3	15	23	ABG72860	Human ribosomal pr
51	5	33.3	15	23	ABP59535	Human ribonucleoti
52	5	33.3	15	24	ABR38294	Human cancer-relat
53	5	33.3	15	24	ABR38351	Human cancer-relat
54	5	33.3	15	24	ABR38352	Human cancer-relat
55	5	33.3	15	24	ABR38391	Human cancer-relat
56	5	33.3	15	24	ABR38392	Human cancer-relat
57	5	33.3	17	19	AAW83113	LRP5 protein fragm
58	5	33.3	18	17	AAW05469	SH3-binding peptid
59	5	33.3	18	18	AAW37677	PPPY motif contai
60	5	33.3	18	18	AAW38909	Peptide resembling
61	5	33.3	18	19	AAW47567	Exendin agonist (1
62	5	33.3	18	19	AAW47569	Exendin agonist (2
63	5	33.3	18	19	AAW47571	Exendin agonist (3
64	5	33.3	18	19	AAW47577	Exendin agonist co
65	5	33.3	18	19	AAW47562	Exendin agonist co
66	5	33.3	18	19	AAW47564	Exendin agonist co
67	5	33.3	18	19	AAW47550	Exendin agonist co
68	5	33.3	18	19	AAW47552	Exendin agonist co
69	5	33.3	18	20	AAW03721	Exendin agonist co
70	5	33.3	18	20	AAW03723	Exendin agonist co
71	5	33.3	18	20	AAW03733	Exendin agonist co
72	5	33.3	18	20	AAW03735	Exendin agonist co
73	5	33.3	18	20	AAW03738	Exendin agonist co
74	5	33.3	18	20	AAW03740	Exendin agonist co
75	5	33.3	18	20	AAW03742	Exendin agonist co
76	5	33.3	18	21	AAW52873	Exendin agonist c
77	5	33.3	18	21	AAW52876	Exendin agonist c
78	5	33.3	18	21	AAW52878	Exendin agonist c
79	5	33.3	18	21	AAW52880	Exendin agonist c
80	5	33.3	18	21	AAW52885	Exendin agonist c
81	5	33.3	18	21	AAW52886	Exendin agonist c
82	5	33.3	18	22	AAW19823	PAK-related sterol

83 Peptide resembling  
84 ActA peptide (aa29  
85 PEST-like amino ac  
86 Peptidase substrat  
87 Peptidase substrat  
88 Peptidase substrat  
89 BOP activated pept  
90 Cyclic polymer der  
91 WW domain ligand p  
92 PPPY motif found  
93 Peptide #67 from p  
94 Daucus carota SERK  
95 Mammalian Ena (Men  
96 FAM-(Pro)4-Lys(eps  
97 Hepatitis GB virus  
98 Ena/VASP homology  
99 "L domain" amino a  
100 Amino acid sequenc

## ALIGNMENTS

## RESULT 1

AAAB72252  
ID AAB72252 standard; peptide; 15 AA.

AC AAB72252;  
XX  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 7.  
XX  
XX Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
XX WO200111937-A2.  
PN  
XX  
XX 22-FEB-2001.  
PD  
XX  
XX 17-AUG-2000; 2000WO-US22818.  
PF  
XX  
XX 17-AUG-1999; 99US-0149311.  
PR  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX (REGE-) REGEN THERAPEUTICS PLC.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
PI  
XX WPI; 2001-202804/20.  
DR  
XX

XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX  
XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system. Bacterial and viral infections and  
CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;  
XX  
XX Query Match 100.0%; Score 15; DB 22; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 3.7e-08; Length 15;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 VLENKFPFPPQETVT 15  
XX |||||||||||  
XX Db 1 VLENKFPFPPQETVT 15  
XX  
XX  
XX RESULT 2  
XX AAB72506  
XX ID AAB72506 standard; Peptide; 15 AA.  
XX AC AAB72506;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #7.  
XX KW Dermatological; oxidative stress regulator; colostrinin.  
XX OS Unidentified.  
XX PN WO200112650-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22665.  
XX PR 17-AUG-1999; 99US-0149310.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2001-218342/22.  
XX  
XX Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX  
XX Claim 6; Page 25; 48pp; English.  
XX  
XX The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
XX SQ Sequence 15 AA;  
XX  
XX Query Match 100.0%; Score 15; DB 22; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 VLENKFPFPPQETVT 15  
XX |||||||||||  
XX Db 1 VLENKFPFPPQETVT 15  
XX  
XX  
XX RESULT 3  
XX AAB72538  
XX ID AAB72538 standard; Peptide; 15 AA.  
XX AC AAB72538;  
XX DT 09-MAY-2001 (first entry)  
XX

```

DE Colostrinin peptide #7.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW Colostrum.
XX
XX Unidentified.
OS
XX WO200112651-A2.
PN
XX 22-FEB-2001.
PD
XX 17-AUG-2000; 2000WO-US22774.
PF
XX 17-AUG-1999; 99US-0149633.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Boldogh I;
PI
XX
XX WPI; 2001-226545/23.
DR
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
PT
XX
XX Claim 6; Page 21; 35pp; English.
PS
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 15 AA;
SQ
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQETVT 15
Db 1 VLEMKFPPPPQETVT 15

RESULT 4
AAB59312
ID AAB59312 standard; Peptide; 15 AA.
XX
AC AAB59312;
XX
XX 21-MAR-2001 (first entry)
DT
XX
DE Ewe colostrinin peptide fragment A-3.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
KW
XX Ovis sp.
OS
XX WO200075173-A2.
PN
XX
XX 14-DEC-2000.
PD
XX
XX 02-JUN-2000; 2000WO-GB02128.
PF
XX
XX 02-JUN-1999; 99GB-0012852.
PR
XX (REGE-) REGEN THERAPEUTICS PLC.
PA
XX
XX Georgiades JA;
PI
XX
XX WPI; 2001-071058/08.
DR
XX
XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
PS
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders, such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 15 AA;
SQ
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQETVT 15
Db 1 VLEMKFPPPPQETVT 15

RESULT 5
AAE20234
ID AAE20234 standard; peptide; 15 AA.
XX
AC AAE20234;
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX Colostrinin constituent peptide #7.
DE
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
PH Modified-site 15
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US22776.
PF
XX
XX 17-AUG-2000; 2000WO-US22776.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Stanton GJ, Hughes TK, Boldogh I;
PI
XX WPI; 2002-269151/31.
PN
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
PS
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
 |||||  
 Db 1 VLEMKFPPPPQETVT 15

# RESULT 6

AA051042  
 ID AAM51042 standard; Peptide; 15 AA.

AC AAM51042;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

DE Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-4, interleukin-6 and interleukin-10.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
 |||||  
 Db 1 VLEMKFPPPPQETVT 15

# RESULT 7

AA014583

ID AAO14583 standard; peptide; 15 AA.

XX AAO14583;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 7.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKPPPPQETVT 15

Db 1 VLEMKPPPPQETVT 15

RESULT 8

AAB59343  
 ID AAB59343 standard; Peptide; 16 AA.

XX AC AAB59343;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment derived sequence #3.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 XX central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS *Ovis sp.*

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REGF-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -

XX PS Claim 8; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

XX Sequence 16 AA;

Query Match 100.0%; Score 15; DB 22; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.9e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKPPPPQETVT 15

Db 2 VLEMKPPPPQETVT 16

RESULT 9

AAR07284

ID AAR07284 standard; protein; 10 AA.

XX AAR07284;

XX DT 31-JAN-1991 (first entry)

XX DE Smooth muscle myosin-2 immunogen for antibody prodn.

XX KW Smooth muscle myosin isoform 2; monoclonal antibody; immunogen;

XX diagnosis; arteriosclerosis.

XX OS *Homo sapiens.*

XX PN WO9011520-A.

XX PD 04-OCT-1990.

XX PF 26-MAR-1990; 90WO-JP00398.

XX PR 28-MAR-1989; 89JP-0075884.

XX PA (YAMS ) YAMASA SHOYU KK.

XX PI Nagai R, Kuroo M, Kato H;

XX DR WPI; 1990-320366/42.

XX PT Antibody against heavy chain of smooth muscle myosin - as reagent  
 PT for histological staining of smooth muscle or diagnosis of blood  
 PT vessel disorders

XX PS Claim 7; Page 42; 61pp; Japanese.

XX CC The oligopeptide is used as immunogen for the prodn. of monoclonal  
 CC antibodies recognising isoform SM-2 of the heavy chain of smooth  
 CC muscle myosin, pref. from heart or skeletal muscle, esp. human.  
 CC The peptide contains the part which differs between isoforms SM1-3.  
 CC The antibodies may be obtained by immunisation with the immunogen,  
 CC followed by cell fusion to produce a hybridoma, cloning and for  
 CC culturing the chosen hybridoma clone. The Ab is a reagent for  
 CC the histological staining of smooth muscle, and is useful in the  
 CC diagnosis of arteriosclerosis, blood vessel disorders etc.  
 CC See also AAR07283-5.

XX SQ Sequence 10 AA;

Query Match 40.0%; Score 6; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQET 13

Db 3 PPPQET 8

RESULT 10

AAR37157

ID AAR37157 standard; Peptide; 5 AA.

XX AC AAR37157;

XX DT 06-JUL-1998 (first entry)

XX DE EVH1 ligand motif.

XX KW Mena protein; mammalian Ena; Enabled; Evi protein; cytoskeleton;  
 KW cell morphology; cell adhesion; cell differentiation; cell growth;  
 KW cell motility; mouse; EVH1 ligand.

XX OS Synthetic.

XX PN WO9801755-A1.

XX PD 15-JAN-1998.



CC The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP  
CC proteins are ligands for the EVH1 domains of  
CC Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The  
CC specification describes a method for modulating cytoskeletal  
CC rearrangement in a cell, or T cell response to T cell receptor  
CC stimulation. The method comprises contacting the cell or T cell with  
CC a Fyb/SLAP complex modulator sufficient to modulate the formation  
CC of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The  
CC method is useful for modulating cytoskeletal rearrangement in a cell  
CC such as a lymphocyte, preferably a T cell, a macrophage or a cell  
CC fragment such as a platelet and for modulating T cell response to a  
CC T cell receptor stimulation. T cell response is increased in a subject  
CC having or at risk of developing infectious disease or cancer and T cell  
CC response is inhibited in a subject having or is at risk of developing an  
CC autoimmune disease or a condition characterized by inflammation. A  
CC composition comprising a Fyb/SLAP complex inhibitor is useful for  
CC increasing platelet aggregation for promoting wound healing or  
CC clotting.

XX Sequence 5 AA;  
SQ

Query Match 33.3%; Score 5; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
DB 1 FPPPP 5

RESULT 13  
AAU09140  
ID AAU09140 standard; peptide; 5 AA.  
AC AAU09140;  
DT 19-DEC-2001 (first entry)  
DE Ena/VASP homology (EVH) proline-rich motif #1.  
XX

KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
KW neurodegeneration; Alzheimer's disease; Down syndrome; trauma; stroke;  
KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
KW Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
KW cancer; ischaemia.

XX Listeria monocytogenes.  
XX  
XX WO200174853-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US10249.  
XX  
XX 03-APR-2000; 2000US-194564P.  
XX  
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
XX Gertler FB, Bear JE, Wehland J, Loureiro JU;  
PI WPI; 2001-626380/72.  
DR  
XX

Regulating cell motility for promoting wound healing and tissue  
PT regeneration, treating, neurodegenerative disease and metastasis, by  
PT inducing or depleting a functional enabled/vasodilator-stimulated  
PT phosphoprotein -  
XX  
XX Example 2; Page 60; 107pp; English.

XX The invention relates to a method of preventing mammalian cell migration,  
CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
CC phosphoprotein (VASP) or promoting cell migration comprising depleting  
CC functional Ena/VASP protein in the mammalian cell. The method is useful  
CC for preventing or promoting mammalian cell migration, preferably tumour  
CC cell migration in vitro or in vivo and to prevent tumour cell metastasis  
CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
CC wound healing, preferably fibroblasts or nerve cells of a tissue type  
CC with the inhibitor to promote actin polymerisation and tissue formation  
CC on a scaffold. The inhibitor is also useful for preventing  
CC neurodegeneration such as in Alzheimer's disease; Down Syndrome,  
CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
CC complex, progressive supranuclear palsy, progressive bulbar palsy,  
CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
CC cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
CC inhibitor is further useful for enhancing learning and memory in a  
CC subject having or at risk of developing a learning disorder such as  
CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
CC is administered in an amount for inhibiting the activity of Mena in a  
CC synapse. Ena/VASP activator is useful for disrupting learning and memory  
CC and the activator is administered in an amount to promote Ena/VASP  
CC protein-FB65 interaction. Inducing the activity of Ena/VASP protein  
CC in immune or haematopoietic cells reduces the ability of the cells to  
CC migrate and this is useful for treating and preventing inflammatory  
CC disorders such as arthritis, allergy, gout, organ transplant.  
CC ulcerative colitis and ischaemic diseases and also for treating cancer  
CC metastasis. The present sequence represents the amino acid sequence  
CC of Ena/VASP homology (EVH) proline-rich motif #1.

XX Sequence 5 AA;  
SQ

Query Match 33.3%; Score 5; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
DB 1 FPPPP 5

RESULT 14  
AAO17762  
ID AAO17762 standard; peptide; 5 AA.  
XX AAO17762;  
XX  
XX 15-AUG-2002 (first entry)  
XX  
XX Zyxine VASP binding motif.  
XX  
XX Zyxine; EVH-1; cardiovascular disease; inflammation; cancer;  
KW Ena-vasodilator-stimulated phosphoprotein homologue; VASP homologue;  
KW cardiant; antiinflammatory; cytostatic.  
XX  
XX Unidentified.  
XX  
XX WO200242777-A2.  
PN  
XX 30-MAY-2002.  
PD  
XX 22-NOV-2001; 2001WO-EP13592.  
PF  
XX 25-NOV-2000; 2000DE-1058596.  
PR  
XX (AVET ) AVENTIS PHARMA DEUT GMBH.  
PA (VASO-) VASOPHARM BIOTECH GMBH.  
XX  
XX Jordan B, Drueckes P, Jarchau T, Walter U;  
PI  
XX



DR WPI; 2002-463650/49.

XX Identifying compounds that modulate Ena-vasodilator-stimulated

PT phosphoprotein homolog (EVH)-1 binding interactions, useful e.g. for

PT treating cardiovascular disease, comprises using antibodies -

XX

XX Example 4; Page 18; 34pp; German.

XX

CC The present invention relates to a method of identifying compounds which

CC modulate the interaction between an EVH-1 (Ena-vasodilator-stimulated

CC phosphoprotein (VASP) homologue) binding domain and an EVH-1 domain. Such

CC compounds can be used for treating cardiovascular diseases, inflammation

CC and neoplastic cell/tissue alterations such as cancer. The present

CC sequence is a VASP binding domain from zyxine described in the

CC exemplification of the invention.

XX

SQ Sequence 5 AA;

Query Match 33.3%; Score 5; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10

Db 1 FPPPP 5

RESULT 15

AAW31441

ID AAW31441 standard; Protein; 6 AA.

AC AAW31441;

XX

DT 04-AUG-1998 (first entry)

XX

DE Transcriptional activator peptide fragment LS46.

XX

XX Activating sequence; Gal4; transcriptional activator; RNA polymerase;

KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;

KW Gal1; DNA binding domain.

XX

OS Synthetic.

OS

PN WO9744447-A2.

XX

PD 27-NOV-1997.

XX

XX

PF 02-MAY-1997; 97WO-US07338.

XX

PR 01-MAY-1997; 97US-0017016.

PR

ER 03-MAY-1996; 96US-0017016.

XX

PA (HARD ) HARVARD COLLEGE.

XX

PI Lu X, Ptashne M, Wu Y;

XX

XX WPI; 1998-018502/02.

DR N-FSDB; AAV02536.

XX

XX New transcriptional activator containing DNA binding domain bound to

PT peptide - useful for controlling gene expression, especially in gene

PT therapy, and in protein-protein interaction assays, does not inhibit

PT other transcription activators

XX

XX Example 1; Page 24; 55pp; English.

PS

CC AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076

CC are fragments used in an assay to determine novel transcriptional

CC activators. The method involves the production of transcriptional

CC activators comprising of a DNA-binding group and a 6-25 amino acid

CC peptide that is covalently bonded to the DNA binding group and does not

CC represent a fragment of a natural transcription activator.

CC Protein-protein interactions are identified in the assay by fusing a

CC

CC DNA-binding domain to a library of DNA fragments and introducing this and

CC a fusion of target protein and a polypeptide containing a region of Gal4

CC which interacts with Gal1p into a cell containing Gal1p and identifying

CC members of the library that interact with the target transcription in a

CC transcription. Such constructs are used to activate transcription in a

CC cell, e.g. for controlling gene activity, particularly in gene therapy

CC (e.g. recognizing a site close to a selected therapeutic gene).

CC Transcription can be activated without blocking other transcriptional

CC activators. They probably act by interacting with a component of the RNA

CC polymerase II holoenzyme, Gal11, the strongest known yeast activator,

CC which provides a more sensitive assay allowing detection of even weak

CC protein-protein interactions. Such activators do not create toxicity

CC problems even when overexpressed.

XX

SQ Sequence 6 AA;

Query Match 33.3%; Score 5; DB 19; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10

Db 1 FPPPP 5

RESULT 16

AAW72259

ID AAW72259 standard; peptide; 7 AA.

XX

AC AAW72259;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostriin derived cytokine inducing peptide SEQ ID 14.

XX

XX Colostriin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder;

KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis; infection.

XX

OS Synthetic.

OS

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US22818.

XX

PR 17-AUG-1999; 99US-0149311.

XX

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX

PT Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostriin as an immunological

PT regulator -

XX

XX Claim 1; Page 34; 50pp; English.

PS

CC Sequences AAW72246 - AAW72275 represent peptides derived from colostriin,

CC a proline rich polypeptide aggregate contained in colostrum. The

CC peptides have immune response modulatory activity, and are capable of

CC inducing cytokines. Colostriin and its derived peptides are useful for

CC inducing cytokine production, for modulating an immunological response

CC and for inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 33.3%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 PPPPQ 11  
 |||||  
 Db 2 PPPPQ 6  
 RESULT 17  
 AAB72512  
 ID AAB72512 standard; Peptide; 7 AA.  
 XX  
 AC AAB72512;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #13.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 KW Unidentified.  
 OS  
 XX WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidizing species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 33.3%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 PPPPQ 11  
 |||||  
 Db 2 PPPPQ 6  
 RESULT 18  
 AAB72544  
 ID AAB72544 standard; Peptide; 7 AA.  
 XX  
 AC AAB72544;  
 XX

DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #13.  
 XX  
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22774.  
 XX  
 PR 17-AUG-1999; 99US-0149633.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 33.3%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 PPPPQ 11  
 |||||  
 Db 2 PPPPQ 6  
 RESULT 19  
 AAB59315  
 ID AAB59315 standard; Peptide; 7 AA.  
 XX  
 AC AAB59315;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment A-7.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB02128.  
 XX  
 PR 02-JUN-1999; 99GB-0012852.  
 XX  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
XX Claim 7; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
XX Sequence 7 AA;  
SQ

Query Match 33.3%; Score 5; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
Db 2 PPPPQ 6

RESULT 20  
AAE20241  
ID AAE20241 standard; peptide; 7 AA.  
XX  
AC AAE20241;  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX  
XX Colostrinin constituent peptide #13.  
DE  
XX  
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnary.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 7 /note= "Optionally C-terminal amide"  
FT  
FT  
XX  
XX WO200213850-A1.  
PN  
XX  
XX 21-FEB-2002.  
PD  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
PF  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
PR  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX  
XX Stanton GJ, Hughes TK, Boldogh I;  
PI WPI; 2002-269151/31.  
XX  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
PT  
XX  
XX Claim 6; Page 25; 51pp; English.  
PS  
XX  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC

CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
CC after a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrinin constituent peptide.  
XX  
XX Sequence 7 AA;  
SQ

Query Match 33.3%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
Db 2 PPPPQ 6

RESULT 21  
AAM51048  
ID AAM51048 standard; Peptide; 7 AA.  
XX  
AC AAM51048;  
XX  
XX 30-MAY-2002 (first entry)  
DT  
XX  
XX Colostrinin constituent peptide.  
DE  
XX  
XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; human.  
KW  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 7 /note= "optional C-terminal amidation"  
FT  
FT  
XX  
XX WO200213849-A1.  
PN  
XX  
XX 21-FEB-2002.  
PD  
XX  
XX 17-AUG-2000; 2000WO-US22775.  
PF  
XX  
XX 17-AUG-2000; 2000WO-US22775.  
PR  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGG-) REGEN THERAPEUTICS PLC.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
PI WPI; 2002-269150/31.  
XX  
XX Modulation of blood cell proliferation in a patient involves use of  
PT blood cell regulator selected from colostrinin, its constituent peptide  
PT and/or analogue -  
PT  
XX  
XX Claim 1; Page 34; 54pp; English.  
PS  
XX  
XX The present sequence is that of a colostrinin constituent peptide  
CC that is used as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. Methods are  
CC claimed for: inducing a cytokine in a cell by contact with an  
CC immunological regulator, where the cell is present in a cell  
CC culture, a tissue, an organ or an organism, and the cell is  
CC mammalian, including human; modulating an immune response in a cell  
CC

CC by contact with the immunological regulator under conditions  
CC effective to induce a cytokine; modulating an immune response in a  
CC patient by administering an immunological regulator under conditions  
CC effective to induce a cytokine, where the immunological regulator  
CC is administered topically or as part of a dietary supplement, and  
CC where the immune response is specific or non specific, an interferon  
CC response or an antibody response; modulating blood cell proliferation  
CC by contacting blood cells with a blood cell regulator, where the  
CC blood cells are present in a cell culture or an organism, are  
CC mammalian or human, and where the blood cells are increased in  
CC number or differentiated; and a method for modulating blood cell  
CC proliferation in a patent. A claimed cytokine-inducing composition  
CC comprises a pharmaceutical carrier and an active agent such as the  
CC present peptide.

XX SQ Sequence 7 AA;  
Query Match 33.3%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
Db 2 PPPPQ 6  
|||||

RESULT 22  
AAO14590  
ID AAO14590 standard; peptide; 7 AA.  
AC AAO14590;  
XX  
XX 27-MAY-2002 (first entry)  
DE Neural cell regulatory colostrinin peptide 13.  
XX  
XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
KW neural cell treatment.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 7 /note= "Optional C-terminal amide"  
FT  
XX WO200213851-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US22777.  
XX  
XX 17-AUG-2000; 2000WO-US22777.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Boldogh I, Stanton JG, Hughes TK;  
XX WPI; 2002-269152/31.  
XX  
XX Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
FT analog -  
XX  
XX Claim 7; Page 21; 37pp; English.  
XX  
XX The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention.  
XX  
SQ Sequence 7 AA;  
Query Match 33.3%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
Db 2 PPPPQ 6  
|||||

RESULT 23  
AAB35516  
ID AAB35516 standard; Peptide; 9 AA.  
XX  
AC AAB35516;  
XX  
XX 14-FEB-2001 (first entry)  
DE S. cerevisiae RNA triphosphatase motif A.  
XX  
XX MRNA cap formation inhibition; RNA guanylyltransferase;  
KW RNA triphosphatase; growth inhibition; antiviral agent;  
KW antiparasitic agent.  
XX  
XX Saccharomycetes cerevisiae.  
XX  
XX WO2000063433-A1.  
XX  
XX 26-OCT-2000.  
XX  
XX 09-NOV-1999; 99WO-US26520.  
XX  
XX 09-NOV-1998; 98US-0189579.  
XX 20-MAY-1999; 99US-0315444.  
XX (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX  
XX Shuman S;  
XX  
XX WPI; 2000-656425/63.  
XX  
XX Screening for a compound that inhibits formation of an organism's 5'  
PT mRNA cap structure for use as e.g. antiviral or antiparasitic agents,  
PT comprises comparing the inhibition of different organism's capping  
PT apparatus in a test organism -  
XX  
XX Disclosure; Page 132; 146pp; English.  
XX  
XX The present invention describes a novel method for use in identifying  
CC compounds which inhibit the formation of an organism's 5' mRNA cap  
CC structure. The cap-forming enzymes differ between organisms, enabling the  
CC inhibitors to be specific to particular viruses, parasites or eukaryotes.  
CC and so they can be used in disease treatment.

XX SQ Sequence 9 AA;  
Query Match 33.3%; Score 5; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEWKF 6  
Db 5 LEWKF 9  
|||||

RESULT 24  
AAB32219  
ID AAB32219 standard; Peptide; 9 AA.

XX AAB32219;  
 XX 08-JAN-2001 (first entry)  
 XX Motif A of RNA triphosphatase.  
 XX RNA guanylyltransferase; mRNA capping; growth inhibition; antiviral;  
 KW antineoplastic agent; antiparasitic; triphosphatase.  
 XX Saccharomyces cerevisiae.  
 XX US6107040-A.  
 XX 22-AUG-2000.  
 XX 09-NOV-1998; 98US-0188579.  
 XX 09-NOV-1998; 98US-0188579.  
 XX (SHUM/) SHUMAN S.  
 XX Shuman S;  
 XX WPI; 2000-578532/54.  
 XX Screening for 5' mRNA cap inhibitors comprising treating host organisms  
 KW with capping apparatus from two different organisms with test compounds  
 KW and comparing growth inhibition -  
 XX Example 9; Figure 4; 62pp; English.  
 XX This invention relates to a method of screening for compounds that  
 CC inhibit the formation of a 5' mRNA cap. The m7GpppN cap is the first  
 CC modification of the 5' terminus of a nascent transcript that occurs  
 CC during the processing of eukaryotic mRNA, and involves the RNA  
 CC triphosphatase and guanylyltransferase enzymes. The method comprises  
 CC replacing the hosts genes encoding 5' mRNA capping functions with genes  
 CC encoding mRNA capping functions from two different organisms, treating  
 CC the modified host cells with a test compound and comparing growth  
 CC inhibition in the two host cells with different modifications. Also  
 CC included in the invention is a method of screening for a compound that  
 CC inhibits the catalytic activity of fungal 5' triphosphatase. The methods  
 CC are used for screening for a compound that inhibits the formation of an  
 CC organisms 5' mRNA cap structure. The method is useful in gene  
 CC biochemical pharmacology and drug discovery. Compounds identified as  
 CC specific inhibitors of capping in mammalian cells are capable of being  
 CC developed as potential antineoplastic agents. The methods also allow for  
 CC the identification of antiviral and antiparasitic agents. Sequences  
 CC AAB32132-B32209 represent peptide motifs of RNA guanylyltransferase  
 CC proteins. RNA guanylyltransferase motif I contains a conserved element  
 CC which is involved in the transfer of GMP from GTP by the enzyme. Motifs  
 CC III, IIIa, IV, V and VI are conserved in the same order and with similar  
 CC spacing in the capping enzymes from fungi, metazoans, DNA viruses and  
 CC trypanosomes. Sequences AAB32210-B32218 represent RNA  
 CC guanylyltransferase proteins. These sequences are used in the  
 CC identification of essential enzymic functional groups used in the capping  
 CC process. Sequences AAB32219-B32242 represent RNA triphosphatase peptide  
 CC motifs, and AAB32243-B32245 represent methyltransferase protein  
 CC sequences. The peptides and proteins are used in examples of the method  
 CC of the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 33.3%; Score 5; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 LEMKF 6  
 Db |||||  
 5 LEMKF 9

RESULT 25  
 AAU09144  
 ID AAU09144 standard; peptide; 9 AA.  
 XX AC AAU09144;  
 XX 19-DEC-2001 (first entry)  
 DT Ena/VASP homology (EVH) proline-rich motif #3.  
 DE  
 XX Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
 KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
 KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
 KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
 KW Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
 KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
 KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
 KW cancer; ischaemia.  
 XX OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 9 /label= OTHER  
 FT /note= "Other = any amino acid"  
 FT WO200174853-A2.  
 FN 11-OCT-2001.  
 XX 30-MAR-2001; 2001WO-US10249.  
 XX 03-APR-2000; 2000US-194564P.  
 XX (WASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 XX Gertler FB, Bear JE, Wehland J, Loureiro JJ;  
 PI WPI; 2001-626380/72.  
 DR Regulating cell motility for promoting wound healing and tissue  
 XX regeneration, treating, neurodegenerative disease and metastasis, by  
 PT inducing or depleting a functional enabled/vasodilator-stimulated  
 PT phosphoprotein -  
 XX Example 6; Page 66; 107pp; English.  
 PS The invention relates to a method of preventing mammalian cell migration,  
 XX comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
 CC phosphoprotein (VASP) or promoting cell migration comprising depleting  
 CC functional Ena/VASP protein in the mammalian cell. The method is useful  
 CC for preventing or promoting mammalian cell migration, preferably tumour  
 CC cell migration in vitro or in vivo and to prevent tumour cell metastasis  
 CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
 CC wound healing, preferably fibroblasts or nerve cells of a tissue type  
 CC with the inhibitor to promote actin polymerisation and tissue formation  
 CC on a scaffold. The inhibitor is also useful for preventing  
 CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
 CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
 CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
 CC complex, progressive supranuclear palsy, progressive bulbar palsy,  
 CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
 CC cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
 CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
 CC inhibitor is further useful for enhancing learning and memory in a  
 CC subject having or at risk of developing a learning disorder such as  
 CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
 CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
 CC is administered in an amount for inhibiting the activity of Ena in a  
 CC synapse. Ena/VASP activator is useful for disrupting learning and memory  
 CC and the activator is administered in an amount to promote Ena/VASP

CC protein-FE65 interaction. Inducing the activity of Ena/VASP protein  
 CC in immune or haematopoietic cells reduces the ability of the cells to  
 CC migrate and this is useful for treating and preventing inflammatory  
 CC disorders such as arthritis, allergy, gout, organ transplant,  
 CC ulcerative colitis and ischaemic diseases and also for treating cancer  
 CC metastasis. The present sequence represents the amino acid sequence  
 CC of Ena/VASP homology (EVH) proline-rich motif #3.  
 XX  
 SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPPP 10  
 Db 1 PPPPP 5  
 |||||  
 |||||

RESULT 26  
 ABJ05692  
 ID ABJ05692 standard; Peptide; 9 AA.  
 XX  
 AC ABJ05692;  
 XX  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE Peptide motif of RNA triphosphatase SEQ ID No 88.  
 XX  
 KW Antimicrobial; fungicide; transformed host organism; 5' mRNA capping;  
 KW eukaryotic gene expression; mRNA 5' cap m7GpppN; enzyme.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PI US6420163-B1.  
 XX  
 PD 16-JUL-2002.  
 XX  
 PF 22-NOV-2000; 2000US-0721362.  
 XX  
 PR 09-NOV-1998; 98US-0188579.  
 XX  
 PA (SHUM/) SHUMAN S.  
 XX  
 PI Shuman S;  
 XX  
 DR WPI; 2002-654639/70.  
 XX  
 PT Transformed host organism for drug screening assays to identify  
 PT candidate drugs, e.g. anti-fungal agents, comprises genes from a second  
 PT organism replacing genes involved in 5' mRNA capping -  
 XX  
 PS Disclosure; Fig 4; 82pp; English.  
 XX  
 CC The invention relates to a transformed host organism, in which the host  
 CC organism's genes encoding entire 5' mRNA capping functions have been  
 CC replaced with replacement genes encoding 5' mRNA capping functions from  
 CC another organism (therefore producing a host organism expressing the  
 CC another organism's complete capping apparatus). The transformed host  
 CC organism may be used to screen for drugs which target an essential aspect  
 CC of eukaryotic gene expression, the formation of the mRNA 5' cap m7GpppN.  
 CC For example, if the transformed host organism was an isogenic yeast  
 CC strain that derived all it's capping activities from fungal sources  
 CC rather than mammalian sources it may be used to identify molecules that  
 CC specifically target the fungal capping apparatus. This sequence  
 CC represents a peptide relating to the formation of the mRNA 5' cap m7GpppN  
 CC of the invention.  
 XX  
 SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPPP 10  
 Db 1 PPPPP 5  
 |||||  
 |||||

RESULT 27  
 ABR27236  
 ID ABR27236 standard; Peptide; 9 AA.  
 XX  
 AC ABR27236;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 187P3F2 HLA peptide #71.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC020283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 401; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
 Db 4 PPPPQ 8  
 |||||  
 |||||

RESULT 28  
 ABR28248  
 ID ABR28248 standard; Peptide; 9 AA.  
 XX

```

AC ABR28248;
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3F2 HLA peptide #1083.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 413; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 33.3%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db |||||
4 PPPPQ 8

RESULT 29
ABR28254
ID ABR28254 standard; Peptide; 9 AA.
XX
XX ABR28254;
AC
XX
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3F2 HLA peptide #1089.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.

XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 413; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 33.3%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db |||||
1 PPPPQ 5

RESULT 30
ABR28437
ID ABR28437 standard; Peptide; 9 AA.
XX
XX ABR28437;
AC
XX
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3F2 HLA peptide #1272.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX

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XX PA (AGEN-) AGENSYS INC.
XX PI Jakovovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 415; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
XX CC
XX CC Query Match 33.3%; Score 5; DB 24; Length 9;
XX CC Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 7 PPPPQ 11
XX DB |||||
XX DB 1 PPPPQ 5
XX
XX RESULT 31
XX ID AAU09138 standard; peptide; 10 AA.
XX AC AAU09138;
XX DT 19-DEC-2001 (first entry)
XX DE Ena/VASP homology (EVH) consensus binding site.
XX KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
XX KW cell migration; Ena/VASP; wound healing; actin polymerisation;
XX KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;
XX KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;
XX KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;
XX KW Tourette's syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;
XX KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;
XX KW inflammatory disorder; arthritis; allergy; gout; organ transplant;
XX KW cancer; ischaemia.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /label= Asp, Gly
XX FT Misc-difference 7 /label= OTHER
XX FT /note= "Other = any amino acid"
XX
XX FN WO200174853-A2.
XX PD 11-OCT-2001.
XX XX
XX PF 30-MAR-2001; 2001WO-US10249.

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XX XX 03-APR-2000; 2000US-194564P.
XX PA (NASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX XX
XX PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;
XX DR WPI; 2001-626380/72.
XX CC Regulating cell motility for promoting wound healing and tissue
XX CC regeneration, treating, neurodegenerative disease and metastasis, by
XX CC inducing or depleting a functional enabled/vasodilator-stimulated
XX CC phosphoprotein
XX CC
XX CC Example 2; Page 59; 107pp; English.
XX CC
XX CC The invention relates to a method of preventing mammalian cell migration,
XX CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated
XX CC phosphoprotein (VASP) or promoting cell migration comprising depleting
XX CC functional Ena/VASP protein in the mammalian cell. The method is useful
XX CC for preventing or promoting mammalian cell migration, preferably tumour
XX CC cell migration in vitro or in vivo and to prevent tumour cell metastasis
XX CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting
XX CC wound healing, preferably fibroblasts or nerve cells of a tissue type
XX CC with the inhibitor to promote actin polymerisation and tissue formation
XX CC on a scaffold. The inhibitor is also useful for preventing
XX CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,
XX CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct
XX CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia
XX CC complex, progressive supranuclear palsy, progressive bulbar palsy,
XX CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts
XX CC cerebellar degeneration, Tourette's syndrome, hypoglycaemia, hypoxia,
XX CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP
XX CC inhibitor is further useful for enhancing learning and memory in a
XX CC subject having or at risk of developing a learning disorder such as
XX CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile
XX CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor
XX CC is administered in an amount for inhibiting the activity of Mena in a
XX CC synapse. Ena/VASP activator is useful for disrupting learning and memory
XX CC and the activator is administered in an amount to promote Ena/VASP
XX CC protein-FB65 interaction. Inducing the activity of Ena/VASP protein
XX CC in immune or haematopoietic cells reduces the ability of the cells to
XX CC migrate and this is useful for treating and preventing inflammatory
XX CC disorders such as arthritis, allergy, gout, organ transplant,
XX CC ulcerative colitis and ischaemic diseases and also for treating cancer
XX CC metastasis. The present sequence represents the amino acid sequence
XX CC of Ena/VASP homology (EVH) consensus binding site.
XX SQ Sequence 10 AA;
XX CC
XX CC Query Match 33.3%; Score 5; DB 22; Length 10;
XX CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 FPPPP 10
XX DB |||||
XX DB 2 FPPPP 6
XX
XX RESULT 32
XX ID ABR27336 standard; Peptide; 10 AA.
XX AC ABR27336;
XX XX
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187B3F2 HLA peptide #171.
XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX XX

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PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 409; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
 |||||  
 Db 1 PPPPQ 5

## RESULT 35

ABR28332  
 ID ABR28332 standard; Peptide; 10 AA.

AC ABR28332;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3F2 HLA peptide #1167.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX

PS Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
 |||||  
 Db 2 PPPPQ 6

## RESULT 36

ABR28354  
 ID ABR28354 standard; Peptide; 10 AA.

XX ABR28354;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3F2 HLA peptide #1189.

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX

PS Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX

SQ Sequence 10 AA;

```

Query Match      33.3%; Score 5; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 4 PPPPQ 8

RESULT 37
ABR28537
ID ABR28537 standard; Peptide; 10 AA.
XX
AC ABR28537;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3P2 HLA peptide #1372.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 416; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 10 AA;

Query Match      33.3%; Score 5; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 2 PPPPQ 6
```

```

RESULT 38
AAG79174
ID AAG79174 standard; peptide; 14 AA.
XX
AC AAG79174;
XX
DT 03-JAN-2002 (first entry)
XX
DE Peptide derived from ActA, and containing EVH1-binding site.
XX
KW ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;
KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
KW infectious disease; cancer; autoimmune disease; inflammation;
KW platelet aggregation; wound healing; clotting.
XX
OS Listeria monocytogenes.
XX
PN WO200174858-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10753.
XX
PR 03-APR-2000; 2000US-194215P.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB ) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
PI Krause M, Sechi AS, Gertler FB, Wehland J;
XX
DR WPI; 2001-616686/71.
XX
PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage
PT activation for treating cancer, autoimmune disease, and infectious
PT disease, comprises contacting with a Fyb/SLAP complex modulator -
XX
PS Example 5; Page 43; 79pp; English.
XX
CC The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
CC ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated
CC phosphoprotein (VASP) proteins. The specification describes a method for
CC modulating cytoskeletal rearrangement in a cell, or T cell response to T
CC cell receptor stimulation. The method comprises contacting the cell or T
CC cell with a Fyb/SLAP complex modulator sufficient to modulate the
CC formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein.
CC The method is useful for modulating cytoskeletal rearrangement in a cell
CC such as a lymphocyte, preferably a T cell, a macrophage or a cell
CC fragment such as a platelet and for modulating T cell response to a
CC T cell receptor stimulation. T cell response is increased in a subject
CC having or at risk of developing infectious disease or cancer and T cell
CC response is inhibited in a subject having or is at risk of developing an
CC autoimmune disease or a condition characterized by inflammation. A
CC composition comprising a Fyb/SLAP complex inhibitor is useful for
CC increasing platelet aggregation for promoting wound healing or
CC clotting. The present sequence represents a peptide derived from
CC ActA, which is used in the course of the invention.
XX
SQ Sequence 14 AA;

Query Match      33.3%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 3 FPPPP 7

RESULT 39
AAB85935
ID AAB85935 standard; peptide; 14 AA.
XX
```

AC AAB85935;  
 DT 30-NOV-2001 (first entry)  
 XX  
 DE 2A11 seed storage protein fragment.  
 XX  
 KW Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;  
 KW 2A11.  
 XX  
 OS Lycopersicon esculentum.  
 XX  
 PN US6281410-B1.  
 XX  
 PD 28-AUG-2001.  
 XX  
 XX 15-JAN-1999; 99US-0232861.  
 XX  
 PR 29-APR-1988; 88US-0188361.  
 PR 02-NOV-1988; 88US-0267685.  
 PR 10-AUG-1993; 93US-0105852.  
 PR 07-JUN-1995; 95US-0484941.  
 PR 07-MAR-1997; 97US-0812665.  
 PR 31-JUL-1986; 86US-0891529.  
 PR 26-MAY-1987; 87US-0054369.  
 PR 28-JUL-1987; 87US-0078538.  
 PR 25-JAN-1988; 88US-0147781.  
 PR 15-MAR-1988; 88US-0168190.  
 XX  
 PA (CALJ ) CALGENE LLC.  
 XX  
 XX Knauf VC, Kridl JC;  
 PI  
 XX WPI; 2001-564354/63.  
 DR  
 XX  
 PT Obtaining a plant that produces a seed with a modified phenotype or  
 PT altering a seed phenotype, comprises transforming a plant cell with a  
 PT DNA construct consisting of operably linked components in the direction  
 PT of transcription -  
 XX  
 PS Example 9; Fig 6; 68pp; English.  
 XX  
 CC The invention provides a method for obtaining a plant which produces  
 CC at least one seed having a modified phenotype. The method involves  
 CC transforming a host plant cell with a DNA construct which consists of  
 CC operably linked components in the direction of transcription, a promoter  
 CC region from a Brassica plant gene, a DNA sequence of interest other than  
 CC the native coding sequence, and a transcription termination region. The  
 CC method is useful for obtaining plants having modified phenotype or for  
 CC altering the phenotype of a plant seed or tissue. The DNA constructs are  
 CC used in manipulating plant cells to provide for regulated transcription,  
 CC such as light inducible transcription, in a plant tissue or plant part of  
 CC interest at particular stages of plant growth or in response to external  
 CC control. These constructs are also used for modulation of expression of  
 CC endogenous products as well as production of exogenous products in the  
 CC seed. The present sequence represents an amino acid fragment of the  
 CC seed storage protein 2A11.  
 XX  
 XX Sequence 14 AA;  
 SQ  
 Query Match 33.3%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PPQET 13  
 Db 8 PPQET 12  
 RESULT 40  
 AAR42641  
 ID AAR42641 standard; peptide; 15 AA.  
 XX  
 AC AAR42641;

XX 25-MAR-2003 (updated)  
 DT 22-APR-1994 (first entry)  
 XX  
 DE N-terminal sequence of protein from BCG culture supernatant.  
 XX  
 KW Tuberculosis; delayed hypersensitivity; antigen; immunogen; vaccine;  
 KW T lymphocyte stimulation; BCG.  
 XX  
 OS Mycobacterium tuberculosis BCG.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 4  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 FT Modified-site 6  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 FT Modified-site 12  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 FT Modified-site 14  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 XX  
 PN WO9319093-A1.  
 XX  
 PD 30-SEP-1993.  
 XX  
 PF 17-MAR-1993; 93WO-FR00268.  
 XX  
 PR 19-MAR-1992; 92FR-0003286.  
 XX  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Marchal G, Romain F;  
 XX  
 XX WPI; 1993-320686/40.  
 DR  
 XX  
 PT New peptide inducing intense delayed hypersensitivity reaction -  
 PT in presence of live, but not dead, Mycobacterium tuberculosis,  
 PT useful diagnostically and in therapeutic immunogens  
 XX  
 PS Claim 2; Page 17; 31pp; French.  
 XX  
 CC A peptide which can initiate delayed hypersensitivity reactions of  
 CC different intensity in the presence of live or dead Mycobacterium  
 CC tuberculosis complex bacteria is isolated from supernatant of BCG  
 CC cell culture. The N-terminal sequence of the peptide has been  
 CC determined.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 15 AA;  
 Query Match 33.3%; Score 5; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PPPPQ 11  
 Db 7 PPPPQ 11  
 RESULT 41  
 AAW39038  
 ID AAW39038 standard; peptide; 15 AA.  
 XX  
 AC AAW39038;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:439.  
 XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX Synthetic.  
 XX WO9730074-A1.  
 XX 21-AUG-1997.  
 XX 14-FEB-1997; 97WO-US02298.  
 XX 16-FEB-1996; 96US-0602999.  
 XX (CYTO-) CYTOGEN CORP.  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 XX Sparks AB, Thorn JM;  
 XX WPI; 1997-424972/39.  
 XX Src homology region 3 binding peptide - used to activate Src  
 XX tyrosine kinase(s) and to stimulate immune response by increasing  
 XX production of certain lymphokine(s), e.g. interleukin-1  
 XX Claim 22; Page 94; 131pp; English.  
 XX The present sequence represents a peptide which resembles a Src homology  
 XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 XX binding peptides can be used in the method to identify inhibitors of  
 XX their binding to their respective SH3 domains, which could be used to  
 XX modulate the pharmacological activity of proteins or polypeptide  
 XX containing the SH3 domain. The peptides can also be used to activate  
 XX Src or Src-related protein tyrosine kinases, to stimulate the immune  
 XX response by increasing the production of certain lymphokines, e.g.  
 XX tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 XX conjugated molecule to certain cellular compartments containing Src or  
 XX Src related proteins.  
 XX Sequence 15 AA;  
 SQ Query Match 33.3%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PPPPQ 11  
 Db 6 PPPPQ 10  
 RESULT 42  
 AAW39006  
 ID AAW39006 standard; peptide; 15 AA.  
 XX AAW39006;  
 XX 27-MAR-1998 (first entry)  
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:405.  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX Synthetic.

XX WO9730074-A1.  
 XX 21-AUG-1997.  
 XX 14-FEB-1997; 97WO-US02298.  
 XX 16-FEB-1996; 96US-0602999.  
 XX (CYTO-) CYTOGEN CORP.  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 XX Sparks AB, Thorn JM;  
 XX WPI; 1997-424972/39.  
 XX Src homology region 3 binding peptide - used to activate Src  
 XX tyrosine kinase(s) and to stimulate immune response by increasing  
 XX production of certain lymphokine(s), e.g. interleukin-1  
 XX Claim 22; Page 93; 131pp; English.  
 XX The present sequence represents a peptide which resembles a Src homology  
 XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 XX binding peptides can be used in the method to identify inhibitors of  
 XX their binding to their respective SH3 domains, which could be used to  
 XX modulate the pharmacological activity of proteins or polypeptide  
 XX containing the SH3 domain. The peptides can also be used to activate  
 XX Src or Src-related protein tyrosine kinases, to stimulate the immune  
 XX response by increasing the production of certain lymphokines, e.g.  
 XX tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 XX conjugated molecule to certain cellular compartments containing Src or  
 XX Src related proteins.  
 XX Sequence 15 AA;  
 SQ Query Match 33.3%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PPPPQ 11  
 Db 6 PPPPQ 10  
 RESULT 43  
 AAW38970  
 ID AAW38970 standard; peptide; 15 AA.  
 XX AAW38970;  
 XX 27-MAR-1998 (first entry)  
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:367.  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX Synthetic.  
 XX WO9730074-A1.  
 XX 21-AUG-1997.

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PF 14-FEB-1997; 97WO-US02298.
XX
PR 16-FEB-1996; 96US-0602999.
XX
PA (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JM;
XX WPI; 1997-424972/39.
XX
PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
PS Claim 22; Page 92; 131pp; English.
XX
CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.
XX
SQ Sequence 15 AA;
Query Match 33.3%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPQ 11
DB 9 PPPPQ 13

RESULT 44
AAW38976
ID AAW38976 standard; peptide; 15 AA.
XX
AC AAW38976;
XX
DT 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:373.
XX
KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS Synthetic.
XX
FN WO9730074-A1.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US02298.
XX
PR 16-FEB-1996; 96US-0602999.
XX
PA (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
XX

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PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
DR WPI; 1997-424972/39.
XX
PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
PS Claim 22; Page 92; 131pp; English.
XX
CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.
XX
SQ Sequence 15 AA;
Query Match 33.3%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPQ 11
DB 6 PPPPQ 10

RESULT 45
AAW38942
ID AAW38942 standard; peptide; 15 AA.
XX
AC AAW38942;
XX
DT 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:339.
XX
KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS Synthetic.
XX
FN WO9730074-A1.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US02298.
XX
PR 16-FEB-1996; 96US-0602999.
XX
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
XX

```

DR WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src

PT tyrosine kinase(s) and to stimulate immune response by increasing

PT production of certain lymphokine(s), e.g. interleukin-1

XX

PS Claim 22; Page 91; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology

CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:

CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which

CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)

CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind

CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3

CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)

CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified

CC peptides can be used in the method to identify inhibitors of

CC their binding to their respective SH3 domains, which could be used to

CC modulate the pharmacological activity of proteins or polypeptide

CC containing the SH3 domain. The peptides can also be used to activate

CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.

CC tumour necrosis factor-alpha and interleukin-1, or to deliver a

CC conjugated molecule to certain cellular compartments containing Src or

CC Src related proteins.

XX

SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPQ 11

DB 6 PPPPQ 10

RESULT 46

AAW38952

ID AAW38952 standard; peptide; 15 AA.

XX

AC AAW38952;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SRQ ID NO:349.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;

KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US02298.

XX

PR 16-FEB-1996; 96US-0602999.

XX

PA (CYTO-) CYTOGEN CORP.

XX

PA (UNIV NORTH CAROLINA.

XX

PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

PI Sparks AB, Thorn JM;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src

PT tyrosine kinase(s) and to stimulate immune response by increasing

PT production of certain lymphokine(s), e.g. interleukin-1

XX

PS Claim 22; Page 91; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology

CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:

CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which

CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)

CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind

CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3

CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)

CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified

CC peptides can be used in the method to identify inhibitors of

CC their binding to their respective SH3 domains, which could be used to

CC modulate the pharmacological activity of proteins or polypeptide

CC containing the SH3 domain. The peptides can also be used to activate

CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.

CC tumour necrosis factor-alpha and interleukin-1, or to deliver a

CC conjugated molecule to certain cellular compartments containing Src or

CC Src related proteins.

XX

SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPQ 11

DB 6 PPPPQ 10

RESULT 47

AAV93014

ID AAV93014 standard; peptide; 15 AA.

XX

AC AAV93014;

XX

DT 08-NOV-2000 (first entry)

XX

DE Transforming growth factor inhibitory peptide P60.

XX

KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;

KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;

KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX

OS Rattus sp.

XX

PN WO200031135-A1.

XX

PD 02-JUN-2000.

XX

PF 23-NOV-1999; 99WO-ES00375.

XX

PR 24-NOV-1998; 98ES-0002465.

XX

PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX

PI Ezquerro Saenz J, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borras Cuesta F;

XX

DR WPI; 2000-411935/35.

XX

PT Peptides that antagonize binding of transforming growth factor beta1,

PT useful for treatment of liver disease, especially cirrhosis, are

PT partial sequences of the factor or its receptors

XX

PS Disclosure; Page 27; 86pp; Spanish.

XX

CC The invention relates to synthetic peptides that antagonise the binding

CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor

CC in vivo which have partial amino acid sequences identical, or similar,

CC with those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133  
 CC represent examples of the peptides of the invention. The peptides act  
 CC by competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors,  
 CC e.g. they are inhibitors of stimulation of collagen synthesis in liver  
 CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade  
 CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of  
 CC liver disease, specifically cirrhosis.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
 |||||  
 DB 10 PPPPQ 14

RESULT 48  
 AAY93015  
 ID AAY93015 standard; peptide; 15 AA.

XX AAY93015;

AC  
 DT 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide P61.

XX Hepatotropic; antagonist; transforming growth factor beta1; TGF- $\beta$ 1;  
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

XX WO200031135-A1.

PN 02-JUN-2000.

PD 23-NOV-1999; 99WO-ES00375.

PF 24-NOV-1998; 98ES-0002465.

PR (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,  
 PT useful for treatment of liver disease, especially cirrhosis, are  
 PT partial sequences of the factor or its receptors -

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor beta1 (TGF- $\beta$ 1) to its receptor  
 CC in vivo which have partial amino acid sequences identical or similar,  
 CC with those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133  
 CC represent examples of the peptides of the invention. The peptides act  
 CC by competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors,  
 CC e.g. they are inhibitors of stimulation of collagen synthesis in liver  
 CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade  
 CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of  
 CC liver disease, specifically cirrhosis.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PPPPQ 11  
 |||||  
 DB 5 PPPPQ 9

RESULT 49

AAG79166  
 ID AAG79166 standard; peptide; 15 AA.

XX AAG79166;

AC  
 DT 03-JAN-2002 (first entry)

XX Synthetic antigenic peptide derived from ActA.

XX ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
 KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
 KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
 KW infectious disease; cancer; autoimmune disease; inflammation;  
 KW platelet aggregation; wound healing; clotting.

XX Synthetic.

OS Listeria monocytogenes.

XX WO200174858-A2.

PN 11-OCT-2001.

PD 03-APR-2001; 2001WO-US10753.

PF 03-APR-2000; 2000US-194215P.

PR (WASI ) MASSACHUSETTS INST TECHNOLOGY.

PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX Krause M, Sechi AS, Gertler FB, Wehlend J;

XX WPI; 2001-616686/71.

XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage  
 PT activation for treating cancer, autoimmune disease, and infectious  
 PT disease, comprises contacting with a Fyb/SLAP complex modulator -

XX Example 1; Page 36; 79pp; English.

XX The present sequence represents an antigenic peptide derived from ActA.  
 CC polyclonal antibodies raised against this peptide were used to screen  
 CC mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP  
 CC proteins are ligands for the EVH1 domains of  
 CC Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins.  
 CC The specification describes a method for modulating cytoskeletal  
 CC rearrangement in a cell, or T cell response to T cell receptor  
 CC stimulation. The method comprises contacting the cell or T cell with a  
 CC Fyb/SLAP complex modulator sufficient to modulate the formation of a  
 CC complex of an Ena/VASP protein and a Fyb/SLAP protein. The method is  
 CC useful for modulating cytoskeletal rearrangement in a cell such as a  
 CC lymphocyte, preferably a T cell, a macrophage or a cell fragment such  
 CC as a platelet and for modulating T cell response to a T cell receptor  
 CC stimulation. T cell response is increased in a subject having or at  
 CC risk of developing infectious disease or cancer and T cell response  
 CC is inhibited in a subject having or is at risk of developing an  
 CC autoimmune disease or a condition characterized by inflammation. A  
 CC composition comprising a Fyb/SLAP complex inhibitor is useful for  
 CC increasing platelet aggregation for promoting wound healing or  
 CC clotting.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 6 FPPPP 10  
 Db |||||  
 4 FPPPP 8

## RESULT 50

ABG72860  
 ID ABG72860 standard; Peptide; 15 AA.

AC ABG72860;

XX 26-FEB-2003 (first entry)

XX Human ribosomal protein 17.05 N-terminal.

XX Human; ribosomal protein 17.05; malignant tumour; haemopathy;  
 KW human immunodeficiency virus; HIV; immunological disease;  
 KW inflammation.

XX Homo sapiens.

XX CN1352106-A.

XX 05-JUN-2002.

XX 06-NOV-2000; 2000CN-0127235.

XX 06-NOV-2000; 2000CN-0127235.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-683308/74.

XX New human ribosomal protein 17.05 polypeptide for treating malignant  
 PT tumors, hemopathy, human immunodeficiency virus infection,  
 PT immunological diseases and various inflammations -

XX Example 5; Page 18 (Disclosure); 33pp; Chinese.

XX The present invention discloses a new kind of polypeptide, human  
 CC ribosomal protein 17.05, polynucleotides encoding the polypeptide and a  
 CC DNA recombination process to produce the polypeptide. The present  
 CC invention also describes applying the polypeptide in treating various  
 CC diseases, such as malignant tumors, haemopathy, human immunodeficiency  
 CC virus (HIV) infection, immunological diseases and various inflammations.  
 CC Also discloses is the antagonist resisting the polypeptide and its  
 CC treatment effect, and the application of the polynucleotides encoding  
 CC human ribosomal protein 17.05. This is the amino acid sequence of the  
 CC novel human ribosomal protein 17.05 N-terminal.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
 Db |||||  
 5 FPPPP 9

## RESULT 51

ABP59535  
 ID ABP59535 standard; Peptide; 15 AA.

XX ABP59535;

XX 03-MAR-2003 (first entry)

XX Human ribonucleotide protein RBM856.43 N-terminal peptide.

XX

KW Human; ribonucleotide protein RBM856.43; infection; cancer; diabetes;  
 KW arrhythmia; hyperthyroidism.

XX Homo sapiens.

XX CN1345752-A.

XX 24-APR-2002.

XX 29-SEP-2000; 2000CN-0125516.

XX 29-SEP-2000; 2000CN-0125516.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-675774/73.

XX Novel polypeptide-ribonucleotide protein RBM 856.43 for curing several  
 PT diseases, such as diabetes, hyperthyroidism, arrhythmic, tumor and  
 PT various infections -

XX Example 5; Page 18 (disclosure); 33pp; Chinese.

XX The present invention provides the protein and coding sequences of human  
 CC ribonucleotide protein RBM856.43. The sequences are useful in the  
 CC treatment of diabetes, hyperthyroidism, arrhythmia, cancer and  
 CC infections. The present sequence is the N-terminus of the protein of the  
 CC invention.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
 Db |||||  
 7 FPPPP 11

## RESULT 52

ABR38294  
 ID ABR38294 standard; Peptide; 15 AA.

XX ABR38294;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3P2 HLA peptide #1425.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;

XX



CC from the invention.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11

DB 4 PPPPQ 8  
 |||||

RESULT 55

ABR38391  
 ID ABR38391 standard; Peptide; 15 AA.

AC ABR38391;  
 XX

DT 19-MAY-2003 (first entry)  
 XX

DE Human cancer-related protein 187P3F2 HLA peptide #1522.  
 XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX

OS Homo sapiens.  
 XX

PN WO200283921-A2.  
 XX

PD 24-OCT-2002.  
 XX

PF 10-APR-2002; 2002WO-US11654.  
 XX

PR 10-APR-2001; 2001US-282739P.  
 PR

PR 10-APR-2001; 2001US-283112P.  
 PR

PR 25-APR-2001; 2001US-286630P.  
 XX

PA (AGEN-) AGENSYS INC.  
 XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX

DR WPI; 2003-075555/07.  
 XX

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX

PS Claim 13; Page 618; 1021pp; English.  
 XX

CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX

QY Sequence 15 AA;  
 |||||

Query Match 33.3%; Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11

DB 4 PPPPQ 8  
 |||||

RESULT 57

AAW83313  
 ID AAW83313 standard; peptide; 17 AA.

XX AC AAW83313;  
 XX

DT 10-FEB-1999 (first entry)  
 |||||

DB 11 PPPPQ 15

RESULT 56

ABR38392  
 ID ABR38392 standard; Peptide; 15 AA.

XX AC ABR38392;  
 XX

DT 19-MAY-2003 (first entry)  
 XX

DE Human cancer-related protein 187P3F2 HLA peptide #1523.  
 XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX

OS Homo sapiens.  
 XX

PN WO200283921-A2.  
 XX

PD 24-OCT-2002.  
 XX

PF 10-APR-2002; 2002WO-US11654.  
 XX

PR 10-APR-2001; 2001US-282739P.  
 PR

PR 10-APR-2001; 2001US-283112P.  
 PR

PR 25-APR-2001; 2001US-286630P.  
 XX

PA (AGEN-) AGENSYS INC.  
 XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX

DR WPI; 2003-075555/07.  
 XX

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX

PS Claim 13; Page 618; 1021pp; English.  
 XX

CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX

QY Sequence 15 AA;  
 |||||

Query Match 33.3%; Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11

DB 9 PPPPQ 13  
 |||||

XX LRP5 protein fragment #1.  
 DE  
 XX  
 KW LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;  
 KW endocytosis; insulin dependent diabetes mellitus; autoimmune disease;  
 KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
 KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9846743-A1.  
 PN  
 XX 22-OCT-1998.  
 XX  
 XX 15-APR-1998; 98WO-GB01102.  
 XX  
 XX 05-JUN-1997; 97US-0048740.  
 PR  
 XX 15-APR-1997; 97US-0043553.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA (WELL ) WELLCOME TRUST LTD.  
 PA  
 XX Caskey CT, Cox RD, Gerhold D, Hammond H, Hess JW;  
 PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
 PI Phillips MS, Todd JA, Twells RCU;  
 XX WPI; 1998-594573/50.  
 DR  
 XX  
 XX New isolated LDL-receptor related protein - used to develop products  
 PT for treating, e.g. elevated triglyceride levels, diabetes,  
 PT autoimmune disorders, inflammation or Alzheimer's disease  
 XX  
 XX Claim 20; Page 126; 200pp; English.  
 PS  
 XX The present invention describes LRP5 (low density lipoprotein (LDL)  
 CC receptor related protein, previously designated LRP-3). The present  
 CC sequence represents a specifically claimed LRP5 protein fragment.  
 CC Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining  
 CC if an individual is susceptible to insulin dependent diabetes mellitus  
 CC (IDDM). The NAMS or proteins can be used for reducing triglyceride levels  
 CC in the serum of an individual. Therapies that affect LRP5 may also be  
 CC useful in the treatment of autoimmune diseases such as  
 CC glomerulonephritis, diseases and disorders involving disruption of  
 CC endocytosis and/or antigen presentation, cytokine clearance and/or  
 CC inflammation, viral infection, pathogenic bacterial toxin contamination,  
 CC elevation of free fatty acids or hypercholesterolemia, type 2 diabetes,  
 CC osteoporosis, Alzheimer's disease and cardiovascular disease. Products  
 CC from the present invention can also be used for detection, diagnosis and  
 CC drug screening.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 33.3%; Score 5; DB 19; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 FPPPP 10  
 Db ||||| 10  
 |||||  
 RESULT 58  
 AAW05469  
 ID AAW05469 standard; Peptide; 18 AA.  
 XX  
 XX AAW05469;  
 AC  
 XX 24-FEB-1998 (first entry)  
 DT  
 XX SH3-binding peptide bSH3020.  
 DE  
 XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
 KW cellular signalling element; cellular structural element; malignancy;  
 KW

KW protein identification; functional domain; protein screening;  
 KW cellular signal transduction process; binding peptide.  
 XX Synthetic.  
 XX WO9631625-A1.  
 FN  
 XX 10-OCT-1996.  
 PD  
 XX 04-APR-1996; 96WO-US04454.  
 PF  
 XX 03-APR-1996; 96US-0630915.  
 PR  
 XX 07-APR-1995; 95US-0417872.  
 PR  
 XX (CVTO-) CYTOGEN CORP.  
 PA (UVNC-) UNIV NORTH CAROLINA.  
 PA  
 XX Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;  
 PI WPI; 1996-465045/46.  
 DR  
 XX Identifying polypeptide(s) having specific functional domain (esp.  
 PT SH3 domain) - comprises detecting selective binding to recognition  
 PT unit, regardless of sequence homology  
 XX  
 XX Example; Fig 12b; 174pp; English.  
 PS  
 XX AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding  
 CC peptides. These sequences were used as parts of multivalent recognition  
 CC unit complexes used in the method of the invention. The method of the  
 CC invention is for identifying polypeptides containing functional domains  
 CC of interest (especially SH3 domains). It comprises contacting a  
 CC multivalent recognition unit (RU) complex with a number of peptides and  
 CC identifying polypeptides having a selective binding affinity for the RU  
 CC complex. The method is based on functional similarities and does not  
 CC rely on sequence similarities. Prior methods only gave limited success  
 CC for identifying proteins containing an SH3 domain due to the minimal  
 CC sequence homology among known SH3 proteins. Multivalent RU complexes are  
 CC particularly suited to screening for polypeptides containing functional  
 CC domains that are similar to, but not identical in sequence to, the  
 CC original target functional domain. The new method enables proteins  
 CC having a common function to be identified. Identification of novel SH3  
 CC proteins will be useful for a better understanding of cell growth,  
 CC malignancy, signal transduction processes, etc. New candidate drugs can  
 CC be identified, and their specificities (e.g. pharmacological activities)  
 CC can be assessed using the method of the invention.  
 XX  
 XX Sequence 18 AA;  
 SQ  
 Query Match 33.3%; Score 5; DB 17; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 FPPPP 10  
 Db ||||| 14  
 |||||  
 RESULT 59  
 AAW37677  
 ID AAW37677 standard; Peptide; 18 AA.  
 XX  
 XX AAW37677;  
 AC  
 XX 23-APR-1998 (first entry)  
 DT  
 XX PPPPY motif containing peptide bSH3020 used to bind WW domains.  
 DE  
 XX Peptide recognition unit; WW domain; cell signalling; growth regulation;  
 KW cytoskeleton organisation; targeted drug screening; modulator;  
 KW WW domain interaction; YAP protein; dystrophin.  
 XX Synthetic.  
 OS

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XX WO9737223-A1.
XX PD
XX PF 09-OCT-1997.
XX PR
XX PF 03-APR-1997; 97WO-US05547.
XX PR
XX PR 03-APR-1996; 96US-0630916.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Kay BK, Pirozzi G;
XX DR WPI; 1997-503234/46.
XX DR
XX PT Identifying cell signalling and growth regulatory polypeptides by
PT reaction with multivalent recognition complex - polypeptides are
PT useful in targetted drug selection
XX
XX Example 6.3; Fig 7; 220pp; English.
XX
XX Peptides AAW37653-77 contain PPPY-like motifs. The PPPY motif is
CC found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
CC containing this residue have been shown to bind the YAP WW domain, but
CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
CC AAW37653-77 were biotinylated and complexed with alkaline streptavidin,
CC and used in a cross affinity mapping experiment. They were tested for
CC their ability to bind to the 12 individual novel WW domains of WWP1
CC (AAW36794), WWP2 (AAW37695), WWP3 (AAW37696) and WWP4 (AAW36797), which
CC were expressed as glutathione-S-transferase expression proteins. The
CC present peptide, derived from a vinculin protein, does not bind to
CC WW domains of the novel proteins. The WW domain is a small functional
CC domain. Its name is derived from the observation that two tryptophan
CC residues, one in the amino terminal portion of the WW domain and one in
CC the carboxyl terminal portion, are conserved. Most proteins containing
CC WW domains have a function involving cell signalling and growth
CC regulation or the organisation of the cytoskeleton. Polypeptides
CC containing a WW domain are identified by treating a multivalent
CC recognition unit complex that has selective binding affinity for a WW
CC domain, with many polypeptides and identifying those with selective
CC affinity for the complex. Proteins containing WW domains are used for
CC targeted drug screening, i.e. to identify potential modulators of
CC specific WW domain interactions.
XX
XX Sequence 18 AA;
XX
XX Query Match 33.3%; Score 5; DB 18; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 FPPPP 10
XX DB 10 FPPPP 14
XX
XX RESULT 60
XX AAW38909
XX ID AAW38909 standard; peptide; 18 AA.
XX AC AAW38909;
XX
XX DT 27-MAR-1998 (first entry)
XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Ah1; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730674-A1.

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XX 21-AUG-1997.
XX PD
XX PF 14-FEB-1997; 97WO-US02298.
XX PR
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;
XX PI Sparks AB, Thorn JW;
XX DR WPI; 1997-424972/39.
XX DR
XX PT Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 90; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC binding peptides can be used in the method to identify inhibitors of
CC their binding to their respective SH3 domains, which could be used to
CC modulate the pharmacological activity of proteins or polypeptide
CC containing the SH3 domain. The peptides can also be used to activate
CC Src or Src-related protein tyrosine kinases, to stimulate the immune
CC response by increasing the production of certain lymphokines, e.g.
CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC conjugated molecule to certain cellular compartments containing Src or
CC Src related proteins.
XX
XX Sequence 18 AA;
XX
XX Query Match 33.3%; Score 5; DB 18; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 FPPPP 10
XX DB 7 FPPPP 11
XX
XX RESULT 61
XX AAW47567
XX ID AAW47567 standard; peptide; 18 AA.
XX AC AAW47567;
XX
XX DT 03-JUL-1998 (first entry)
XX DE Exendin agonist (18).
XX
XX Exendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 18
XX /note= "amidated"
XX
XX WO9805351-A1.

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XX PD 12-FEB-1998.
XX PF
XX PR 08-AUG-1997; 97WO-US14199.
XX PF 08-AUG-1997; 97WO-US14199.
XX PR 08-AUG-1996; 96US-0694954.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX DR WPI; 1998-145351/13.
XX PT Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS Example 21; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX SQ Sequence 18 AA;
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FPPPP 10
DB 13 FPPPP 17
RESULT 62
AAW47569
ID AAW47569 standard; peptide; 18 AA.
AC AAW47569;
XX DT 03-JUL-1998 (first entry)
XX DE Extendin agonist (20).
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 11 /note= "tert-butylglycine"
XX FT Modified-site 18 /note= "amidated"
XX PN WO9805351-A1.
XX PD 12-FEB-1998.
XX PF 08-AUG-1997; 97WO-US14199.
XX PR 08-AUG-1996; 96US-0694954.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX DR WPI; 1998-145351/13.
XX PT Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS Example 21; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX SQ Sequence 18 AA;
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FPPPP 10
DB 13 FPPPP 17
RESULT 63
AAW47571
ID AAW47571 standard; peptide; 18 AA.
AC AAW47571;
XX DT 03-JUL-1998 (first entry)
XX DE Extendin agonist (22).
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 18 /note= "amidated"
XX FT Modified-site 11 /note= "tert-butylglycine"
XX PN WO9805351-A1.
XX PD 12-FEB-1998.
XX PF 08-AUG-1997; 97WO-US14199.
XX PR 08-AUG-1996; 96US-0694954.
XX PA (AMYL-) AMYLIN PHARM INC.

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PF 08-AUG-1997; 97WO-US14199.
XX PF
XX PR 08-AUG-1996; 96US-0694954.
XX PA (AMYL-) AMYLIN PHARM INC.
XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX DR WPI; 1998-145351/13.
XX PT Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS Example 23; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX SQ Sequence 18 AA;
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FPPPP 10
DB 13 FPPPP 17
RESULT 63
AAW47571
ID AAW47571 standard; peptide; 18 AA.
AC AAW47571;
XX DT 03-JUL-1998 (first entry)
XX DE Extendin agonist (22).
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 18 /note= "amidated"
XX FT Modified-site 11 /note= "tert-butylglycine"
XX PN WO9805351-A1.
XX PD 12-FEB-1998.
XX PF 08-AUG-1997; 97WO-US14199.
XX PR 08-AUG-1996; 96US-0694954.
XX PA (AMYL-) AMYLIN PHARM INC.

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XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX DR WPI; 1998-145351/13.
XX PT Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS Example 25; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX CC Sequence 18 AA;
XX Query Match 33.3%; Score 5; DB 19; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 FPPPP 10
XX DB |||||
XX 13 FPPPP 17

RESULT 64
AAW47577
ID AAW47577 standard; peptide; 18 AA.
XX AC AAW47577;
XX DT 03-JUL-1998 (first entry)
XX DE Extendin agonist (28).
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 14 /label= Hyp
XX FT Modified-site 15 /label= Hyp
XX FT Modified-site 16 /label= Hyp
XX FT Modified-site 17 /label= Hyp
XX FT Modified-site 18 /label= Hyp
XX FT Modified-site 18 /note= "amidated"
XX PN WO9805351-A1.
XX PD 12-FEB-1998.
XX PF 08-AUG-1997; 97WO-US14199.
XX PP 08-AUG-1996; 97WO-US14199.
XX PA (AWYL-) AMYLIN PHARM INC.

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PR 08-AUG-1996; 96US-0694954.
XX (AWYL-) AMYLIN PHARM INC.
XX PA Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX PI WPI; 1998-145351/13.
XX DR Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS Example 31; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX CC Sequence 18 AA;
XX Query Match 33.3%; Score 5; DB 19; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 FPPPP 10
XX DB |||||
XX 13 FPPPP 17

RESULT 65
AAW47562
ID AAW47562 standard; peptide; 18 AA.
XX AC AAW47562;
XX DT 03-JUL-1998 (first entry)
XX DE Extendin agonist (13).
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 8 /note= "pentyglycine"
XX FT Modified-site 18 /note= "amidated"
XX PN WO9805351-A1.
XX PD 12-FEB-1998.
XX PF 08-AUG-1997; 97WO-US14199.
XX PP 08-AUG-1996; 96US-0694954.
XX PA (AWYL-) AMYLIN PHARM INC.

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XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;  
 XX DR WPI; 1998-145351/13.  
 XX PT Regulating gastrointestinal motility using exendins or their  
 XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
 XX impaired glucose tolerance etc., also in diagnostic investigations  
 XX PS Example 16; Fig 8; 70pp; English.  
 XX CC The present sequence is an exendin agonist, which reduces gastric  
 XX motility and delays gastric emptying. It can be used to treat spasm  
 XX (where associated with acute diverticulitis or disorders of the  
 XX biliary tract or sphincter of Oddi), postprandial dumping syndrome  
 XX and hyperglycaemia (particularly associated with type 2 diabetes),  
 XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an  
 XX exendin agonist is administered to prevent stomach contents passing  
 XX into the intestines, then the stomach pumped) and obesity. It can  
 XX also be administered to subjects undergoing gastrointestinal  
 XX diagnostic investigation, particularly radiological or by magnetic  
 XX resonance imaging.  
 XX CC Exendins, components of Gila monster venom, have some sequence  
 XX similarity to glucagon-like peptides (GLP). They are GLP agonists  
 XX and have been suggested (US5424286) for treatment of diabetes and  
 XX prevention of hyperglycaemia.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

Qy 6 FPPPP 10  
 Db 13 FPPPP 17

# RESULT 66

AAW47564  
 ID AAW47564 standard; peptide; 18 AA.

AC AAW47564;

DT 03-JUL-1998 (first entry)

DE Exendin agonist (15).

XX Exendin agonist; gastric motility; gastric emptying; treatment;  
 XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
 XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;  
 XX obesity; Gila monster venom.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 9 /note= "pentylglycine"

FT Modified-site 18 /note= "amidated"

FT WO9805351-A1.

PN 12-FEB-1998.

PD 08-AUG-1997; 97WO-US14199.

PF 08-AUG-1996; 96US-0694954.

PR (AMYL-) AMYLIN PHARM INC.

XX Beeley NRA, Gedulin B, Prickett KS, Young AA;

XX

DR WPI; 1998-145351/13.  
 XX Regulating gastrointestinal motility using exendins or their  
 XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
 XX impaired glucose tolerance etc., also in diagnostic investigations  
 XX PS Example 18; Fig 8; 70pp; English.

XX CC The present sequence is an exendin agonist, which reduces gastric  
 XX motility and delays gastric emptying. It can be used to treat spasm  
 XX (where associated with acute diverticulitis or disorders of the  
 XX biliary tract or sphincter of Oddi), postprandial dumping syndrome  
 XX and hyperglycaemia (particularly associated with type 2 diabetes),  
 XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an  
 XX exendin agonist is administered to prevent stomach contents passing  
 XX into the intestines, then the stomach pumped) and obesity. It can  
 XX also be administered to subjects undergoing gastrointestinal  
 XX diagnostic investigation, particularly radiological or by magnetic  
 XX resonance imaging.  
 XX CC Exendins, components of Gila monster venom, have some sequence  
 XX similarity to glucagon-like peptides (GLP). They are GLP agonists  
 XX and have been suggested (US5424286) for treatment of diabetes and  
 XX prevention of hyperglycaemia.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

Qy 6 FPPPP 10  
 Db 13 FPPPP 17

# RESULT 67

AAW47550  
 ID AAW47550 standard; peptide; 18 AA.

AC AAW47550;

DT 03-JUL-1998 (first entry)

DE Exendin agonist (1).

XX Exendin agonist; gastric motility; gastric emptying; treatment;  
 XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
 XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;  
 XX obesity; Gila monster venom.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 18 /note= "amidated"

FT WO9805351-A1.

PN 12-FEB-1998.

PD 08-AUG-1997; 97WO-US14199.

PF 08-AUG-1996; 96US-0694954.

PR (AMYL-) AMYLIN PHARM INC.

XX Beeley NRA, Gedulin B, Prickett KS, Young AA;

XX WPI; 1998-145351/13.

XX Regulating gastrointestinal motility using exendins or their  
 XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
 XX impaired glucose tolerance etc., also in diagnostic investigations



```

XX Example 4; Fig 8; 70pp; English.
XX
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX
SQ Sequence 18 AA;
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 13 FPPPP 17

RESULT 68
AAW47552
ID AAW47552 standard; peptide; 18 AA.
XX
AC AAW47552;
XX
XX 03-JUL-1998 (first entry)
XX
DE Extendin agonist (3).
XX
KW Extendin agonist; gastric motility; gastric emptying; treatment;
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
KW obesity; Gila monster venom.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 18
FT /note= "amidated"
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX
XX Example 6; Fig 8; 70pp; English.
XX
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm

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XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX
SQ Sequence 18 AA;
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 13 FPPPP 17

RESULT 69
AAW03721
ID AAW03721 standard; peptide; 18 AA.
XX
AC AAW03721;
XX
XX 08-JUN-1999 (first entry)
XX
DE Extendin agonist compound 1.
XX
KW Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 18
FT /note= "C-terminal amide"
XX
XX WO9907404-A1.
XX
XX 18-FEB-1999.
XX
XX 06-AUG-1998; 98WO-US16387.
XX
XX 08-AUG-1997; 97US-0055404.
XX
XX (AMYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Prickett KS;
XX WPI; 1999-180403/15.
XX
XX New extendin agonists - useful in the treatment of Type I and II
XX PT diabetes
XX
XX Claim 17; Fig 1A-B; 70pp; English.
XX
XX The invention relates to extendin agonists which slow gastric emptying
XX CC and lower plasma glucose levels. The extendin agonists are used to treat
XX CC Type I and II diabetes, disorders which would be benefited by agents
XX CC which lower plasma glucose levels, and disorders which would be benefited
XX CC by agents useful in delaying and/or slowing gastric emptying. Delayed
XX CC gastric emptying is a useful diagnostic aid in gastro-intestinal
XX CC radiological examinations. Sequences AAW03721-51 represent specifically
XX CC claimed examples of the extendin agonist compounds of the invention.
XX CC (Also see AAW03720 for extendin generic peptide formula and description).
XX

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SQ Sequence 18 AA;
  Query Match      33.3%; Score 5; DB 20; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
   |||||
Db 13 FPPPP 17

RESULT 70
AAV03723
ID AAY03723 standard; peptide; 18 AA.
XX
AC AAY03723;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extentin agonist compound 3.
XX
KW Extentin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 18
   /note= "C-terminal amide"
XX
PN WO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US16387.
XX
PR 08-AUG-1997; 97US-0055404.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extentin agonists - useful in the treatment of Type I and II
PT diabetes
XX
PS Claim 17; Fig 1A-B; 70pp; English.
XX
CC The invention relates to extentin agonists which slow gastric emptying
CC and lower plasma glucose levels. The extentin agonists are used to treat
CC Type I and II diabetes, disorders which would be benefited by agents
CC which lower plasma glucose levels, and disorders which would be benefited
CC by agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extentin agonist compounds of the invention.
CC (Also see AAY03720 for extentin generic peptide formula and description).
XX
SQ Sequence 18 AA;
  Query Match      33.3%; Score 5; DB 20; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
   |||||
Db 13 FPPPP 17

RESULT 71
AAV03733
ID AAY03733 standard; peptide; 18 AA.

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XX
AC AAY03733;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extentin agonist compound 13.
XX
KW Extentin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 8
   /note= "pentylglycine"
FT Modified-site 18
   /note= "C-terminal amide"
XX
PN WO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US16387.
XX
PR 08-AUG-1997; 97US-0055404.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extentin agonists - useful in the treatment of Type I and II
PT diabetes
XX
PS Claim 17; Fig 1A-B; 70pp; English.
XX
CC The invention relates to extentin agonists which slow gastric emptying
CC and lower plasma glucose levels. The extentin agonists are used to treat
CC Type I and II diabetes, disorders which would be benefited by agents
CC which lower plasma glucose levels, and disorders which would be benefited
CC by agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extentin agonist compounds of the invention.
CC (Also see AAY03720 for extentin generic peptide formula and description).
XX
SQ Sequence 18 AA;
  Query Match      33.3%; Score 5; DB 20; Length 18;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
   |||||
Db 13 FPPPP 17

RESULT 72
AAV03735
ID AAY03735 standard; peptide; 18 AA.
XX
AC AAY03735;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extentin agonist compound 15.
XX
KW Extentin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX

```

FH Key Location/Qualifiers  
 FT Modified-site 9  
 FT Modified-site 18 /note= "pentylglycine"  
 FT Modified-site 18 /note= "C-terminal amide"  
 XX WO9907404-A1.  
 PN 18-FEB-1999.  
 PD 06-AUG-1998; 98WO-US16387.  
 PF 08-AUG-1997; 97US-0055404.  
 PR (AMYL-) AMYLIN PHARM INC.  
 XX Bealey NRA, Prickett KS;  
 XX WPI; 1999-180403/15.  
 XX New extendin agonists - useful in the treatment of Type I and II diabetes  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 CC The invention relates to extendin agonists which slow gastric emptying and lower plasma glucose levels. The extendin agonists are used to treat Type I and II diabetes, disorders which would be benefited by agents which lower plasma glucose levels, and disorders which would be benefited by agents useful in delaying and/or slowing gastric emptying. Delayed gastric emptying is a useful diagnostic aid in gastro-intestinal radiological examinations. Sequences AAY03721-51 represent specifically claimed examples of the extendin agonist compounds of the invention. (Also see AAY03720 for extendin generic peptide formula and description).  
 XX Sequence 18 AA;  
 PS Query Match 33.3%; Score 5; DB 20; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FPPPP 10  
 Db 13 FPPPP 17  
 RESULT 73  
 AAY03738  
 ID AAY03738 standard; peptide; 18 AA.  
 AC AAY03738;  
 DT 08-JUN-1999 (first entry)  
 DE Extendin agonist compound 18.  
 XX Extendin; agonist; diabetes; disorder; plasma glucose; gastric; diagnostic; gastro-intestinal; radiological.  
 KW Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 18 /note= "C-terminal amide"  
 FT WO9907404-A1.  
 PN 18-FEB-1999.  
 PD 06-AUG-1998; 98WO-US16387.  
 PF 08-AUG-1997; 97US-0055404.  
 PR (AMYL-) AMYLIN PHARM INC.  
 XX Bealey NRA, Prickett KS;  
 XX WPI; 1999-180403/15.  
 XX New extendin agonists - useful in the treatment of Type I and II diabetes  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 CC The invention relates to extendin agonists which slow gastric emptying and lower plasma glucose levels. The extendin agonists are used to treat Type I and II diabetes, disorders which would be benefited by agents which lower plasma glucose levels, and disorders which would be benefited by agents useful in delaying and/or slowing gastric emptying. Delayed gastric emptying is a useful diagnostic aid in gastro-intestinal radiological examinations. Sequences AAY03721-51 represent specifically claimed examples of the extendin agonist compounds of the invention. (Also see AAY03720 for extendin generic peptide formula and description).  
 XX Sequence 18 AA;  
 PS Query Match 33.3%; Score 5; DB 20; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FPPPP 10  
 Db 13 FPPPP 17  
 RESULT 74  
 AAY03740  
 ID AAY03740 standard; peptide; 18 AA.  
 AC AAY03740;  
 DT 08-JUN-1999 (first entry)  
 DE Extendin agonist compound 20.  
 XX Extendin; agonist; diabetes; disorder; plasma glucose; gastric; diagnostic; gastro-intestinal; radiological.  
 KW Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 11 /note= "text-butylglycine"  
 FT Modified-site 18 /note= "C-terminal amide"  
 FT WO9907404-A1.  
 PN 18-FEB-1999.  
 PD 06-AUG-1998; 98WO-US16387.  
 PF 08-AUG-1997; 97US-0055404.  
 PR (AMYL-) AMYLIN PHARM INC.  
 XX Bealey NRA, Prickett KS;  
 XX WPI; 1999-180403/15.  
 XX New extendin agonists - useful in the treatment of Type I and II diabetes  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 CC The invention relates to extendin agonists which slow gastric emptying

PA (AMYL-) AMYLIN PHARM INC.  
 XX Bealey NRA, Prickett KS;  
 XX WPI; 1999-180403/15.  
 XX New extendin agonists - useful in the treatment of Type I and II diabetes  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 CC The invention relates to extendin agonists which slow gastric emptying and lower plasma glucose levels. The extendin agonists are used to treat Type I and II diabetes, disorders which would be benefited by agents which lower plasma glucose levels, and disorders which would be benefited by agents useful in delaying and/or slowing gastric emptying. Delayed gastric emptying is a useful diagnostic aid in gastro-intestinal radiological examinations. Sequences AAY03721-51 represent specifically claimed examples of the extendin agonist compounds of the invention. (Also see AAY03720 for extendin generic peptide formula and description).  
 XX Sequence 18 AA;  
 PS Query Match 33.3%; Score 5; DB 20; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FPPPP 10  
 Db 13 FPPPP 17  
 RESULT 74  
 AAY03740  
 ID AAY03740 standard; peptide; 18 AA.  
 AC AAY03740;  
 DT 08-JUN-1999 (first entry)  
 DE Extendin agonist compound 20.  
 XX Extendin; agonist; diabetes; disorder; plasma glucose; gastric; diagnostic; gastro-intestinal; radiological.  
 KW Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 11 /note= "text-butylglycine"  
 FT Modified-site 18 /note= "C-terminal amide"  
 FT WO9907404-A1.  
 PN 18-FEB-1999.  
 PD 06-AUG-1998; 98WO-US16387.  
 PF 08-AUG-1997; 97US-0055404.  
 PR (AMYL-) AMYLIN PHARM INC.  
 XX Bealey NRA, Prickett KS;  
 XX WPI; 1999-180403/15.  
 XX New extendin agonists - useful in the treatment of Type I and II diabetes  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 CC The invention relates to extendin agonists which slow gastric emptying

CC and lower plasma glucose levels. The exendin agonists are used to treat  
CC Type I and II diabetes, disorders which would be benefited by agents  
CC which lower plasma glucose levels, and disorders which would be benefited  
CC by agents useful in delaying and/or slowing gastric emptying. Delayed  
CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
CC radiological examinations. Sequences AAY03721-51 represent specifically  
CC claimed examples of the exendin agonist compounds of the invention.  
CC (Also see AAY03720 for exendin generic peptide formula and description).

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
| | | | |  
Db 13 FPPPP 17

RESULT 75  
AAY03742  
ID AAY03742 standard; peptide; 18 AA.

AC AAY03742;

XX 08-JUN-1999 (first entry)

XX Exendin agonist compound 22.

XX Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
KW diagnostic; gastro-intestinal; radiological.

XX Synthetic.

XX Key Location/Qualifiers  
FT Modified-site 18  
FT /note= "C-terminal amide"

XX WO9907404-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16387.

XX 08-AUG-1997; 97US-0055404.

XX (AMYL-) AMYLIN PHARM INC.

XX Beeley NRA, Prickett KS;

XX WPI; 1999-180403/15.

XX New exendin agonists - useful in the treatment of Type I and II  
PT diabetes

XX Claim 17; Fig 1D-E; 70pp; English.

XX The invention relates to exendin agonists which slow gastric emptying  
CC and lower plasma glucose levels. The exendin agonists are used to treat  
CC Type I and II diabetes, disorders which would be benefited by agents  
CC which lower plasma glucose levels, and disorders which would be benefited  
CC by agents useful in delaying and/or slowing gastric emptying. Delayed  
CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
CC radiological examinations. Sequences AAY03721-51 represent specifically  
CC claimed examples of the exendin agonist compounds of the invention.  
CC (Also see AAY03720 for exendin generic peptide formula and description).

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 20; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
| | | | |  
Db 13 FPPPP 17

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Title: US-09-641-801-7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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7	5	33.3	9	9	US-09-823-240-7
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9	5	33.3	14	9	US-09-825-144-12
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12	5	33.3	15	12	US-10-161-791-349
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14	5	33.3	15	12	US-10-161-791-373
15	5	33.3	15	12	US-10-161-791-405

16	5	33.3	15	12	US-10-161-791-439	Sequence 439, App
17	5	33.3	17	12	US-10-331-907-403	Sequence 403, App
18	5	33.3	18	9	US-09-879-957-165	Sequence 165, App
19	5	33.3	18	11	US-09-949-510-4	Sequence 4, Appli
20	5	33.3	18	12	US-10-161-791-305	Sequence 305, App
21	5	33.3	18	15	US-10-185-050-109	Sequence 109, App
22	5	33.3	20	9	US-09-735-450-4	Sequence 4, Appli
23	5	33.3	20	12	US-10-161-791-368	Sequence 368, App
24	4	26.7	4	12	US-10-352-704-21	Sequence 21, Appl
25	4	26.7	4	12	US-10-376-121A-134	Sequence 134, App
26	4	26.7	4	12	US-10-376-121A-135	Sequence 135, App
27	4	26.7	4	15	US-10-222-455-33	Sequence 33, Appl
28	4	26.7	5	8	US-08-424-550B-716	Sequence 716, App
29	4	26.7	5	9	US-09-823-240-4	Sequence 4, Appli
30	4	26.7	5	9	US-09-785-921A-15	Sequence 15, Appl
31	4	26.7	5	12	US-10-315-964A-422	Sequence 422, App
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33	4	26.7	5	12	US-10-317-252A-422	Sequence 422, App
34	4	26.7	5	12	US-10-352-704-23	Sequence 23, Appl
35	4	26.7	5	12	US-10-376-121A-120	Sequence 120, App
36	4	26.7	5	14	US-10-014-485A-72	Sequence 72, Appl
37	4	26.7	5	15	US-10-174-105A-72	Sequence 72, Appl
38	4	26.7	5	15	US-10-185-050-3	Sequence 3, Appli
39	4	26.7	5	15	US-10-096-986-9	Sequence 9, Appli
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41	4	26.7	6	9	US-09-803-136-21	Sequence 21, Appl
42	4	26.7	6	12	US-10-352-704-25	Sequence 25, Appl
43	4	26.7	6	14	US-10-078-547-3	Sequence 3, Appli
44	4	26.7	6	14	US-10-078-547-13	Sequence 13, Appl
45	4	26.7	6	14	US-10-078-547-14	Sequence 14, Appl
46	4	26.7	6	14	US-10-078-547-19	Sequence 19, Appl
47	4	26.7	6	14	US-10-078-547-21	Sequence 21, Appl
48	4	26.7	6	15	US-10-192-257-5	Sequence 5, Appli
49	4	26.7	7	9	US-09-825-144-8	Sequence 8, Appli
50	4	26.7	7	11	US-09-281-495-17	Sequence 17, Appl
51	4	26.7	7	12	US-10-032-214-312	Sequence 312, App
52	4	26.7	7	12	US-09-261-894-91	Sequence 91, Appl
53	4	26.7	7	15	US-10-192-257-6	Sequence 6, Appli
54	4	26.7	7	15	US-10-314-057-8	Sequence 8, Appli
55	4	26.7	7	15	US-10-235-236-3	Sequence 3, Appli
56	4	26.7	7	15	US-10-104-607B-3	Sequence 3, Appli
57	4	26.7	8	10	US-09-843-245-1	Sequence 1, Appli
58	4	26.7	8	12	US-10-022-066-378	Sequence 378, App
59	4	26.7	8	12	US-10-376-121A-96	Sequence 96, Appl
60	4	26.7	8	12	US-10-376-121A-99	Sequence 99, Appl
61	4	26.7	8	12	US-10-376-121A-196	Sequence 196, App
62	4	26.7	8	12	US-10-376-121A-197	Sequence 197, App
63	4	26.7	8	12	US-10-376-121A-198	Sequence 198, App
64	4	26.7	8	12	US-10-376-121A-199	Sequence 199, App
65	4	26.7	8	12	US-10-376-121A-210	Sequence 210, App
66	4	26.7	8	12	US-10-376-121A-211	Sequence 211, App
67	4	26.7	8	12	US-10-376-121A-213	Sequence 213, App
68	4	26.7	8	12	US-10-376-121A-215	Sequence 215, App
69	4	26.7	8	12	US-10-376-121A-216	Sequence 216, App
70	4	26.7	8	12	US-10-376-121A-217	Sequence 217, App
71	4	26.7	8	15	US-10-226-007-452	Sequence 452, App
72	4	26.7	8	15	US-10-226-007-465	Sequence 465, App
73	4	26.7	8	15	US-10-226-007-478	Sequence 478, App
74	4	26.7	8	15	US-10-226-007-491	Sequence 491, App
75	4	26.7	8	15	US-10-226-007-738	Sequence 738, App
76	4	26.7	8	15	US-10-226-007-751	Sequence 751, App
77	4	26.7	8	15	US-10-226-007-764	Sequence 764, App
78	4	26.7	8	15	US-10-226-007-777	Sequence 777, App
79	4	26.7	8	15	US-10-226-007-881	Sequence 881, App
80	4	26.7	8	15	US-10-226-007-894	Sequence 894, App
81	4	26.7	8	15	US-10-226-007-907	Sequence 907, App
82	4	26.7	8	15	US-10-226-007-920	Sequence 920, App
83	4	26.7	8	15	US-10-226-007-1024	Sequence 1024, Ap
84	4	26.7	8	15	US-10-226-007-1037	Sequence 1037, Ap
85	4	26.7	8	15	US-10-226-007-1050	Sequence 1050, Ap
86	4	26.7	8	15	US-10-226-007-1063	Sequence 1063, Ap
87	4	26.7	8	15	US-10-226-007-1167	Sequence 1167, Ap
88	4	26.7	8	15	US-10-226-007-1180	Sequence 1180, Ap

89 4 26.7 8 15 US-10-226-007-1193 Sequence 1193, Ap  
90 4 26.7 8 15 US-10-226-007-1206 Sequence 1206, Ap  
91 4 26.7 8 15 US-10-226-007-1492 Sequence 1492, Ap  
92 4 26.7 8 15 US-10-226-007-1493 Sequence 1493, Ap  
93 4 26.7 8 15 US-10-226-007-1495 Sequence 1495, Ap  
94 4 26.7 9 9 US-09-823-240-8 Sequence 8, Appli  
95 4 26.7 9 9 US-09-835-232-11 Sequence 11, Appl  
96 4 26.7 9 11 US-09-938-864-76 Sequence 76, Appl  
97 4 26.7 9 11 US-09-938-864-96 Sequence 96, Appl  
98 4 26.7 9 11 US-09-938-864-97 Sequence 97, Appl  
99 4 26.7 9 11 US-09-938-864-156 Sequence 156, App  
100 4 26.7 9 11 US-09-938-864-157 Sequence 157, App

ALIGNMENTS

RESULT 1  
US-10-281-652-7  
; Sequence 7, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-7

Query Match 100.0%; Score 15; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15

RESULT 2  
US-09-825-144-15  
; Sequence 15, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 5

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-144-15  
Query Match 33.3%; Score 5; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 FPPPP 10  
Db 1 FPPPP 5  
RESULT 3  
US-09-823-240-3  
; Sequence 3, Application US/09823240  
; Patent No. US2002004813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jorgen Wehland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-823-240-3  
Query Match 33.3%; Score 5; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 FPPPP 10  
Db 1 FPPPP 5  
RESULT 4  
US-10-192-381-47  
; Sequence 47, Application US/10192381  
; Publication No. US20030170807A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS  
; TITLE OF INVENTION: AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/10/192,381  
; CURRENT FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US/09/377,285  
; PRIOR FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: optimal ligand  
US-10-192-381-47

Query Match 33.3%; Score 5; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
|||  
Db 1 FPPPP 5

## RESULT 5

US-10-281-652-14  
; Sequence 14, Application US/10281652  
; Publication No. US20030091066A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1993-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-14

Query Match 33.3%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|||  
Db 2 PPPPQ 6

## RESULT 6

US-09-825-144-10  
; Sequence 10, Application US/09825144  
; Patent No. US200020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-144-10

Query Match 33.3%; Score 5; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
|||  
Db 1 FPPPP 5

## RESULT 7

US-09-823-240-7  
; Sequence 7, Application US/09823240  
; Patent No. US20020048813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jorgen Wehland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (9)...(9)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-823-240-7

Query Match 33.3%; Score 5; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
|||  
Db 1 FPPPP 5

## RESULT 8

US-09-823-240-1  
; Sequence 1, Application US/09823240  
; Patent No. US20020048813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jorgen Wehland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT

ORGANISM: Listeria monocytogenes

FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa is Asp or Glu  
NAME/KEY: UNSURE  
LOCATION: (7)...(7)  
OTHER INFORMATION: Xaa is any amino acid

US-09-823-240-1

Query Match 33.3%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
Db 2 FPPPP 6

RESULT 9

US-09-825-144-12  
Sequence 12, Application US/09825144  
Patent No. US20020037286A1  
GENERAL INFORMATION:  
APPLICANT: Matthias Krause  
APPLICANT: Antonio S. Sechi  
APPLICANT: Frank B. Gertler  
APPLICANT: Jorgen Wehland  
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
FILE REFERENCE: M0656/7065  
CURRENT APPLICATION NUMBER: US/09/825,144  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/194,215  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Listeria monocytogenes  
US-09-825-144-12

Query Match 33.3%; Score 5; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
Db 3 FPPPP 7

RESULT 10

US-09-825-144-1  
Sequence 1, Application US/09825144  
Patent No. US20020037286A1  
GENERAL INFORMATION:  
APPLICANT: Matthias Krause  
APPLICANT: Antonio S. Sechi  
APPLICANT: Frank B. Gertler  
APPLICANT: Jorgen Wehland  
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
FILE REFERENCE: M0656/7065  
CURRENT APPLICATION NUMBER: US/09/825,144  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/194,215  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Listeria monocytogenes  
US-09-825-144-1

Query Match 33.3%; Score 5; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
Db 4 FPPPP 8

RESULT 11

US-10-161-791-339  
Sequence 339, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 339:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-339

Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPP 11  
Db 6 PPPPP 10

RESULT 12

US-10-161-791-349  
Sequence 349, Application US/10161791  
Publication No. US20030186863A1



;  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 349:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-349  
  
Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 PPPPQ 11  
Db 6 PPPPQ 10  
  
RESULT 13  
US-10-161-791-367  
; Sequence 367, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas

;  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 367:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-367  
  
Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 PPPPQ 11  
Db 9 PPPPQ 13  
  
RESULT 14  
US-10-161-791-373  
; Sequence 373, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 373:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-373

Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
Db 6 PPPPQ 10

## RESULT 15

US-10-161-791-405  
Sequence 405, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

US-10-161-791-405  
Sequence 405, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid

TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-405

Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
Db 6 PPPPQ 10

## RESULT 16

US-10-161-791-439  
Sequence 439, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 439:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-439

US-10-161-791-439  
Sequence 439, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 439:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-439

Query Match 33.3%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
Db 6 PPPPQ 10

## RESULT 17

```

US-10-331-907-403
; Sequence 403, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hess, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1e Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-Apr-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-Apr-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 403:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-331-907-403
Query Match 33.3%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 6 FPPPP 10

RESULT 18
US-09-879-957-165
; Sequence 165, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;
; US-09-949-510-4
; Sequence 4, Application US/09949510
; Publication No. US20030077840A1
; GENERAL INFORMATION:
; APPLICANT: Chait et al.
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF
; TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC
; TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY
; FILE REFERENCE: Seq. List 1-6
; CURRENT APPLICATION NUMBER: US/09/949,510
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-949-510-4
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;
; US-09-879-957-165
; Sequence 165, Application US/08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-879-957-165
Query Match 33.3%; Score 5; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 10 FPPPP 14

RESULT 19
US-09-949-510-4
; Sequence 4, Application US/09949510
; Publication No. US20030077840A1
; GENERAL INFORMATION:
; APPLICANT: Chait et al.
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF
; TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC
; TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY
; FILE REFERENCE: Seq. List 1-6
; CURRENT APPLICATION NUMBER: US/09/949,510
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-949-510-4
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;
; US-09-641-801-7-oligo.rapb
; Title of Invention: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-879-957-165
Query Match 33.3%; Score 5; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 10 FPPPP 14

RESULT 19
US-09-949-510-4
; Sequence 4, Application US/09949510
; Publication No. US20030077840A1
; GENERAL INFORMATION:
; APPLICANT: Chait et al.
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF
; TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC
; TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY
; FILE REFERENCE: Seq. List 1-6
; CURRENT APPLICATION NUMBER: US/09/949,510
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-949-510-4
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QETVT 15

Db 4 QETVT 8

RESULT 20

US-10-161-791-305  
; Sequence 305, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-305

Query Match 33.3%; Score 5; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10

Db 7 FPPPP 11

RESULT 21

US-10-185-050-109  
; Sequence 109, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.

Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:  
US-10-185-050-109

Query Match 33.3%; Score 5; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10

Db 10 FPPPP 14

RESULT 22

US-09-735-450-4  
; Sequence 4, Application US/09735450  
; Patent No. US2002025323A1  
; GENERAL INFORMATION:  
; APPLICANT: Paterson, Yvonne R  
; APPLICANT: Gunn III, George R  
; APPLICANT: Peters, Christian  
; TITLE OF INVENTION: Compositions and Methods for Enhancing Immunogenicity  
; TITLE OF INVENTION: of Antigens  
; FILE REFERENCE: PENN-0741  
; CURRENT APPLICATION NUMBER: US/09/735,450  
; CURRENT FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 09/537,642  
; PRIOR FILING DATE: 2000-03-29  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-735-450-4

```
Query Match      33.3%; Score 5; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 FPPPP 10
Db      10 FPPPP 14

RESULT 23
US-10-161-791-368
; Sequence 368, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-368

Query Match      33.3%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPPP 11
Db      13 PPPPP 17

RESULT 24
US-10-352-704-21
; Sequence 21, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-352-704-21

Query Match      26.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 25
US-10-376-121A-134
; Sequence 134, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 134:  
US-10-376-121A-134  
Query Match 26.7%; Score 4; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PPPP 10  
DB 1 PPPP 4  
RESULT 26  
US-10-376-121A-135  
Sequence 135, Application US/10376121A  
Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 135:  
US-10-376-121A-135  
Query Match 26.7%; Score 4; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PPPP 10  
DB 1 PPPP 4  
RESULT 27  
US-10-222-455-33  
Sequence 33, Application US/10222455  
Publication No. US2003009983A1  
GENERAL INFORMATION:  
APPLICANT: Holmes, Christopher P.  
TITLE OF INVENTION: Cyclic and Substituted Immobilized  
MOLECULAR SYNTHESIS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/222,455  
FILING DATE: 16-Aug-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/647,618  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: US 07/972,007  
FILING DATE: 05-NOV-1992  
APPLICATION NUMBER: US 07/796,727  
FILING DATE: 22-NOV-1991  
APPLICATION NUMBER: US 07/805,727  
FILING DATE: 06-DEC-1991  
APPLICATION NUMBER: US 07/624,120  
FILING DATE: 06-DEC-1990  
APPLICATION NUMBER: US 07/492,462  
FILING DATE: 07-MAR-1990  
APPLICATION NUMBER: US 07/362,901  
FILING DATE: 07-JUN-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Matthew B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 16528J-000141US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-222-455-33

Query Match      26.7%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 28
US-08-424-550B-716
; Sequence 716, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-716

Query Match      26.7%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLEM 4
Db      1 VLEM 4
```

```
RESULT 29
US-09-823-240-4
; Sequence 4, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureio
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-823-240-4

Query Match      26.7%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      2 PPPP 5

RESULT 30
US-09-785-921A-15
; Sequence 15, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: LIT-PI-529
; CURRENT APPLICATION NUMBER: US/09/785,921A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-09-785-921A-15

Query Match      26.7%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 31
US-10-315-964A-422
; Sequence 422, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
```

; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 422  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-315-964A-422

Query Match 26.7%; Score 4; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4  
|||  
Db 2 VLEM 5

RESULT 32  
US-10-317-251A-422  
; Sequence 422, Application US/10317251A  
; Publication No. US20030148957A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M2  
; CURRENT APPLICATION NUMBER: US/10/317,251A  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 422  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-251A-422

Query Match 26.7%; Score 4; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4  
|||  
Db 2 VLEM 5

RESULT 33  
US-10-317-252A-422  
; Sequence 422, Application US/10317252A  
; Publication No. US20030148958A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company

; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M  
; CURRENT APPLICATION NUMBER: US/10/317,252A  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 422  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-252A-422

Query Match 26.7%; Score 4; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4  
|||  
Db 2 VLEM 5

RESULT 34  
US-10-352-704-23  
; Sequence 23, Application US/10352704  
; Publication No. US20030176690A1  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Rumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on a Solid Support and Apparatus Permitting its Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; STATE: D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/10/352,704  
; FILING DATE: 28-Jan-2003  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,556A  
; FILING DATE: 14-DEC-1994  
; APPLICATION NUMBER: FR 9315164  
; FILING DATE: 16-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR



; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-352-704-23

Query Match 26.7%; Score 4; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 1 PPPP 4

RESULT 35  
US-10-376-121A-120  
; Sequence 120, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS: 218  
; ADDRESSEE: Patrea L. Pabst  
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/376,121A  
; FILING DATE: 27-Mar-2003  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/867,819  
; FILING DATE: April 13, 1992  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: January 31, 1991  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV(2)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-817-8473  
; TELEFAX: (404)-817-8588  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 120:  
US-10-376-121A-120

Query Match 26.7%; Score 4; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 1 PPPP 4

Db 1 PPPP 4

RESULT 36  
US-10-014-485A-72  
; Sequence 72, Application US/10014485A  
; Publication No. US20020168684A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: COMB, Michael J.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIE  
; FILE REFERENCE: CST-138 CIP2  
; CURRENT APPLICATION NUMBER: US/10/014,485A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 72  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: MOD RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 4 is phosphorylated  
US-10-014-485A-72

Query Match 26.7%; Score 4; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QETV 14  
Db 2 QETV 5

RESULT 37  
US-10-174-105A-72  
; Sequence 72, Application US/10174105A  
; Publication No. US20030068652A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIF  
; FILE REFERENCE: CST-138 CIP3  
; CURRENT APPLICATION NUMBER: US/10/174,105A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 72  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
; NAME/KEY: MOD RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 4 is phosphorylated  
US-10-174-105A-72

Query Match 26.7%; Score 4; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QETV 14  
DB 2 QETV 5

## RESULT 38

US-10-185-050-3  
; Sequence 3, Application US/10185050  
; Publication No. US2003007757A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.

## TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

PEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

## NUMBER OF SEQUENCES: 233

## CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

## SOFTWARE: Patentin Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997

## ATTORNEY/AGENT INFORMATION:

NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872

## REFERENCE/DOCKET NUMBER: 1101-208-999

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 3:

## SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>

## TOPOLOGY: unknown

## MOLECULE TYPE: peptide

## SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-185-050-3

Query Match 26.7%; Score 4; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 1 PPPP 4

## RESULT 39

US-10-096-986-9  
; Sequence 9, Application US/10096986  
; Publication No. US2003008346A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.

Richardson, Charles  
Chambers, James  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Crissman, John W.

TITLE OF INVENTION: NO. US2003008346A1 Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Sam

## NUMBER OF SEQUENCES: 117

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

## SOFTWARE: Patentin Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/096,986  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/444,791  
FILING DATE: 22-No. US2003008346A1-1999  
APPLICATION NUMBER: US 08/482,085

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31,801

REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

## INFORMATION FOR SEQ ID NO: 9:

## SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

## TOPOLOGY: linear

## MOLECULE TYPE: peptide

## SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-096-986-9

Query Match 26.7%; Score 4; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 2 PPPP 5

## RESULT 40

US-10-281-652-12  
; Sequence 12, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND

```
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-12

Query Match          26.7%; Score 4; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PPPP 9
      ||||
Db      1 PPPP 4

RESULT 41
US-09-803-126-21
; Sequence 21, Application US/09803126
; Patent No. US20020099190A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Alan R.
; APPLICANT: Deng, Gary G.
; APPLICANT: Rubanyi, Gabor M.
; TITLE OF INVENTION: Estrogen-Regulated Unconventional Myosin-Related
; FILE REFERENCE: 015303-00031005
; CURRENT APPLICATION NUMBER: US/09/803,126
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/188,488
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Peptide
US-09-803-126-21

Query Match          26.7%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      1 PPPP 4

RESULT 42
US-10-352-704-25
; Sequence 25, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
```

```
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-352-704-25

Query Match          26.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      1 PPPP 4

RESULT 43
US-10-078-547-3
; Sequence 3, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
```

```
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: profilin motif
US-10-078-547-3
Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 PPPP 10
        |||||
Db       2 PPPP 5
```

## RESULT 44

```
US-10-078-547-13
; Sequence 13, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: PPPPPP domain of WASP
US-10-078-547-13
```

```
Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 PPPP 10
        |||||
Db       1 PPPP 4
```

## RESULT 45

```
US-10-078-547-14
; Sequence 14, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
```

```
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: ABM-2 motif
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-078-547-14
```

```
Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 PPPP 10
        |||||
Db       2 PPPP 5
```

## RESULT 46

```
US-10-078-547-19
; Sequence 19, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: APPPPP motif, WIP
US-10-078-547-19
```

```
Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 PPPP 10
        |||||
Db       2 PPPP 5
```

## RESULT 47

```
US-10-078-547-21
; Sequence 21, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
```

APPLICANT: Narayanaswamy Ramesh  
APPLICANT: Miguel A. de la Fuente  
APPLICANT: Ines M. Anton  
APPLICANT: Raif S. Geha  
TITLE OF INVENTION: WIP, A WASP-Associated Protein  
FILE REFERENCE: 1242.1022-005  
CURRENT APPLICATION NUMBER: US/10/078,547  
CURRENT FILING DATE: 2002-02-19  
PRIOR APPLICATION NUMBER: 09/599,287  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: PCT/US98/27501  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/101,457  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/068,533  
PRIOR FILING DATE: 1997-12-23  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 21  
LENGTH: 6  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
OTHER INFORMATION: profilin-binding consensus sequence  
NAME/KEY: VARIANT  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa = A, G, L or S  
NAME/KEY: VARIANT  
LOCATION: 1  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-078-547-21

Query Match 26.7%; Score 4; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 2 PPPP 5

RESULT 48  
US-10-192-257-5  
Sequence 5, Application US/10192257  
Publication No. US20030021786A1  
GENERAL INFORMATION:  
APPLICANT: Aphton Corporation  
TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition  
FILE REFERENCE: 1102865-0057  
CURRENT APPLICATION NUMBER: US/10/192,257  
CURRENT FILING DATE: 2002-07-09  
PRIOR APPLICATION NUMBER: US 60/303,868  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Hypothetical spacer peptide  
US-10-192-257-5

Query Match 26.7%; Score 4; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 2 PPPP 5

RESULT 49  
US-09-825-144-8  
Sequence 8, Application US/09825144  
Patent No. US20020037286A1  
GENERAL INFORMATION:  
APPLICANT: Matthias Krause  
APPLICANT: Antonio S. Sechl  
APPLICANT: Frank B. Gertler  
APPLICANT: Jorgen Wehland  
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
FILE REFERENCE: M0656/7065  
CURRENT APPLICATION NUMBER: US/09/825,144  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/194,215  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Listeria monocytogenes  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa is Phe, Leu, or Trp  
US-09-825-144-8

Query Match 26.7%; Score 4; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 4 PPPP 7

RESULT 50  
US-09-281-495-17  
Sequence 17, Application US/09281495  
Publication No. US20030059765A1  
GENERAL INFORMATION:  
APPLICANT: Pomerantz, Roger J  
APPLICANT: Bouhmandan, Mohamad  
APPLICANT: Duan, Ling-Xun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROVIDING A PROTEIN TO A  
TITLE OF INVENTION: VIRION  
FILE REFERENCE: 9855-25U1  
CURRENT APPLICATION NUMBER: US/09/281,495  
CURRENT FILING DATE: 1999-03-30  
EARLIER APPLICATION NUMBER: US 60/079,822  
EARLIER FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Vpr-Specific  
OTHER INFORMATION: Polypeptide Binding Region  
US-09-281-495-17

Query Match 26.7%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPP 9  
Db 4 FPPP 7

RESULT 51  
US-10-032-214-312

```
; Sequence 312, Application US/10032214
; Publication No. US2003013881A1
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-106730US
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09/888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 312
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-10-032-214-312

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 52
US-09-261-894-91
; Sequence 91, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
```

```
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-91

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKPP 7
Db 3 MKPP 6

RESULT 53
US-10-192-257-6
; Sequence 6, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical spacer peptide
US-10-192-257-6

Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 54
US-10-314-057-8
; Sequence 8, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: ACGIUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
```

```

; LENGTH: 7
; TYPE: PRT
; ORGANISM: human or synthetic peptide
US-10-314-057-8

Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 55
US-10-235-236-3
; Sequence 3, Application US/10235236
; Publication No. US20030086941A1
; GENERAL INFORMATION:
; APPLICANT: Michaeli, Dov
; Caplin, Martyn E.
; Watson, Susan A.
; Grimes, Stephen
; TITLE OF INVENTION: Immunogenic Compositions
; to the CCK-B/Gastrin Receptor and Methods for
; the Treatment of Tumors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White & Case LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,236
; FILING DATE: 04-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,201
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-0032
; TELEPHONE: (212) 819-8200
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-235-236-3

Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 56
US-10-235-236-3
; Sequence 3, Application US/10235236
; Publication No. US20030086941A1
; GENERAL INFORMATION:
; APPLICANT: Michaeli, Dov
; Caplin, Martyn E.
; Watson, Susan A.
; Grimes, Stephen
; TITLE OF INVENTION: Immunogenic Compositions
; to the CCK-B/Gastrin Receptor and Methods for
; the Treatment of Tumors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White & Case LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,236
; FILING DATE: 04-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,201
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-0032
; TELEPHONE: (212) 819-8200
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-235-236-3

Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 57
US-09-843-245-1
; Sequence 1, Application US/09843245
; Patent No. US20020164672A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Peter S.
; APPLICANT: Ramjaun, Antoine Rachid
; TITLE OF INVENTION: REGULATION OF JNK ACTIVITY BY MODULATION OF THE
; TITLE OF INVENTION: INTERACTION BETWEEN THE ENDOCYTIC PROTEIN ENDOPHILIN
; TITLE OF INVENTION: AND THE GERMINAL CENTER KINASE-LIKE KINASE
; FILE REFERENCE: 9555.116US01
; CURRENT APPLICATION NUMBER: US/09/843,245
; CURRENT FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-843-245-1

Query Match          26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 4 PPPP 7

RESULT 58
US-10-022-066-378
; Sequence 378, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
US-10-022-066-378
```

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US-10-104-607B-3
; Sequence 3, Application US/10104607B
; Publication No. US20030091574A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Combination Treatment of Pancreatic Cancer
; FILE REFERENCE: 1102865-0052
; CURRENT APPLICATION NUMBER: US/10/104,607B
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278,294
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical synthetic peptide spacer
US-10-104-607B-3

Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 57
US-09-843-245-1
; Sequence 1, Application US/09843245
; Patent No. US20020164672A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Peter S.
; APPLICANT: Ramjaun, Antoine Rachid
; TITLE OF INVENTION: REGULATION OF JNK ACTIVITY BY MODULATION OF THE
; TITLE OF INVENTION: INTERACTION BETWEEN THE ENDOCYTIC PROTEIN ENDOPHILIN
; TITLE OF INVENTION: AND THE GERMINAL CENTER KINASE-LIKE KINASE
; FILE REFERENCE: 9555.116US01
; CURRENT APPLICATION NUMBER: US/09/843,245
; CURRENT FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-843-245-1

Query Match          26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 4 PPPP 7

RESULT 58
US-10-022-066-378
; Sequence 378, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
US-10-022-066-378
```

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; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 378
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-378

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      5 PPPP 8

RESULT 59
US-10-376-121A-96
; Sequence 96, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8
; SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-10-022-066-378

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      5 PPPP 8

RESULT 60
US-10-376-121A-99
; Sequence 99, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-376-121A-99

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      1 PPPP 4
```



Db 1 PPPP 4

RESULT 61

US-10-376-121A-196

; Sequence 196, Application US/10376121A

; Publication No. US20030216544A1

; GENERAL INFORMATION:

; APPLICANT: Harley, John

; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

; AUTOANTIBODIES

; NUMBER OF SEQUENCES: 218

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: Suite 2000, 1201 West Peachtree Street, N.E.

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/376,121A

; FILING DATE: 27-Mar-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/867,819

; FILING DATE: April 13, 1992

; APPLICATION NUMBER: 07/648,205

; FILING DATE: January 31, 1991

; APPLICATION NUMBER: 07/472,947

; FILING DATE: January 31, 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-817-8473

; TELEFAX: (404)-817-8588

; INFORMATION FOR SEQ ID NO: 196:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 196:

US-10-376-121A-196

Query Match 26.7%; Score 4; DB 12; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10

Db 5 PPPP 8

RESULT 62

US-10-376-121A-197

; Sequence 197, Application US/10376121A

; Publication No. US20030216544A1

; GENERAL INFORMATION:

; APPLICANT: Harley, John

; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

; AUTOANTIBODIES

; NUMBER OF SEQUENCES: 218

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: Suite 2000, 1201 West Peachtree Street, N.E.

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/376,121A

; FILING DATE: 27-Mar-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/867,819

; FILING DATE: April 13, 1992

; APPLICATION NUMBER: 07/648,205

; FILING DATE: January 31, 1991

; APPLICATION NUMBER: 07/472,947

; FILING DATE: January 31, 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-817-8473

; TELEFAX: (404)-817-8588

; INFORMATION FOR SEQ ID NO: 197:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 197:

US-10-376-121A-197

Query Match 26.7%; Score 4; DB 12; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10

Db 4 PPPP 7

RESULT 63

US-10-376-121A-198

; Sequence 198, Application US/10376121A

; Publication No. US20030216544A1

; GENERAL INFORMATION:

; APPLICANT: Harley, John

; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

; AUTOANTIBODIES

; NUMBER OF SEQUENCES: 218

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: Suite 2000, 1201 West Peachtree Street, N.E.

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/376,121A

; FILING DATE: 27-Mar-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/867,819

```
/
/ FILING DATE: April 13, 1992
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-817-8473
/ TELEFAX: (404)-817-8588
/ INFORMATION FOR SEQ ID NO: 198:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 198:
US-10-376-121A-198

Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      3 PPPP 6

RESULT 64
US-10-376-121A-199
/ Sequence 199, Application US/10376121A
/ Publication No. US20030216544A1
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: Suite 2000, 1201 West Peachtree Street, N.E.
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3400
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/376,121A
/ FILING DATE: 27-Mar-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/867,819
/ FILING DATE: April 13, 1992
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-817-8473
/ TELEFAX: (404)-817-8588
/ INFORMATION FOR SEQ ID NO: 199:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
```

```
/
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-376-121A-199

Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      1 PPPP 4

RESULT 65
US-10-376-121A-210
/ Sequence 210, Application US/10376121A
/ Publication No. US20030216544A1
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: Suite 2000, 1201 West Peachtree Street, N.E.
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3400
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/376,121A
/ FILING DATE: 27-Mar-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/867,819
/ FILING DATE: April 13, 1992
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-817-8473
/ TELEFAX: (404)-817-8588
/ INFORMATION FOR SEQ ID NO: 210:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-10-376-121A-210

Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      3 PPPP 6
```

RESULT 66  
US-10-376-121A-211  
; Sequence 211, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/376,121A  
; FILING DATE: 27-Mar-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/867,819  
; FILING DATE: April 13, 1992  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: January 31, 1991  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-817-8473  
; TELEFAX: (404)-817-8588  
; INFORMATION FOR SEQ ID NO: 211:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-817-8473  
; TELEFAX: (404)-817-8588  
; INFORMATION FOR SEQ ID NO: 211:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:  
US-10-376-121A-211  
Query Match 26.7%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 PPPP 10  
Db 2 PPPP 5  
RESULT 67  
US-10-376-121A-213  
; Sequence 213, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: GA

COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 213:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 213:  
US-10-376-121A-213  
Query Match 26.7%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 PPPP 10  
Db 1 PPPP 4  
RESULT 68  
US-10-376-121A-215  
; Sequence 215, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/376,121A  
; FILING DATE: 27-Mar-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/867,819  
; FILING DATE: April 13, 1992  
; APPLICATION NUMBER: 07/648,205

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;
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
;   NAME: Pabst, Patrea L.
;   REGISTRATION NUMBER: 31,284
;   REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV(2)
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (404)-817-8473
;     TELEFAX: (404)-817-8588
;   INFORMATION FOR SEQ ID NO: 215:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 8 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-10-376-121A-215
Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      3 PPPP 6

RESULT 69
US-10-376-121A-216
; Sequence 216, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
;   APPLICANT: Harley, John
;   TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
;     AUTOCANTIBODIES
;   NUMBER OF SEQUENCES: 218
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Patrea L. Pabst
;     STREET: Suite 2000, 1201 West Peachtree Street, N.E.
;     CITY: Atlanta
;     STATE: GA
;     COUNTRY: USA
;     ZIP: 30309-3400
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     FILING DATE: 27-Mar-2003
;     APPLICATION NUMBER: US/10/376,121A
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/867,819
;     FILING DATE: April 13, 1992
;     APPLICATION NUMBER: 07/648,205
;     FILING DATE: January 31, 1991
;     APPLICATION NUMBER: 07/472,947
;     FILING DATE: January 31, 1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV(2)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (404)-817-8473
;       TELEFAX: (404)-817-8588
;     INFORMATION FOR SEQ ID NO: 216:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 8 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-376-121A-217
Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      3 PPPP 6

RESULT 71
US-10-376-121A-217
; Sequence 217, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
;   APPLICANT: Harley, John
;   TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
;     AUTOCANTIBODIES
;   NUMBER OF SEQUENCES: 218
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Patrea L. Pabst
;     STREET: Suite 2000, 1201 West Peachtree Street, N.E.
;     CITY: Atlanta
;     STATE: GA
;     COUNTRY: USA
;     ZIP: 30309-3400
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     FILING DATE: 27-Mar-2003
;     APPLICATION NUMBER: US/10/376,121A
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/867,819
;     FILING DATE: April 13, 1992
;     APPLICATION NUMBER: 07/648,205
;     FILING DATE: January 31, 1991
;     APPLICATION NUMBER: 07/472,947
;     FILING DATE: January 31, 1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV(2)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (404)-817-8473
;       TELEFAX: (404)-817-8588
;     INFORMATION FOR SEQ ID NO: 217:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 8 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-376-121A-217
Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      1 PPPP 4

RESULT 71
US-10-376-121A-217
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-376-121A-216
Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      2 PPPP 5

RESULT 70
US-10-376-121A-217
; Sequence 217, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
;   APPLICANT: Harley, John
;   TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
;     AUTOCANTIBODIES
;   NUMBER OF SEQUENCES: 218
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Patrea L. Pabst
;     STREET: Suite 2000, 1201 West Peachtree Street, N.E.
;     CITY: Atlanta
;     STATE: GA
;     COUNTRY: USA
;     ZIP: 30309-3400
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent In Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     FILING DATE: 27-Mar-2003
;     APPLICATION NUMBER: US/10/376,121A
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/867,819
;     FILING DATE: April 13, 1992
;     APPLICATION NUMBER: 07/648,205
;     FILING DATE: January 31, 1991
;     APPLICATION NUMBER: 07/472,947
;     FILING DATE: January 31, 1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV(2)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (404)-817-8473
;       TELEFAX: (404)-817-8588
;     INFORMATION FOR SEQ ID NO: 217:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 8 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-376-121A-217
Query Match      26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
Db      1 PPPP 4

RESULT 71
US-10-376-121A-217
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US-10-226-007-452
; Sequence 452, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 452
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-452

Query Match          26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 72
US-10-226-007-465
; Sequence 465, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 465
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-465

Query Match          26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 2 PPPP 5

RESULT 73
US-10-226-007-478
; Sequence 478, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

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; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 478
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-478

Query Match          26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 74
US-10-226-007-491
; Sequence 491, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 491
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-491

Query Match          26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 4 PPPP 7

RESULT 75
US-10-226-007-738
; Sequence 738, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738
; LENGTH: 8

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; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-738
Query Match      26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
       ||||
Db      1 PPPP 4

Search completed: November 25, 2003, 20:25:33
Job time : 30.8404 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 16.3564 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKFPPTQETVT 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

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Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/PCtUS COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-641-803-7
2	5	33.3	5	2	US-08-867-941-26
3	5	33.3	5	3	US-09-074-658-26
4	5	33.3	6	2	US-08-867-941-47
5	5	33.3	6	3	US-09-074-658-47
6	5	33.3	7	4	US-09-641-803-14
7	5	33.3	9	3	US-09-188-579-88
8	5	33.3	9	3	US-09-315-444-88
9	5	33.3	9	4	US-09-721-362-88
10	5	33.3	15	1	US-08-302-771-1
11	5	33.3	15	3	US-08-602-999A-339
12	5	33.3	15	3	US-08-602-999A-349
13	5	33.3	15	3	US-08-602-999A-367
14	5	33.3	15	3	US-08-602-999A-373
15	5	33.3	15	3	US-08-602-999A-405
16	5	33.3	15	3	US-08-602-999A-439
17	5	33.3	15	4	US-09-500-124-339
18	5	33.3	15	4	US-09-500-124-349
19	5	33.3	15	4	US-09-500-124-367
20	5	33.3	15	4	US-09-500-124-373
21	5	33.3	15	4	US-09-500-124-405
22	5	33.3	15	4	US-09-500-124-439
23	5	33.3	17	4	US-09-060-299-403
24	5	33.3	17	4	US-09-402-923A-403
25	5	33.3	18	3	US-08-630-316A-109
26	5	33.3	18	3	US-08-602-999A-305
27	5	33.3	18	4	US-08-630-915A-165

28	5	33.3	18	4	US-09-304-799-4	Sequence 4, Appli
29	5	33.3	18	4	US-09-500-124-305	Sequence 305, App
30	5	33.3	20	3	US-08-602-999A-368	Sequence 368, App
31	5	33.3	20	4	US-09-500-124-368	Sequence 368, App
32	4	26.7	4	1	US-07-972-007-33	Sequence 33, Appl
33	4	26.7	4	1	US-08-351-058A-1	Sequence 1, Appli
34	4	26.7	4	1	US-08-647-618-33	Sequence 33, Appl
35	4	26.7	4	2	US-08-358-556A-21	Sequence 21, Appl
36	4	26.7	4	4	US-09-295-996B-6	Sequence 6, Appli
37	4	26.7	4	4	US-09-057-162-33	Sequence 33, Appl
38	4	26.7	4	4	US-09-295-846B-9	Sequence 9, Appli
39	4	26.7	4	4	US-09-551-737C-9	Sequence 9, Appli
40	4	26.7	4	5	PCT-US92-09964-1	Sequence 1, Appli
41	4	26.7	5	1	US-08-351-058A-5	Sequence 5, Appli
42	4	26.7	5	1	US-08-477-509B-9	Sequence 9, Appli
43	4	26.7	5	2	US-08-358-556A-23	Sequence 23, Appl
44	4	26.7	5	3	US-08-630-916A-3	Sequence 3, Appli
45	4	26.7	5	3	US-08-482-085B-9	Sequence 9, Appli
46	4	26.7	5	3	US-08-476-509B-38	Sequence 38, Appl
47	4	26.7	5	4	US-09-444-791A-9	Sequence 9, Appli
48	4	26.7	5	4	US-09-295-996B-7	Sequence 7, Appli
49	4	26.7	5	4	US-08-469-260A-716	Sequence 716, App
50	4	26.7	5	4	US-09-641-803-12	Sequence 12, Appl
51	4	26.7	5	4	US-09-119-507B-3	Sequence 3, Appli
52	4	26.7	5	4	US-08-488-446-716	Sequence 716, App
53	4	26.7	5	4	US-09-295-846B-10	Sequence 10, Appl
54	4	26.7	5	4	US-09-551-737C-10	Sequence 10, Appl
55	4	26.7	5	4	US-08-897-556A-3	Sequence 3, Appli
56	4	26.7	5	4	US-08-897-556A-105	Sequence 105, App
57	4	26.7	5	4	US-08-467-344A-716	Sequence 716, App
58	4	26.7	5	5	PCT-US92-09964-5	Sequence 5, Appli
59	4	26.7	6	1	US-08-151-219-5	Sequence 5, Appli
60	4	26.7	6	1	US-08-188-223-4	Sequence 4, Appli
61	4	26.7	6	1	US-08-188-223-11	Sequence 11, Appl
62	4	26.7	6	2	US-08-358-556A-25	Sequence 25, Appl
63	4	26.7	6	3	US-08-968-466-4	Sequence 4, Appli
64	4	26.7	6	3	US-08-968-466-11	Sequence 11, Appl
65	4	26.7	6	3	US-09-001-984C-35	Sequence 35, Appl
66	4	26.7	6	4	US-08-478-546B-4	Sequence 4, Appli
67	4	26.7	6	4	US-08-478-546B-11	Sequence 11, Appl
68	4	26.7	6	4	US-09-396-347F-35	Sequence 35, Appl
69	4	26.7	6	4	US-09-119-507B-117	Sequence 117, App
70	4	26.7	6	5	PCT-US94-13205-5	Sequence 5, Appli
71	4	26.7	7	1	US-08-151-219-3	Sequence 3, Appli
72	4	26.7	7	1	US-08-188-223-9	Sequence 9, Appli
73	4	26.7	7	1	US-08-188-223-10	Sequence 10, Appl
74	4	26.7	7	2	US-08-968-676-91	Sequence 91, Appl
75	4	26.7	7	2	US-08-680-326-73	Sequence 73, Appl
76	4	26.7	7	3	US-08-968-466-9	Sequence 9, Appli
77	4	26.7	7	3	US-08-968-466-10	Sequence 10, Appl
78	4	26.7	7	4	US-09-343-011B-8	Sequence 8, Appli
79	4	26.7	7	4	US-08-478-546B-9	Sequence 9, Appli
80	4	26.7	7	4	US-08-478-546B-10	Sequence 10, Appl
81	4	26.7	7	4	US-09-281-495-17	Sequence 17, Appl
82	4	26.7	7	4	US-09-076-372-3	Sequence 3, Appli
83	4	26.7	7	5	PCT-US94-13205-3	Sequence 3, Appli
84	4	26.7	8	1	US-07-989-290-4	Sequence 4, Appli
85	4	26.7	8	1	US-08-271-698-4	Sequence 4, Appli
86	4	26.7	8	2	US-08-468-596-4	Sequence 4, Appli
87	4	26.7	8	2	US-08-769-745-22	Sequence 22, Appl
88	4	26.7	8	4	US-09-343-011B-9	Sequence 9, Appli
89	4	26.7	8	4	US-09-295-996B-10	Sequence 10, Appl
90	4	26.7	8	4	US-09-295-996B-14	Sequence 14, Appl
91	4	26.7	8	4	US-09-295-846B-13	Sequence 13, Appl
92	4	26.7	8	4	US-09-295-846B-17	Sequence 17, Appl
93	4	26.7	8	4	US-09-551-737C-13	Sequence 13, Appl
94	4	26.7	8	4	US-09-551-737C-17	Sequence 17, Appl
95	4	26.7	9	2	US-08-340-283-125	Sequence 125, App
96	4	26.7	9	3	US-09-188-573-106	Sequence 106, App
97	4	26.7	9	3	US-09-315-444-106	Sequence 106, App
98	4	26.7	9	3	US-09-001-984C-17	Sequence 17, Appl
99	4	26.7	9	4	US-09-343-011B-6	Sequence 6, Appli
100	4	26.7	9	4	US-09-295-996B-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-09-641-803-7  
; Sequence 7, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-7

Query Match 100.0%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
Db 1 VLEMKFPPPPQETVT 15

RESULT 2  
US-08-867-941-26  
; Sequence 26, Application US/08867941  
; Patent No. 5977337  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Du, Run-Pan  
; APPLICANT: Wang, Quijun  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,941  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-867-941-26

Query Match 33.3%; Score 5; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEMKF 6  
Db 1 LEMKF 5

RESULT 3  
US-09-074-658-26  
; Sequence 26, Application US/09074658  
; Patent No. 6184371  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Run-Pan Du  
; APPLICANT: Quijun Wang  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/074,658  
; FILING DATE: 08-MAY-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-795  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-074-658-26

Query Match 33.3%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEMKF 6  
Db 1 LEMKF 5

RESULT 4  
US-08-867-941-47



; Sequence 47, Application US/08867941  
; Patent No. 5977337  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Du, Run-Pan  
; APPLICANT: Wang, Quijun  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,941  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-867-941-47  
  
Query Match 33.3%; Score 5; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LEMKF 6  
Db 2 LEMKF 6  
  
RESULT 5  
US-09-074-658-47  
; Sequence 47, Application US/09074658  
; Patent No. 6184371  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Run-Pan Du  
; APPLICANT: Quijun Wang  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/074,658  
; FILING DATE: 08-MAY-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-795  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-074-658-47  
  
Query Match 33.3%; Score 5; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LEMKF 6  
Db 2 LEMKF 6  
  
RESULT 6  
US-09-641-803-14  
; Sequence 14, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-14  
  
Query Match 33.3%; Score 5; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 PPPPQ 11  
Db 2 PPPPQ 6  
  
RESULT 7  
US-09-188-579-88  
; Sequence 88, Application US/091885798  
; Patent No. 6107040  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
; FILE REFERENCE: D6185  
; CURRENT APPLICATION NUMBER: US/09/188,579B

; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 114  
; SEQ ID NO 88  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; OTHER INFORMATION: Motif A of RNA triphosphatase.  
US-09-188-579-88

Query Match 33.3%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6  
| | | | |  
Db 5 LEMKF 9

RESULT 8  
US-09-315-444-88  
; Sequence 88, Application US/09315444A  
; Patent No. 6232070  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
; FILE REFERENCE: D6185CIP  
; CURRENT APPLICATION NUMBER: US/09/315,444A  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: US 09/188,579  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 88  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; OTHER INFORMATION: Motif A of RNA triphosphatase.  
US-09-315-444-88

Query Match 33.3%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6  
| | | | |  
Db 5 LEMKF 9

RESULT 9  
US-09-721-362-88  
; Sequence 88, Application US/09721362  
; Patent No. 6420163  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
; FILE REFERENCE: D6185CIP/D  
; CURRENT APPLICATION NUMBER: US/09/721,362  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 09/315,444  
; PRIOR FILING DATE: 1999-05-20  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 88  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; OTHER INFORMATION: Motif A of RNA triphosphatase.  
US-09-721-362-88

Query Match 33.3%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6  
| | | | |  
Db 5 LEMKF 9

RESULT 10  
US-08-302-771-1  
; Sequence 1, Application US/08302771  
; Patent No. 559541  
; GENERAL INFORMATION:  
; APPLICANT: MARCHAL, GILLES  
; APPLICANT: ROMAIN, FELIX  
; TITLE OF INVENTION: PEPTIDE SEQUENCE CAPABLE OF INDUCING  
; TITLE OF INVENTION: A  
; TITLE OF INVENTION: DELAYED-TYPE HYPERSENSITIVITY REACTION IN THE PRESENCE  
; TITLE OF INVENTION: OF  
; TITLE OF INVENTION: LIVING BACTERIA OF THE MYCOBACTERIUM TUBERCULOSIS  
; TITLE OF INVENTION: COMPLEX  
; TITLE OF INVENTION: AND ITS APPLICATIONS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
; ADDRESSEE: NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302,771  
; FILING DATE: OCTOBER 17, 1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92 03 286  
; FILING DATE: 19-MAR-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 12  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 14  
US-08-302-771-1

Query Match 33.3%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11  
| | | | |  
Db 7 PPPPQ 11

```
RESULT 11
US-08-602-999A-339
; Sequence 339, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: O'QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLWES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-339

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 13
US-08-602-999A-367
; Sequence 367, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: O'QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLWES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-339

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 12
US-08-602-999A-349
; Sequence 349, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: O'QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLWES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-339

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 6 PPPPQ 10
```

REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 367:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-367

Query Match 33.3%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
Db 9 PPPPQ 13

RESULT 14  
US-08-602-999A-373  
; Sequence 373, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 373:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-373

Query Match 33.3%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
Db 6 PPPPQ 10

RESULT 15  
US-08-602-999A-405  
; Sequence 405, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 405:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-405

Query Match 33.3%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
Db 6 PPPPQ 10

RESULT 16  
US-08-602-999A-439  
; Sequence 439, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.

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CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 349:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-349

Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPPQ 11  
      |||||  
Db 6 PPPPQ 10

RESULT 19  
US-09-500-124-367  
Sequence 367, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
OPERATING SYSTEM: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 367:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-367

Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPPQ 11  
      |||||

Db 9 PPPPQ 13

RESULT 20  
US-09-500-124-373  
Sequence 373, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
OPERATING SYSTEM: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 373:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-373

Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPPQ 11  
      |||||  
Db 6 PPPPQ 10

RESULT 21  
US-09-500-124-405  
Sequence 405, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-405  
Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 PPPPQ 11  
Db 6 PPPPQ 10  
RESULT 22  
US-09-500-124-439  
Sequence 439, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: O'QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 439:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-439  
Query Match 33.3%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 7 PPPPQ 11  
Db 6 PPPPQ 10  
RESULT 23  
US-09-060-299-403  
Sequence 403, Application US/09060299  
Patent No. 6545137  
GENERAL INFORMATION:  
APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Merriman, Tony R  
APPLICANT: Metzker, Michael L  
TITLE OF INVENTION: No. 6545137el Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vandertye  
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,299  
FILING DATE: 15-APR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:

NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 403:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-060-299-403

Query Match 33.3%; Score 5; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
DB 6 FPPPP 10

RESULT 24  
US-09-402-923A-403  
; Sequence 403, Application US/09402923A  
; Patent No. 6555654  
; GENERAL INFORMATION:  
; APPLICANT: Todd, John A  
; Hess, John W  
; Caskey, Charles T  
; Cox, Roger D  
; Gerhold, David  
; Hammond, Holly  
; Hey, Patricia  
; Kawaguchi, Yoshihiko  
; Merriman, Tony R  
; Metzker, Michael L

TITLE OF INVENTION: No. 6555654e1 LDL-Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US  
ZIP: VA 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,923A  
FILING DATE: 14-Feb-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01102  
FILING DATE: 15-APR-1998  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-81  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 403:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-81  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 403:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-09-402-923A-403  
SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Query Match 33.3%; Score 5; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
DB 6 FPPPP 10

RESULT 25  
US-08-630-916A-109  
; Sequence 109, Application US/08630916A  
; Patent No. 601137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-109

Query Match 33.3%; Score 5; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10  
DB 10 FPPPP 14

RESULT 26  
US-08-602-999A-305  
; Sequence 305, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.



```

; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-305

```

```

Query Match 33.3%; Score 5; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 FPPPP 10
Db 7 FPPPP 11

```

```

RESULT 27
US-08-630-915A-165
; Sequence 165, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-915A-165

```

```

Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 FPPPP 10
Db 10 FPPPP 14

```

```

RESULT 28
US-09-304-799-4
; Sequence 4, Application US/09304799
; Patent No. 6391649
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE ANALYSIS OF PROTEINS AND OTHER BIOLOGICAL
; FILE REFERENCE: 1119-0002
; CURRENT APPLICATION NUMBER: US/09/304,799
; CURRENT FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-304-799-4

```

```

Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 11 QETVT 15
Db 4 QETVT 8

```

```

RESULT 29
US-09-500-124-305
; Sequence 305, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-305

Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
DB 7 FPPPP 11
|||||
;
; RESULT 30
; US-08-602-999A-368
; Sequence 368, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; OPERATION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
```

```
;
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-368

Query Match 33.3%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
DB 13 PPPPQ 17
|||||
;
; RESULT 31
; US-500-124-368
; Sequence 368, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; OPERATION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
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TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-368

Query Match 33.3%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 11  
Db 13 PPPP 17

## RESULT 32

US-07-972-007-33  
; Sequence 33, Application US/07972007  
; Patent No. 5527681  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; TITLE OF INVENTION: Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Stewart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,007  
FILING DATE: 19921105

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5527681v1, Vernon A.

REGISTRATION NUMBER: 32,483

REFERENCE/DOCKET NUMBER: 11509-57-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-972-007-33

Query Match 26.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 1 PPPP 4

## RESULT 33

US-08-351-058A-1  
; Sequence 1, Application US/08351058A  
; Patent No. 5550215  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,058A  
FILING DATE: 28-NOV-1994  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,940

FILING DATE: 19-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,727

FILING DATE: 22-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Swiss, Gerald F.

REGISTRATION NUMBER: 30,113

REFERENCE/DOCKET NUMBER: 000324-015

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-7400

TELEFAX: 415-854-8275

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-351-058A-1

Query Match 26.7%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 1 PPPP 4

## RESULT 34

US-08-647-618-33  
; Sequence 33, Application US/08647618  
; Patent No. 5770456  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; TITLE OF INVENTION: Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/647,618

FILING DATE: 13-MAY-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/972,007

FILING DATE: 05-NOV-1992

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,727
; FILING DATE: 06-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/624,120
; FILING DATE: 06-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/492,462
; FILING DATE: 07-MAR-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/362,901
; FILING DATE: 07-JUN-1989
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-000141US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-647-618-33

Query Match 26.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 35
US-08-358-556A-21
; Sequence 21, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-556A-21

Query Match 26.7%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 36
US-09-295-996B-6
; Sequence 6, Application US/09295996B
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
; US-09-295-996B-6

Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 37
US-09-057-162-33
; Sequence 33, Application US/09057162
; Patent No. 6468740
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Cyclic and Substituted Immobilized
; MOLECULAR SYNTHESIS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,162  
FILING DATE: 08-Apr-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/647,618  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: US 07/972,007  
FILING DATE: 05-NOV-1992  
APPLICATION NUMBER: US 07/796,727  
FILING DATE: 22-NOV-1991  
APPLICATION NUMBER: US 07/805,727  
FILING DATE: 06-DEC-1991  
APPLICATION NUMBER: US 07/624,120  
FILING DATE: 06-DEC-1990  
APPLICATION NUMBER: US 07/492,462  
FILING DATE: 07-MAR-1990  
APPLICATION NUMBER: US 07/362,901  
FILING DATE: 07-JUN-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Matthew B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 16528J-000141US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-057-162-33

Query Match 26.7%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
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|  
Db 1 PPPP 4

RESULT 38  
US-09-295-846B-9  
; Sequence 9, Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
US-09-295-846B-9

Query Match 26.7%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
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|  
Db 1 PPPP 4  
RESULT 39  
US-09-551-737C-9  
; Sequence 9, Application US/09551737C  
; Patent No. 6566129  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Schlesinger, Yaagov  
; APPLICANT: Nauwelaers, Sabine M. I.  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223C1  
; CURRENT APPLICATION NUMBER: US/09/551,737C  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/295,846  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking region  
US-09-551-737C-9

Query Match 26.7%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
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|  
|  
|  
Db 1 PPPP 4

RESULT 40  
PCT-US92-09964-1  
; Sequence 1, Application PC/TUS9209964  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09964  
; FILING DATE: 19921119  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11509-51-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
US-09-551-737C-9

SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US92-09964-1

Query Match 26.7%; Score 4; DB 5; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
 ||||  
 Db 1 PPPP 4

RESULT 41  
 US-08-351-058A-5  
 ; Sequence 5, Application US/08351058A  
 ; Patent No. 5550215  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holmes, Christopher P.  
 ; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis  
 ; STREET: P.O. Box 1404  
 ; CITY: Alexandria  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22313-1404  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/351,058A  
 ; FILING DATE: 28-NOV-1994  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/978,940  
 ; FILING DATE: 19-NOV-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/796,727  
 ; FILING DATE: 22-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Swiss, Gerald F.  
 ; REGISTRATION NUMBER: 30,113  
 ; REFERENCE/DOCKET NUMBER: 000324-015  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-854-7400  
 ; TELEFAX: 415-854-8275  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-351-058A-5

Query Match 26.7%; Score 4; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
 ||||  
 Db 1 PPPP 4

RESULT 42

US-08-477-509B-9  
 ; Sequence 9, Application US/08477509B  
 ; Patent No. 5770697  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ferrari, Franco A  
 ; APPLICANT: Cappello, Joseph  
 ; APPLICANT: Crissman, John W  
 ; APPLICANT: Dorman, Mary A  
 ; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
 ; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
 ; NUMBER OF SEQUENCES: 112  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,509B  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/175,155  
 ; FILING DATE: 29-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/053,049  
 ; FILING DATE: 22-APR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/114,618  
 ; FILING DATE: 29-OCT-1987  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 06/927,258  
 ; FILING DATE: 04-NOV-1986  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Trecartin, Richard F.  
 ; REGISTRATION NUMBER: 31,801  
 ; REFERENCE/DOCKET NUMBER: A-55186-7/RPT/MTK  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-781-1989  
 ; TELEFAX: 415-398-3249  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-477-509B-9

Query Match 26.7%; Score 4; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
 ||||  
 Db 2 PPPP 5

RESULT 43  
 US-08-358-556A-23  
 ; Sequence 23, Application US/08358556A  
 ; Patent No. 5869643  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chatelein, Francois  
 ; APPLICANT: Kumarev, Viktor  
 ; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
 ; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its

```
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-556A-23
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Query Match 26.7%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7 PPPP 10
Db 1 PPPP 4
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```
RESULT 44
US-08-630-916A-3
; Sequence 3, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-916A-3
```

```
Query Match 26.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 PPPP 10
Db 1 PPPP 4
```

```
RESULT 45
US-08-482-085B-9
; Sequence 9, Application US/08482085B
; Patent No. 6018030
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Richardson, Charles
; APPLICANT: Chambers, James
; APPLICANT: Causey, Stuart
; APPLICANT: Pollock, Thomas J.
; APPLICANT: Cappello, Joseph W.
; APPLICANT: Crissman, John W.
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,085B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
```

TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-9

Query Match 26.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPP 10  
Db 2 PPPP 5

RESULT 46  
US-08-476-509B-38  
Sequence 38, Application US/08476509B  
Patent No. 6034212  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/476,509B  
FILING DATE: 01-DEC-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-476-509B-38

Query Match 26.7%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPP 10  
Db 1 PPPP 4

RESULT 47  
US-09-444-791A-9  
Sequence 9, Application US/09444791A  
Patent No. 6355776  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
Richardson, Charles  
Chambers, James  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Crissman, John W.  
TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/444,791A  
FILING DATE: 22-NOV-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-444-791A-9

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPP 10  
Db 2 PPPP 5

RESULT 48  
US-09-295-996B-7  
Sequence 7, Application US/09295996B



```
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
US-09-295-996B-7

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
   |||||
Db 1 PPPP 4

RESULT 49
US-08-469-260A-716
; Sequence 716, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-716

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEM 4
   |||||
Db 1 VLEM 4

RESULT 50
US-09-641-803-12
; Sequence 12, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-12

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPP 9
   |||||
Db 1 FPPP 4

RESULT 51
US-09-119-507B-3
; Sequence 3, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: SITE
; LOCATION: (2)..(5)
; OTHER INFORMATION: The Proline at these positions is a
; OTHER INFORMATION: hydroxyproline.
US-09-119-507B-3
```

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 2 PPPP 5

RESULT 52  
US-08-488-446-716  
; Sequence 716; Application US/08488446  
; Patent No. 6558898  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 716:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-488-446-716

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4  
DB 1 VLEM 4

RESULT 53  
US-09-295-846B-10

; Sequence 10; Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
US-09-295-846B-10

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 1 PPPP 4

RESULT 54  
US-09-551-737C-10  
; Sequence 10; Application US/09551737C  
; Patent No. 6566129  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Schlesinger, Yaagov  
; APPLICANT: Nauwelaers, Sabine M. I.  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223C1  
; CURRENT APPLICATION NUMBER: US/09/551,737C  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/295,846  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking region  
US-09-551-737C-10

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10  
DB 1 PPPP 4

RESULT 55  
US-08-897-556A-3  
; Sequence 3; Application US/08897556A  
; Patent No. 6570062  
; GENERAL INFORMATION:  
; APPLICANT: KIELSZEWSKI, MARCIA J.  
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/897,556A  
FILING DATE: 21-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: OHU-02908  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
MOLECULE TYPE: unknown  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2-5  
OTHER INFORMATION: /note= "The proline at these positions is a hydroxyproline."  
US-08-897-556A-3

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 7 PPPP 10  
Db 2 PPPP 5

RESULT 56  
US-08-897-556A-105  
; Sequence 105, Application US/08897556A  
; Patent No. 6570062  
; GENERAL INFORMATION:  
; APPLICANT: KIELSEWSKI, MARCIA J.  
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/897,556A  
; FILING DATE: 21-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-02908  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2..5  
OTHER INFORMATION: /note= "The proline at positions 2,  
OTHER INFORMATION: 3, 4, and 5 is a hydroxyproline."  
US-08-897-556A-105

Query Match 26.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 2 PPPP 5

RESULT 57  
US-08-467-344A-716  
; Sequence 716, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; TAMI J. PILOT-MATIAS  
; GEORGE J. DAWSON  
; GEORGE G. SCHLAUDER  
; SURESH M. DESAI  
; THOMAS P. LEARY  
; ANTHONY SCOTT MUERHOFF  
; JAMES C. ERKER  
; SHERI L. BUIJK  
; ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 716:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 716:
US-08-467-344A-716

Query Match      26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4
Db 1 VLEM 4

RESULT 58
PCT-US92-09964-5
; Sequence 5, Application PC/TUS2209964
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09964
; FILING DATE: 19921119
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-51-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
PCT-US92-09964-5

Query Match      26.7%; Score 4; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 59
US-08-151-219-5
; Sequence 5, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
```

```
;
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-5

Query Match      26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 60
US-08-188-223-4
; Sequence 4, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
```

```

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; US-08-188-223-4
;
; Query Match 26.7%; Score 4; DB 1; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
;
; QY 7 PPPP 10
; Db 2 PPPP 5
;
; RESULT 61
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
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; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTOR
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; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
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; US-08-968-466-4
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; Query Match 26.7%; Score 4; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 7 PPPP 10
; Db 2 PPPP 5
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; RESULT 64
; US-08-968-466-11
; Sequence 11, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
;
; US-08-968-466-11
;
; Query Match 26.7%; Score 4; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 7 PPPP 10
; Db 2 PPPP 5
;
; RESULT 65
; US-09-001-984C-35
; Sequence 35, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Leal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
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; US-09-001-984C-35
;
; Query Match 26.7%; Score 4; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 11 QETV 14
; Db 1 QETV 4
;
; RESULT 66
; US-08-478-546B-4
; Sequence 4, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
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; TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; US-08-478-546B-4

Query Match 26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 67
US-08-478-546B-11
; Sequence 11, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TUMORS WITH IMMUNOGENS AGAINST GONADOTROPIN-RELEASING HORMONE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; US-08-478-546B-11
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Query Match 26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7 PPPP 10
Db 2 PPPP 5
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RESULT 68
US-09-396-347F-35
; Sequence 35, Application US/09396347F
; Patent No. 6506384
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T.
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: 32004-169276
; CURRENT APPLICATION NUMBER: US/09/396,347F
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/001,984
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
; US-09-396-347F-35
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Query Match 26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 QETV 14
Db 1 QETV 4
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RESULT 69
US-09-119-507B-117
; Sequence 117, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
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APPLICANT: Kieliszewski, Marcia J.  
TITLE OF INVENTION: No. 6548642e1 Synthetic Genes for Plant Gums  
FILE REFERENCE: OHU-03417  
CURRENT APPLICATION NUMBER: US/09/119,507B  
CURRENT FILING DATE: 1998-07-20  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 117  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (2), (5)  
OTHER INFORMATION: The Proline at these positions is a  
OTHER INFORMATION: hydroxyproline.  
US-09-119-507B-117  
Query Match 26.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PPPP 10  
Db 2 PPPP 5  
RESULT 70  
PCT-US94-13205-5  
Sequence 5, Application PC/TUS9413205  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,219  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-09-119-507B-117  
Query Match 26.7%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PPPP 10  
Db 2 PPPP 5  
RESULT 71  
PCT-US94-13205-5  
Sequence 3, Application US/08151219  
Patent No. 5468494  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,219  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-151-219-3  
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QY 7 PPPP 10  
Db 3 PPPP 6  
RESULT 72  
US-08-188-223-9  
Sequence 9, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen

PCT-US94-13205-5  
Query Match 26.7%; Score 4; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
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QY 7 PPPP 10  
Db 2 PPPP 5  
RESULT 71  
US-08-151-219-3  
Sequence 3, Application US/08151219  
Patent No. 5468494  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,219  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-151-219-3  
Query Match 26.7%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PPPP 10  
Db 3 PPPP 6  
RESULT 72  
US-08-188-223-9  
Sequence 9, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen



APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
OTHER INFORMATION: /note= "spacer"  
US-08-188-223-9

Query Match 26.7%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 2 PPPP 5

RESULT 73  
US-08-188-223-10  
Sequence 10, Application US/08188223  
Patent No. 568566  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: C-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..7  
OTHER INFORMATION: /note= "spacer"  
US-08-188-223-10

Query Match 26.7%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
Db 3 PPPP 6

RESULT 74  
US-08-968-676-91  
Sequence 91, Application US/08968676  
Patent No. 5919639  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,676  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-968-676-91

Query Match 26.7%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFP 7  
|||  
Db 3 MKFP 6

## RESULT 75

US-08-680-326-73  
; Sequence 73, Application US/08680326  
; Patent No. 5925733  
; GENERAL INFORMATION:  
; APPLICANT: ROSE, TIMOTHY M.  
; APPLICANT: BOSCH, MARINX  
; APPLICANT: STRAND, KURT  
; APPLICANT: TODARO, GEORGE J.  
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES  
; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL  
; TITLE OF INVENTION: FIBROMATOSIS  
; NUMBER OF SEQUENCES: 152  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/680,326  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 29938-20001.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-680-326-73

Query Match 26.7%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ETVT 15  
|||  
Db 3 ETVT 6

Search completed: November 25, 2003, 20:16:03  
Job time : 17.3564 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 13.8032 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPFKLVKVEFPFP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 9616862 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4	26.7	11	2 S33519	probable secreted
2	3	20.0	5	2 C41225	copper resistance
3	3	20.0	6	2 A61049	halo-toxin - Pseud
4	3	20.0	8	2 A42689	major postsynaptic
5	3	20.0	9	2 A60356	118K stomach cance
6	3	20.0	9	2 I54379	Gene NF2 protein -
7	3	20.0	9	2 S66635	alpha-2-macroglobu
8	3	20.0	9	2 PC7073	ubiquinol-cytochro
9	3	20.0	10	2 GXHU1	gastric juice pept
10	3	20.0	10	2 B33143	pneumadin - human
11	3	20.0	10	2 A33443	pneumadin - rat
12	3	20.0	10	2 S65728	hemoglobin, extrac
13	3	20.0	10	2 S43625	cytochrome-c oxida
14	3	20.0	11	2 S66606	quinoline 2-oxidor
15	3	20.0	11	2 PA0028	protein QA300042 -
16	3	20.0	12	2 S26559	T-cell receptor be
17	3	20.0	12	2 A20907	Ig kappa chain J1
18	3	20.0	12	2 PH1466	T-cell receptor be
19	3	20.0	13	2 S21152	tryptophyllin-rela
20	3	20.0	13	2 H64124	hypothetical prote
21	3	20.0	13	2 B44957	protein L7 - commo
22	3	20.0	13	2 A26999	carboxylesterase (
23	3	20.0	13	2 S23638	Ig kappa chain J s
24	3	20.0	13	2 S65612	tubulin alpha-chain
25	3	20.0	13	2 S01904	H+-transporting tw
26	3	20.0	14	2 S14336	mastoparan B - hor
27	3	20.0	14	2 PC7075	guanylate cyclase
28	3	20.0	14	2 PH0753	T-cell receptor be
29	3	20.0	14	2 PH0762	T-cell receptor be

30	3	20.0	15	2 S10891	ubiquitin thiolest
31	3	20.0	15	2 PA0027	protein QA100006 -
32	3	20.0	15	2 PA0026	protein QA300027 -
33	3	20.0	15	2 PA0024	protein QA300050 -
34	3	20.0	15	2 PT0082	protein QA600023 -
35	3	20.0	15	2 S13973	chlorophyll a/b-bi
36	3	20.0	15	2 S43321	RNA-binding protei
37	3	20.0	15	2 PS0452	32K protein 3306 -
38	3	20.0	15	2 C61511	milk band B protei
39	3	20.0	15	2 S03955	acidic fibroblast
40	3	20.0	15	2 PQ0074	T-cell receptor be
41	3	20.0	15	2 PH0752	T-cell receptor be
42	3	20.0	15	2 PH0760	T-cell receptor be
43	3	20.0	15	2 PT0093	ubiquitin thiolest
44	3	20.0	16	2 I40065	shikimate 5-dehydr
45	3	20.0	16	2 A53337	regulatory protein
46	3	20.0	16	2 S34444	braz protein - Sta
47	3	20.0	16	2 D45193	zinc finger protei
48	3	20.0	16	2 PH0758	T-cell receptor be
49	3	20.0	16	2 PH0759	T-cell receptor be
50	3	20.0	16	2 S33590	beta-crystallin A3
51	3	20.0	17	2 I54269	vitamin D binding
52	3	20.0	17	2 S50901	chlorophyll a/b-bi
53	3	20.0	17	2 S15064	hypothetical prote
54	3	20.0	17	2 A35550	adrenocortical cel
55	3	20.0	17	2 A60889	olfactory glycopro
56	3	20.0	17	2 G85956	hypothetical prote
57	3	20.0	17	4 I76673	hypothetical COL1
58	3	20.0	18	2 G02018	proteasome chain L
59	3	20.0	18	2 S09731	photosystem I prot
60	3	20.0	18	2 A29558	pigment-dispersing
61	3	20.0	18	2 S54272	CTC 75 protein - h
62	3	20.0	18	4 I54078	hypothetical PML/R
63	3	20.0	19	2 B56613	virion morphogenes
64	3	20.0	19	2 T02624	hypothetical prote
65	3	20.0	19	2 S19532	globin - polychaet
66	3	20.0	19	2 S19613	globin - polychaet
67	3	20.0	19	2 S43624	cytochrome-c oxida
68	3	20.0	19	2 S02808	nucleolin - bovine
69	3	20.0	20	2 S77981	cytochrome-c oxida
70	3	20.0	20	2 B53875	creatine kinase (E
71	3	20.0	20	2 A53875	creatine kinase (E
72	3	20.0	20	2 A45806	T-cell receptor be
73	3	20.0	20	2 A54538	39k major outer me
74	3	20.0	20	2 S57286	translation elonga
75	3	20.0	20	2 S09720	2S albumin small c
76	3	20.0	20	2 B30208	hypothetical prote
77	3	20.0	20	2 A34859	heliothermine - Mex
78	3	20.0	20	2 A25335	myosin-light-chain
79	3	20.0	20	2 S58382	hypothetical prote
80	3	20.0	20	2 S03954	acidic fibroblast
81	3	20.0	20	2 A41439	acid ribonuclease
82	3	20.0	20	2 S03508	T-cell receptor al
83	3	20.0	20	2 S68341	procathepsin L - g
84	3	20.0	20	2 A61526	major milk gland p
85	2	13.3	4	2 A02147	phagocytosis-stimu
86	2	13.3	4	2 T46627	hypothetical prote
87	2	13.3	4	2 S53508	starvation-induced
88	2	13.3	5	2 T14908	hypothetical prote
89	2	13.3	5	2 JS0319	subesophageal gang
90	2	13.3	6	2 S02617	alcohol dehydrogen
91	2	13.3	6	2 A35890	RNA-directed DNA p
92	2	13.3	6	2 B34835	dnaa protein - Pse
93	2	13.3	6	2 A60986	N-formyl oligopept
94	2	13.3	6	2 B60110	repetitive protein
95	2	13.3	6	2 A61140	sperm acrosomal pr
96	2	13.3	6	2 I51317	bHLH transcription
97	2	13.3	6	2 H48394	glycoprotein compo
98	2	13.3	6	2 S78764	ribosomal protein
99	2	13.3	6	2 A20186	faty-acid synthas
100	2	13.3	6	2 I48126	alpha-tubulin - Ch

## ALIGNMENTS

## RESULT 1

S33519  
probable secreted protein - Acholeplasma laidlawii (fragment)  
C;Species: Acholeplasma laidlawii  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Oct-1999  
C;Accession: S33519  
R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.  
submitted to the EMBL Data Library, June 1993  
A;Description: Sequence regions from Acholeplasma laidlawii which restore export of beta  
A;Reference number: S33518  
A;Accession: S33519  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <BOY>  
A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 26.7%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLKV 9  
|||  
Db 3 KLKV 6

## RESULT 2

C41225  
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
C;Species: Pseudomonas syringae pv. tomato  
C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C;Accession: C41225  
R;Cha, J.S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem  
A;Reference number: A41225; MUID:92020961; PMID:1924351  
A;Accession: C41225  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <CHA>

Query Match 20.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKL 7  
|||  
Db 2 PKL 4

## RESULT 3

A61049  
halo-toxin - Pseudomonas syringae pv. mori  
C;Species: Pseudomonas syringae pv. mori  
A;Note: host mulberry tree  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
C;Accession: A61049  
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;  
Chem. Lett. 00, 679-680, 1989  
A;Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri  
A;Reference number: A61049  
A;Accession: A61049  
A;Molecule type: protein  
A;Residues: 1-6 <KAL>  
A;Note: sequence confirmed by synthesis  
C;Comment: This toxin is one of the etiological agents of halo bright disease in mulber  
C;Keywords: toxin

Query Match 20.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 1 PPP 3

## RESULT 4

A42689  
major postsynaptic density protein - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 26-May-1994  
C;Accession: A42689  
R;Wu, K.; Huang, Y.; Adler, J.; Black, I.B.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992  
A;Title: On the identity of the major postsynaptic density protein.  
A;Reference number: A42689; MUID:92212958; PMID:1313576  
A;Accession: A42689  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <WUA>

Query Match 20.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9  
|||  
Db 2 LKV 4

## RESULT 5

A60356  
118K stomach cancer antigen - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 17-Mar-1999  
C;Accession: A60356  
R;Shiraishi, Y.  
Int. J. Cancer 45, 783-787, 1990  
A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens  
A;Reference number: A60356; MUID:90216080; PMID:2333853  
A;Accession: A60356  
A;Molecule type: protein  
A;Residues: 1-9 <SHI>  
C;Keywords: glycoprotein

Query Match 20.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3  
|||  
Db 3 LKP 5

## RESULT 6

I54379  
gene NF2 protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C;Accession: I54379  
R;Arai, E.; Ikeuchi, T.; Nakamura, Y.  
Hum. Mol. Genet. 3, 937-939, 1994  
A;Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a  
A;Reference number: I54379; MUID:95038750; PMID:77951241  
A;Accession: I54379  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-9 <RES>  
A;Cross-references: GB:S75841; NID:g861532; PIDN:AAD14190.1; PID:g4261890  
C;Genetics:

A;Gene: GDB:NF2  
A;Cross-references: GDB:120232; OMIM:101000  
A;Map position: 22q12.2-22q12.2



A:Molecule type: protein  
A:Residues: 1-10 <FUS>

Query Match 20.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKV 9  
|||  
Db 8 LKV 10

#### RESULT 13

S43625  
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 20-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 18-Jul-1997  
C:Accession: S43625

R;Freund, R.; Kadenbach, B.  
Eur. J. Biochem. 221, 1111-1116, 1994  
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase  
A:Reference number: S43624; MUID:94237150; PMID:8181469

A:Accession: S43625  
A:Molecule type: protein

A:Residues: 1-10 <FRE>  
A:Note: the source is designated as Salmo gairdneri

C:Genetics:

A:Genome: nuclear

C:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||  
Db 4 KVE 6

#### RESULT 14

S66606  
quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)  
C:Species: Comamonas testosteroni  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C:Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.  
Eur. J. Biochem. 232, 536-544, 1995  
A:Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni  
A:Reference number: S66606; MUID:96035889; PMID:7556204

A:Accession: S66606  
A:Molecule type: protein

A:Residues: 1-11 <SCH>

A:Experimental source: strain 53

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3  
|||  
Db 8 LKP 10

#### RESULT 15

PA0028  
protein QA300042 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0028

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPB, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
A:Reference number: PA0001

A:Accession: PA0028

A:Molecule type: protein

A:Residues: 1-11 <KAM>

A:Experimental source: seed

C:Keywords: seed

Query Match 20.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
Db 6 PPP 8

#### RESULT 16

S26559

T-cell receptor beta chain (clone Cw3/Cas15) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C:Accession: S26559

R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; V

J. Exp. Med. 176, 439-447, 1992

A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A:Reference number: S26512; MUID:92364546; PMID:1380061

A:Accession: S26559

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Cross-references: EMBL:X68009

A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas15

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 8 EVF 10

#### RESULT 17

A20907

IG kappa chain J1 region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 21-Jul-2000

C:Accession: A20907; A53275

R;Emorine, L.; Max, E.E.

Nucleic Acids Res. 11, 8877-8890, 1983

A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals mult

A:Reference number: A20907; MUID:84169523; PMID:6324107

A:Accession: A20907

A:Molecule type: DNA

A:Residues: 1-12 <EMO>

A:Cross-references: GB:X00232; NID:gl582; PIDN:CAA25052.1; PID:gl364236

R;Ayadi, R.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275; MUID:91372868; PMID:1909995

A:Accession: A53275

A:Molecule type: DNA

A:Residues: 1-12 <AYA>

A:Note: sequence extracted from NCBI backbone (NCBI:56069, NCBIP:56161)  
C:Comment: This J1 segment may not be functional because of a short space between the

C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||

Db 8 KVE 10

## RESULT 18

PH1466

T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995

C:Accession: PH1466

R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K

J. Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompatib

A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1466

A:Molecule type: mRNA

A:Residues: 1-12 &lt;AS&gt;

A:Experimental source: cytolytic T-lymphocyte

C:Superfamily: immunoglobulin homology

C:Keywords: receptor; T-cell

Query Match 20.0%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12

|||

Db 8 EVF 10

## RESULT 19

S21152

tryptophyllin-related peptide - two-colored leaf frog

C:Species: Phyllomedusa bicolor (two-colored leaf frog)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C:Accession: S21152

R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.

FEBS Lett. 302, 151-154, 1992

A:Title: Identification and characterization of two dermorphins from skin extracts of th

A:Reference number: S21152; MUID:92339502; PMID:1633846

A:Accession: S21152

A:Molecule type: protein

A:Residues: 1-13 &lt;MG&gt;

A:Experimental source: skin

C:Superfamily: unassigned animal peptides

Query Match 20.0%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4

|||

Db 3 KPF 5

## RESULT 20

H64124

hypothetical protein H11460 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 31-Oct-1997

C:Accession: H64124

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.I.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: H64124

A&gt;Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-13 &lt;TIGR&gt;

A:Cross-references: GB:U32824; GB:I42023; NID:G1574299; PID:G1574306; TIGR:H11460

Query Match 20.0%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

6 KLK 8

|||

Db

4 KLK 6

|||

## RESULT 21

B44957

protein L7 - common tobacco (cv. Samsun NN) (fragment)

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 30-Sep-1993

C:Accession: B44957

R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.

Plant Cell Physiol. 31, 215-221, 1990

A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacu

A:Reference number: A44957

A:Accession: B44957

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 &lt;TAK&gt;

Query Match

20.0%; Score 3; DB 2; Length 13;

Best Local Similarity

100.0%; Pred. No. 3.3e+03;

Matches 3; Conservative

0; Mismatches 0; Indels

0; Gaps 0;

QY

2 KPF 4

|||

Db

9 KPF 11

## RESULT 22

A26999

carboxylesterase (EC 3.1.1.1), intestinal - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 07-Feb-1997

C:Accession: A26999

R:McGhee, J.D.

Biochemistry 26, 4101-4107, 1987

A:Title: Purification and characterization of a carboxylesterase from the intestine of

A:Reference number: A26999; MUID:88000636; PMID:3651439

A:Accession: A26999

A:Molecule type: protein

A:Residues: 1-13 &lt;MCG&gt;

C:Keywords: carboxylic ester hydrolase; intestine

Query Match

20.0%; Score 3; DB 2; Length 13;

Best Local Similarity

100.0%; Pred. No. 3.3e+03;

Matches 3; Conservative

0; Mismatches 0; Indels

0; Gaps 0;

QY

8 KVE 10

|||

Db

10 KVE 12

## RESULT 23

S23638

IG kappa chain J segment (J-kappa-1) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C:Accession: S23638

R:Huber, C.; Klobeck, H.G.; Zachau, H.G.

Eur. J. Immunol. 22, 1561-1565, 1992

A:Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kap

A:Reference number: S23637; MUID:92289816; PMID:1601042

A:Accession: S23638

A&gt;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-13 &lt;HUB&gt;

A:Cross-references: EMBL:X63370

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991

C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||  
DB 8 KVE 10

# RESULT 24

S65612  
tubulin alpha-chain - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C;Accession: S65612  
R;Ruediger, M.; Plessmann, U.; Ruediger, A.H.; Weber, K.  
FEBS Lett. 364, 147-151, 1995  
A;Title: Beta tubulin of bull sperm is polyglycylated.  
A;Reference number: S65611; MUID:95269788; PMID:7750559  
A;Accession: S65612  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <RUE>

Query Match 20.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11  
|||  
DB 5 VEV 7

# RESULT 25

S01904  
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloroplast  
C;Species: chloroplast Arabidopsis thaliana (mouse-ear cress)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 03-Jun-2002  
C;Accession: S01904  
R;Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.  
Nucleic Acids Res. 16, 10372, 1988  
A;Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon-subunit and elongator tRNA  
A;Reference number: S01903; MUID:89057486; PMID:2904134  
A;Accession: S01904  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-13 <CHE>  
A;Cross-references: EMBL:X12889; NID:g11332; PIDN:CAA31380.1; PID:g829297  
C;Genetics:

A;Gene: atpB  
A;Genome: chloroplast  
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|||  
DB 10 KLK 12

# RESULT 26

S14336  
mastoparan B - hornet (Vespa basalis)  
C;Species: Vespa basalis  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Apr-1999  
C;Accession: S14336  
R;Ho, C.L.; Hwang, L.L.  
Biochem. J. 274, 453-456, 1991  
A;Title: Structure and biological activities of a new mastoparan isolated from the venom

A;Reference number: S14336; MUID:91174755; PMID:2006909

A;Accession: S14336

A;Molecule type: protein

A;Residues: 1-14 <HOC>

A;Experimental source: venom

C;Function:

A;Description: possesses a potent hemolytic activity which acts in synergy with the lei

C;Keywords: amidated carboxyl end; mast cell; venom

F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|||  
DB 2 KLK 4

# RESULT 27

PC7075  
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C;Accession: PC7075  
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.  
Electrophoresis 21, 1853-1871, 2000  
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of  
A;Reference number: PC7072  
A;Accession: PC7075  
A;Molecule type: protein  
A;Residues: 1-14 <TSU>  
A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum  
C;Keywords: brain; phosphorus-oxygen lyase

Query Match 20.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
DB 12 EVF 14

# RESULT 28

PH0753  
T-cell receptor beta chain (H3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PH0753  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex:  
allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0753

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Cross-references: EMBL:X60846; NID:g51199; PIDN:CAA43237.1; PID:g51200

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
DB 10 EVF 12

# RESULT 29

PH0762



T-cell receptor beta chain (K1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PH0762  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0762  
A;Molecule type: mRNA  
A;Residues: 1-14 <CAS>  
A;Cross-references: EMBL:X60856; NID:g52768; PIDN:CAA43246.1; PID:g52769  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12  
|||  
Db 10 EVF 12

RESULT 30  
S10891  
ubiquitin thiolesterase (EC 3.1.2.15) PGP9.5 - human (fragment)  
N;Alternate names: ubiquitin carboxyl-terminal hydrolase, neuron-specific  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C;Accession: S10891  
R;Day, I.N.M.; Hinks, L.J.; Thompson, R.J.  
Biochem. J. 268, 521-524, 1990  
A;Title: The structure of the human gene encoding protein gene product 9.5 (PGP9.5), a nuclear protein.  
A;Reference number: S10891; MUID:90303237; PMID:2163617  
A;Accession: S10891  
A;Molecule type: DNA  
A;Residues: 1-15 <DAY>  
A;Cross-references: EMBL:X17377; NID:g35441; PIDN:CAA35249.1; PID:g296799  
C;Genetics:  
A;Introns: 11/3  
C;Superfamily: human ubiquitin thiolesterase  
C;Keywords: thiolester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3  
|||  
Db 3 LKP 5

RESULT 31  
PA0027  
protein QA10006 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0027  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of plant proteins and standardization of  
A;Reference number: PA0001  
A;Accession: PA0027  
A;Molecule type: protein  
A;Residues: 1-15 <KAM>  
A;Experimental source: callus

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9  
|||  
Db 2 LKV 4

RESULT 32  
PA0026  
protein QA300027 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0026  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of plant proteins and standardization of  
A;Reference number: PA0001  
A;Accession: PA0026  
A;Molecule type: protein  
A;Residues: 1-15 <KAM>  
A;Experimental source: leaf

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9  
|||  
Db 2 LKV 4

RESULT 33  
PA0024  
protein QA300050 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0024  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of plant proteins and standardization of  
A;Reference number: PA0001  
A;Accession: PA0024  
A;Molecule type: protein  
A;Residues: 1-15 <KAM>  
A;Experimental source: seed

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5  
|||  
Db 6 PFP 8

RESULT 34  
PT0082  
protein QA600023 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 06-Jun-1997  
C;Accession: PT0082  
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995  
A;Description: Two dimensional electrophoresis of plant proteins and standardization of  
A;Reference number: PN0173  
A;Accession: PT0082  
A;Molecule type: protein  
A;Residues: 1-15 <TSU>  
A;Experimental source: leaf

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKL 7

```

Db          |||
           5 PKL 7

RESULT 35
SI3973
Chlorophyll a/b-binding protein type II - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: SI3973
R:Jainis, P.; Junge, W.
Eur. J. Biochem. 193, 731-736, 1990
A:Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the P
A:Reference number: SI3973; MUID:91065379; PMID:2174365
A:Accession: SI3973
A:Molecule type: protein
A:Residues: 1-15 <UAH>
C:Genetics:
A:Genome: nuclear
C:Keywords: chlorophyll; chloroplast; light-harvesting complex; thylakoid; transmembrane

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
   |||
Db 4 EVF 6

RESULT 36
S43321
RNA-binding protein - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 01-Feb-1999
C:Accession: S43321
R:Lakhani, S.; Khanna, N.C.; Tewari, K.K.
Plant Mol. Biol. 23, 963-979, 1993
A:Title: Nascent transcript-binding protein of the pea chloroplast transcriptionally act
A:Reference number: S43321; MUID:94083566; PMID:8260634
A:Accession: S43321
A:Molecule type: protein
A:Residues: 1-15 <LAK>
C:Function:
A:Description: probably involved in the transcription of chloroplast genes
C:Keywords: RNA binding

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
   |||
Db 10 KVE 12

RESULT 37
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pi 5.3.

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;

```

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
   |||
Db 6 PFP 8

RESULT 38
C61511
milk band B protein - Australian echidna (fragment)
C:Species: Tachyglossus aculeatus (Australian echidna)
C:Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C:Accession: C61511
R:Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
Comp. Biochem. Physiol. B 99, 99-118, 1991
A:Title: Some monotreme milk "whey" and blood proteins.
A:Reference number: A61511; MUID:92070088; PMID:1959333
A:Accession: C61511
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GRI>
C:Keywords: glycoprotein

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFP 14
   |||
Db 13 PFP 15

RESULT 39
S03955
acidic fibroblast growth factor - dog (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Canis lupus familiaris (dog)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03955
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Scha
Eur. J. Biochem. 181, 67-73, 1989
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine f
A:Reference number: S03953; MUID:89231704; PMID:2714282
A:Accession: S03955
A:Molecule type: protein
A:Residues: 1-15 <QUI>
C:Keywords: growth factor

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
   |||
Db 5 PKL 7

RESULT 40
PQ0074
T-cell receptor beta chain (BTB82) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0074
R:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0074
A:Molecule type: mRNA
A:Residues: 1-15 <TAN>
A:Experimental source: T cell
C:Genetics:
A:Gene: BTB82

```

## C;Keywords: receptor

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 3 EVF 5

## RESULT 41

PH0752  
T-cell receptor beta chain (C1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PH0752  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0752  
A;Molecule type: mRNA  
A;Residues: 1-15 <CAS>  
A;Cross-references: EMBL:X60845; NID:g50230; PIDN:CAA43236.1; PID:g50231  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 11 EVF 13

## RESULT 42

PH0760  
T-cell receptor beta chain (H2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C;Accession: PH0760  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0760  
A;Molecule type: mRNA  
A;Residues: 1-15 <CAS>  
A;Cross-references: EMBL:X60855; NID:g51194; PIDN:CAA43245.1; PID:g51195  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 11 EVF 13

## RESULT 43

PT0093  
ubiquitin thiolesterase (EC 3.1.2.15) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 18-Sep-1998  
C;Accession: PT0093; PNO045  
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, July 1998

## A;Description: Proteome analysis of mouse brain.

A;Reference number: PT0091  
A;Accession: PT0093  
A;Molecule type: Protein  
A;Residues: 1-15 <KAW>  
A;Experimental source: brain, striatum  
R;Kato, H.  
Kawasaki Igakkaishi 22, 245-259, 1996  
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neu  
A;Reference number: PNO041  
A;Accession: PNO045  
A;Molecule type: protein  
A;Residues: 1-15 <KAT>  
A;Experimental source: neuroblastoma cell  
C;Comment: The molecular mass is 28,000 and the pI is 5.0.  
C;Keywords: brain; thiolester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3  
|||  
Db 3 LKP 5

## RESULT 44

I40065  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C;Species: Buchnera aphidicola  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C;Accession: I40065  
R;Rounbakhsh, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (enc  
A;Reference number: I40061; MUID:95212914; PMID:7535281  
A;Accession: I40065  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-16 <RES>  
A;Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718  
C;Genetics:  
A;Gene: aroE  
C;Keywords: oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPK 6  
|||  
Db 9 FPK 11

## RESULT 45

A53337  
regulatory protein tyrR - Escherichia coli (fragment)  
C;Species: Escherichia coli  
C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 07-May-1999  
C;Accession: A53337  
R;Argaet, V.P.; Wilson, T.J.; Davidson, B.E.  
J. Biol. Chem. 269, 5171-5178, 1994  
A;Title: Purification of the Escherichia coli regulatory protein TyrR and analysis of  
A;Reference number: A53337; MUID:94148980; PMID:8106498  
A;Accession: A53337  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <ARG>

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 4 EVF 6

## RESULT 46

S34444  
bla2 protein - Staphylococcus aureus plasmid p1258 (fragment)  
C:Species: Staphylococcus aureus  
C:Date: 22-Nov-1993 #sequence\_revision 09-Mar-1996 #text\_change 07-May-1999  
C:Accession: S34444  
R;Wang, P.Z.; Projan, S.J.; Novick, R.P.  
Nucleic Acids Res. 19, 4000, 1991  
A:Title: Nucleotide sequence of beta-lactamase regulatory genes from staphylococcal plasmid p1258  
A:Reference number: S34444; MUID:91319567; PMID:1861992  
A:Accession: S34444  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-16 <WAN>  
A:Cross-references: EMBL:M62650  
A:Experimental source: strain RN11  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C:Genetics:  
A:Gene: bla2  
A:Genome: plasmid p1258

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|||  
Db 4 KLK 6

## RESULT 47

D45193  
zinc finger protein ZNF60 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 01-Jan-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: D45193  
R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.  
Genomics 13, 999-1007, 1992  
A:Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile sites  
A:Reference number: A43284; MUID:92372070; PMID:1505991  
A:Accession: D45193  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <LIC>  
A:Cross-references: GB:M88369; NID:g340475; PIDN:AAA61327.1; PID:g340476  
A:Note: sequence extracted from NCBI backbone (NCBIN:111662, NCBIPI:111664)

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4  
|||  
Db 6 KPF 8

## RESULT 48

PH0758  
T-cell receptor beta chain (E22) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C:Accession: PH0758  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1 allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0758

A:Molecule type: mRNA  
A:Residues: 1-16 <CAS>  
A:Cross-references: EMBL:X60853; NID:g50743; PIDN:CAA43243.1; PID:g50744  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 12 EVF 14

## RESULT 49

PH0759  
T-cell receptor beta chain (QB7.3.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C:Accession: PH0759  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1 allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0759  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS>  
A:Cross-references: EMBL:X60854; NID:g53878; PIDN:CAA43244.1; PID:g53879  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12  
|||  
Db 12 EVF 14

## RESULT 50

S33590  
beta-crystallin A3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 17-Mar-1999  
C:Accession: S33590  
R;David, L.L.; Shearer, T.R.  
FEBS Lett. 324, 265-270, 1993  
A:Title: beta-crystallins insolubilized by calpain II in vitro contain cleavage sites  
A:Reference number: S33586; MUID:94009594; PMID:8405363  
A:Accession: S33590  
A:Molecule type: protein  
A:Residues: 1-16 <DAV>

Query Match 20.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||  
Db 6 KVE 8

## RESULT 51

I54269  
vitamin D binding protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C:Accession: I54269  
R;Braun, A.; Bichlmaier, R.; Muller, B.; Cleve, H.  
Hum. Genet. 90, 526-532, 1993

A;Title: Molecular evaluation of an Alu repeat including a polymorphic variable poly(da)  
A;Reference number: I54269; MUID:93154720; PMID:8381387  
A;Accession: I54269  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-17 <RES>  
A;Cross-references: GB:SS4074; NID:9264876; PIDN:AD13872.1; PID:g4261572  
C;Superfamily: serum albumin; serum albumin repeat homology

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12  
|||  
Db 13 EVF 15

RESULT 52  
S50901  
Chlorophyll a/b-binding protein Lhcb4 - spinach (fragment)  
N;Alternate names: light-harvesting complex LHCIIa protein  
C;Species: Spinacia oleracea (spinach)  
C;Date: 19-Mar-1997 #sequence\_revision 23-Apr-1999 #text\_change 23-Apr-1999  
C;Accession: S50901  
R;Walters, R.G.; Kuban, A.V.; Horton, P.  
Eur. J. Biochem. 226, 1063-1069, 1994  
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexylphosphoribosyl pyrophosphate  
A;Reference number: S50900; MUID:95112835; PMID:7813461  
A;Accession: S50901  
A;Molecule type: protein  
A;Residues: 1-17 <WAL>  
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosynthesis

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12  
|||  
Db 9 EVF 11

RESULT 53  
S15064  
Hypothetical protein A - Trypanosoma brucei (fragment)  
C;Species: Trypanosoma brucei  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Sep-1997  
C;Accession: S15064; S12677  
R;Clayton, C.E.  
Submitted to the EMBL Data Library, April 1990  
A;Reference number: S15063  
A;Accession: S15064  
A;Molecule type: DNA  
A;Residues: 1-17 <CLA>  
A;Cross-references: EMBL:X52586; NID:gl0397; PID:g10402  
R;Vijayarath, S.; Ernest, I.; Itzhaki, J.E.; Sherman, D.; Mowatt, M.R.; Michels, P.A.  
Nucleic Acids Res. 18, 2967-2975, 1990  
A;Title: The genes encoding fructose biphosphate aldolase in Trypanosoma brucei are interrupted  
A;Reference number: S12673; MUID:90272402; PMID:2349093  
A;Accession: S12677  
A;Molecule type: DNA  
A;Residues: 1-9 <VIJ>  
A;Cross-references: EMBL:X52586

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEV 11  
|||  
Db 5 VEV 7

RESULT 54  
A35550  
Adrenocortical cell major secreted protein - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993  
C;Accession: A35550  
R;Shi, D.L.; Savona, C.; Gagnon, J.; Cochet, C.; Chambaz, E.M.; Feige, J.J.  
J. Biol. Chem. 265, 2881-2887, 1990  
A;Title: Transforming growth factor-beta stimulates the expression of alpha-2-macroglobulin  
A;Reference number: A35550; MUID:90153919; PMID:1689294  
A;Accession: A35550  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17 <SHI>

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3  
|||  
Db 4 LKP 6

RESULT 55  
A60889  
Olfactory glycoprotein RB-8 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: A60889  
R;Schwob, J.E.; Gottlieb, D.I.  
J. Neurosci. 8, 3470-3480, 1988  
A;Title: Purification and characterization of an antigen that is spatially segregated  
A;Reference number: A60889; MUID:89010968; PMID:3171685  
A;Accession: A60889  
A;Molecule type: protein  
A;Residues: 1-17 <SCH>  
A;Note: this protein was purified from whole brain  
C;Comment: The monoclonal antibody RB-8 binds this integral membrane glycoprotein on t  
C;Keywords: glycoprotein; membrane protein; olfaction

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10  
|||  
Db 10 KVE 12

RESULT 56  
G85956  
Hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDI  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C;Accession: G85956  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimailanta, E.; Potamouis, K.; Apodac  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: G85956  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-17 <STO>  
A;Cross-references: GB:AE005174; NID:gl2517539; PIDN:AGS8115.1; GSPDB:GN00145; UWGP:Z  
C;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z4331

Query Match 20.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5  
|||  
Db 6 PFP 8

## RESULT 57

176673  
hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)  
N;Alternate names: COII/ND5 protein  
C;Species: mitochondrion Mus musculus (house mouse)  
C;Date: 12-Aug-1996 #sequence\_revision 16-Jul-1998 #text\_change 20-Apr-2000  
C;Accession: I76673; I76674  
R;Nelson, I.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.  
Mamm. Genome 4, 680-683, 1993  
A;Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic mice  
A;Reference number: I57011; MUID:94108239; PMID:8281018

A;Accession: I76673  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-17 <NEL1>  
A;Cross-references: GB:S88119; NID:g544777  
A;Accession: I76674  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 8-17 <NEL2>

A;Cross-references: GB:S88119; NID:g544777  
A;Comment: This is the hypothetical translation of a sequence believed to result from a  
C;Genetics:

A;Gene: COII/ND5  
A;Genome: mitochondrion  
A;Genetic code: SGC1  
C;Keywords: fusion protein; mitochondrion  
F.1-7/Region: cytochrome-c oxidase chain II  
F.8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match 20.0%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|||  
Db 4 KLK 6

## RESULT 58

G02018  
proteasome chain LMP7 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 22-Jun-1999  
C;Accession: G02018  
R;Kim, T.

submitted to the EMBL Data Library, July 1995  
A;Reference number: G09054  
A;Accession: G02018

A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-18 <KIM>

A;Cross-references: EMBL:U32862; NID:g1045468; PIDN:AAA80234.1; PID:g1045469  
C;Genetics:

A;Gene: LMP7  
C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||  
Db 10 KVE 12

## RESULT 59

## S09731

photosystem I protein psal - spinach chloroplast (fragment)  
C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 19-Jan-1996  
C;Accession: S09731  
R;Ikemuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.

FEBS Lett. 263, 274-278, 1990  
A;Title: Polypeptide composition of higher plant photosystem I complex. Identification

A;Reference number: S09730; MUID:90242987; PMID:2185953  
A;Accession: S09731

A;Molecule type: protein  
A;Residues: 1-18 <IK>  
C;Genetics:

A;Gene: psal

A;Genome: chloroplast

A;Superfamily: photosystem I protein psal

C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; t

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFP 13  
|||  
Db 14 VFP 16

## RESULT 60

## A29558

pigment-dispersing hormone - eastern lubber grasshopper  
C;Species: Romalea guttata (eastern lubber grasshopper)

C;Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 03-Mar-1994  
C;Accession: A29558  
R;Rao, K.R.; Mohrher, C.J.; Riehm, J.P.; Zahn, C.A.; Norton, S.; Johnson, L.; Tarr,

J. Biol. Chem. 262, 2672-2675, 1987

A;Title: Primary structure of an analog of crustacean pigment-dispersing hormone from

A;Reference number: A29558; MUID:87137516; PMID:3818616  
A;Accession: A29558

A;Molecule type: protein

A;Residues: 1-18 <RAO>

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7  
|||  
Db 12 PKL 14

## RESULT 61

## S54272

CTC 75 protein - human

C;Species: Homo sapiens (man)

C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999

C;Accession: S54272

R;Gensch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.  
EMBO J. 14, 791-800, 1995

A;Title: Purification of the sequence-specific transcription factor CTCBF, involved in

A;Reference number: S54272; MUID:95188883; PMID:7882982

A;Accession: S54272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <GEN>

Query Match 20.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||

Db 9 KVE 11

## RESULT 62

I54078

hypothetical PML/RARA mutant fusion protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Feb-1997

C;Accession: I54078

R;Yoshida, H.; Naoe, T.; Fukutani, H.; Kiyoi, H.; Kubo, K.; Ohno, R.

A;Title: Analysis of the joining sequences of the t(15;17) translocation in human acute

rt stretches

A;Reference number: I54078; MUID:95194921; PMID:7534109

A;Accession: I54078

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-18 &lt;RES&gt;

A;Cross-references: GB:S76369; NID:g913695

C;Comment: This sequence is the chimeric product of a translocation mutation.

C;Genetics:

A;Gene: PML/RARA

A;Map position: 15q22/17q12

C;Keywords: fusion protein; leukemia

Query Match 20.0%; Score 3; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12

Db 2 EVF 4

## RESULT 63

B56613

viroion morphogenesis late F alternate orf - phage Mu (fragment)

C;Species: phage Mu

C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995

C;Accession: B56613

R;Baxa, C.A.; Chiang, L.; Howe, M.M.

DNA Seq. 2, 329-333, 1992

A;Title: DNA sequence characterization of the G gene region of bacteriophage Mu.

A;Reference number: A56613; MUID:92338399; PMID:1385991

A;Accession: B56613

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-19 &lt;BAX&gt;

A;Note: sequence extracted from NCBI backbone (NCBIN:109379, NCBIPI:109381)

Query Match 20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3

Db 4 LKP 6

## RESULT 64

T02624

hypothetical protein At2g25990 [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein T19L18.20

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 02-Feb-2001

C;Accession: T02624; B84655

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, August 1998

A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.

A;Reference number: Z14681

A;Accession: T02624

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-19 &lt;ROU&gt;

A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413713

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84655

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-19 &lt;STO&gt;

A;Cross-references: GB:AE002093; NID:g3413713; PIDN:AAC31236.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g25990; T19L18.20

A;Map position: 2

Query Match 20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLK 8

Db 8 KLK 10

## RESULT 65

S19532

globin - polychaete (Eudistylia vancouveri) (fragment)

N;Alternate names: chlorocruorin

C;Species: Eudistylia vancouveri

C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998

C;Accession: S19532

R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O

J. Mol. Biol. 222, 1109-1129, 1991

A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular

A;Reference number: S19532; MUID:92106333; PMID:1762147

A;Accession: S19532

A;Molecule type: protein

A;Residues: 1-19 &lt;QAB&gt;

A;Experimental source: plume

C;Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dode

C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9

Db 8 LKV 10

## RESULT 66

S19613

globin - polychaete (Eudistylia vancouveri) (fragment)

C;Species: Eudistylia vancouveri

C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 05-Dec-1998

C;Accession: S19613

R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O

J. Mol. Biol. 222, 1109-1129, 1991

A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular

A;Reference number: S19613; MUID:92106333; PMID:1762147

A;Accession: S19613

A;Molecule type: protein

A;Residues: 1-19 &lt;QAB&gt;

A;Experimental source: plume

C;Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dode

C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKV 9  
|||

Db 8 LKV 10  
|||

RESULT 67

S43624  
cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rainbow trout (fragment)

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 20-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 16-Jul-1999

C;Accession: S43624

R;Freund, R.; Kadenbach, B.  
Eur. J. Biochem. 221, 1111-1116, 1994

A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase

A;Reference number: S43624; MUID:94237150; PMID:8181469

A;Accession: S43624

A;Molecule type: protein

A;Residues: 1-19 <PRE>

A;Note: the source is designated as Salmo gairdneri

C;Genetics:

A;Genome: nuclear

C;Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11  
|||

Db 6 VEV 8  
|||

RESULT 68

S02808  
nucleolin - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993

C;Accession: S02808

R;Sapp, M.; Richter, A.; Weisshart, K.; Caizergues-Ferrer, M.; Amalric, F.; Wallace, M.C.  
Eur. J. Biochem. 179, 541-548, 1989

A;Title: Characterization of a 48-kDa nucleic-acid-binding fragment of nucleolin.

A;Reference number: S02808; MUID:89153087; PMID:2920725

A;Accession: S02808

A;Molecule type: protein

A;Residues: 1-19 <SAP>

Query Match 20.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||

Db 16 KVE 18  
|||

RESULT 69

S77981  
cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)

C;Species: Thunnus obesus (bigeye tuna)

C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 26-Feb-1998

C;Accession: S77981

R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980

A;Accession: S77981

A;Molecule type: protein

A;Residues: 1-20 <ARN>

A;Experimental source: heart; liver

C;Genetics:

A;Genome: nuclear

C;Function:

A;Pathway: oxidative phosphorylation; respiratory chain

C;Superfamily: mammalian cytochrome-c oxidase chain Va

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||

Db 4 KVE 6  
|||

RESULT 70

B53875  
creatine kinase (EC 2.7.3.2) CK-I - coho salmon (fragment)

C;Species: Oncorhynchus kisutch (coho salmon)

C;Date: 26-Sep-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1997

C;Accession: B53875

R;White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.  
J. Protein Chem. 11, 489-494, 1992

A;Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB

A;Reference number: A53875; MUID:93080727; PMID:1449598

A;Accession: B53875

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-20 <WHI>

A;Experimental source: Brockmann body, principal islet

A;Note: sequence extracted from NCBI backbone (NCBIP:120600)

C;Superfamily: creatine kinase; creatine kinase repeat homology

C;Keywords: phosphotransferase

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|||

Db 8 KLK 10  
|||

RESULT 71

A53875  
creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)

C;Species: Oncorhynchus kisutch (coho salmon)

C;Date: 26-Sep-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1997

C;Accession: A53875

R;White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.  
J. Protein Chem. 11, 489-494, 1992

A;Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB

A;Reference number: A53875; MUID:93080727; PMID:1449598

A;Accession: A53875

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-20 <WHI>

A;Experimental source: Brockmann body, principal islet

A;Note: sequence extracted from NCBI backbone (NCBIP:120599)

C;Superfamily: creatine kinase; creatine kinase repeat homology

C;Keywords: phosphotransferase

Query Match 20.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|||

Db 14 KVE 16  
|||

RESULT 72

A45806  
T-cell receptor beta chain C region type 1 - human (fragment)

C;Species: Homo sapiens (man)



C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Jul-1999  
 C;Accession: A45806  
 R;Dent, A.L.; Fink, P.J.; Hedrick, S.M.  
 J. Immunol. 143, 322-328, 1989  
 A;Title: Characterization of an alternative exon of the murine T cell receptor beta chain  
 A;Reference number: A45806; MUID:89278666; PMID:2525149  
 A;Accession: A45806  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-20 <DEN>  
 A;Cross-references: GB:M27225; NID:G339373; PIDN:AAA61099.1; PID:G553781  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFP 13  
 |||  
 Db 5 VFP 7

## RESULT 73

A54538  
 39k major outer membrane protein - Actinobacillus actinomycetemcomitans (strain 14) (L14)  
 C;Species: Actinobacillus actinomycetemcomitans  
 C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 28-Oct-1994  
 C;Accession: A54538  
 R;Koikeguchi, S.; Kato, K.; Nishimura, F.; Kurihara, H.; Murayama, Y.  
 FEMS Microbiol. Lett. 77, 85-90, 1991  
 A;Title: Isolation and partial characterization of a 39 kDa major outer membrane protein  
 A;Reference number: A54538  
 A;Accession: A54538  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <XOK>

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10  
 |||  
 Db 10 KVE 12

## RESULT 74

S57286  
 translation elongation factor aEF-1 beta - Sulfolobus solfataricus (fragments)  
 C;Species: Sulfolobus solfataricus  
 C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
 C;Accession: S57286  
 R;Arcari, P.; Raimo, G.; Ianniciello, G.; Gallo, M.; Bocchini, V.  
 Biochim. Biophys. Acta 1263, 86-88, 1995  
 A;Title: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.  
 A;Reference number: S57268; MUID:95359209; PMID:7632739  
 A;Accession: S57286  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <ARC>

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9  
 |||  
 Db 7 LKV 9

## RESULT 75

S09720

2S albumin small chain nII - rape (fragments)  
 C;Species: Brassica napus (rape)  
 C;Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
 C;Accession: S09720  
 R;Monsalve, R.L.; Menéndez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
 FEBS Lett. 263, 27-32, 1990  
 A;Title: beta-turns as structural motifs for the proteolytic processing of seed protein  
 A;Reference number: S. 720; MUID:90542974; PMID:2185951  
 A;Accession: S09720  
 A;Molecule type: protein  
 A;Residues: 1-9;10-20 <KN>  
 A;Experimental source: seed  
 A;Note: 1-Sei was also found

Query Match 20.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKL 7  
 |||  
 Db 8 PKL 10

Search completed: November 25, 2003, 18:28:19  
 Job time: 14.8036 hours

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 7.26064 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPPKLKVEVFPPF 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: listing first 100 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	20.0	10	1 COXA_ONCMY	P80328 oncorhynchu
2	3	20.0	10	1 GATU_HUMAN	P01358 homo sapien
3	3	20.0	10	1 PNEU_HUMAN	P22103 homo sapien
4	3	20.0	10	1 PNEU_RAT	P21996 rattus norv
5	3	20.0	11	1 CSIS_BACSU	P81095 bacillus su
6	3	20.0	11	1 Q2OA_COMTE	P80464 comamonas t
7	3	20.0	13	1 IDHP_RAT	P56574 rattus norv
8	3	20.0	14	1 MAST_VESBA	P21654 vespa basal
9	3	20.0	15	1 FGF1_CANFA	P18651 canis famil
10	3	20.0	15	1 RMI2_YEAST	P36522 saccharomyc
11	3	20.0	15	1 UBL1_MONDO	P50103 monodelphis
12	3	20.0	15	1 VORA_METTM	P80907 methanobact
13	3	20.0	17	1 YALA_TRYBB	P17961 trypanosoma
14	3	20.0	19	1 COXA_THUOB	P80327 oncorhynchu
15	3	20.0	20	1 COXA_THUOB	P80972 thunnus obe
16	3	20.0	20	1 JHBP_BOMMO	P81627 bombyx mori
17	3	20.0	20	1 MI17_BOVIN	P35451 bos taurus
18	3	20.0	20	1 OM4V_VIBAL	P83149 vibrio algi
19	3	20.0	20	1 OMP1_ACTAC	P20242 actinobacil
20	3	20.0	20	1 TRYL_STREX	P80420 streptomyce
21	2	13.3	4	1 TUFT_HUMAN	P01858 homo sapien
22	2	13.3	5	1 PAP2_PARMA	P81864 pardachirus
23	2	13.3	5	1 SUGA_ACHDO	P19991 acheta dome
24	2	13.3	5	1 UC22_MAIZE	P80628 zea mays (m
25	2	13.3	6	1 OVM_LEPDE	P42985 leptonotars
26	2	13.3	7	1 CCF1_ENTFA	P20104 enterococcu
27	2	13.3	7	1 FAR1_HELTI	P41871 helisoma tr
28	2	13.3	7	1 FAR4_PANRE	P41875 panagrellus
29	2	13.3	7	1 TPFY_PACDA	P83455 pachymedusa
30	2	13.3	7	1 UF04_MOUSE	P83642 mus musculu
31	2	13.3	7	1 UN06_PINPS	P81675 pinus pinas
32	2	13.3	8	1 AN02_BOTJA	Q10582 bothrops ja
33	2	13.3	8	1 LPMS_STAEP	P23211 staphylococ

34	2	13.3	8	1 PPK3_PERAM	P82692 periplaneta
35	2	13.3	8	1 PPK3_PERAM	P82618 periplaneta
36	2	13.3	8	1 RS7_MYCIT	P33564 mycobacteri
37	2	13.3	9	1 BUK_CLOPA	P81337 clostridium
38	2	13.3	9	1 CCAE_CARMA	P38556 carcinus ma
39	2	13.3	9	1 CONO_CONGE	P05486 conus geogr
40	2	13.3	9	1 COW_CONVE	P83047 conus ventr
41	2	13.3	9	1 FAR4_CALVO	P41859 calliphora
42	2	13.3	9	1 FAR5_ASCSU	P43170 ascaris suu
43	2	13.3	9	1 FIBB_ERYPA	P19346 erythrocebu
44	2	13.3	9	1 KNL3_BOWVA	P83058 bombina var
45	2	13.3	9	1 LMT3_LOCMI	P81489 locusta mig
46	2	13.3	9	1 SAMP_MUSCA	P19095 mustelus ca
47	2	13.3	9	1 ULAK_MOUSE	P99031 mus musculu
48	2	13.3	9	1 UPA3_HUMAN	P30089 homo sapien
49	2	13.3	10	1 ANGL1_BOTJA	Q10581 bothrops ja
50	2	13.3	10	1 ANGT_BOVIN	P01017 bos taurus
51	2	13.3	10	1 ANGT_CHICK	P01018 gallus gall
52	2	13.3	10	1 BPP_VIPAS	P31351 vipera aspi
53	2	13.3	10	1 COXK_ONCMY	P80332 oncorhynchu
54	2	13.3	10	1 COXQ_RABIT	P80336 oryctolagus
55	2	13.3	10	1 COXQ_SHEEP	P80337 ovis aries
56	2	13.3	10	1 FARP_PANRE	P82660 panagrellus
57	2	13.3	10	1 FARP_LOCMI	P38553 locusta mig
58	2	13.3	10	1 GON1_CHEPR	P80677 chelyosoma
59	2	13.3	10	1 GON1_PETMA	P80378 petromyzon
60	2	13.3	10	1 GON3_PETMA	P30948 petromyzon
61	2	13.3	10	1 LCMS_LEUMA	P21144 leucophaea
62	2	13.3	10	1 MALE_KLEPN	Q05564 klebsiella
63	2	13.3	10	1 ODP2_BOVIN	P11180 bos taurus
64	2	13.3	10	1 PVK_LOCMI	P83382 locusta mig
65	2	13.3	10	1 Q2O8_COMTE	P80465 comamonas t
66	2	13.3	10	1 RCA_PINPS	P81084 pinus pinas
67	2	13.3	10	1 RL16_ACHLA	P29221 acholepiasm
68	2	13.3	10	1 SLAP_BACTG	P49325 bacillus th
69	2	13.3	10	1 SPI_HALRO	Q10997 halocynthia
70	2	13.3	10	1 SVK_CAMUP	O46464 campylobact
71	2	13.3	10	1 TEMK_RANTE	P56923 rana tempor
72	2	13.3	10	1 TXNB_RANR1	P29135 rana ridibu
73	2	13.3	10	1 UHA3_HUMAN	P40930 homo sapien
74	2	13.3	10	1 UPA5_HUMAN	P30091 homo sapien
75	2	13.3	10	1 URE3_MORMO	P17339 morganelia
76	2	13.3	10	1 XYNB_DICB4	P80717 dictyoglomu
77	2	13.3	11	1 ANGT_CRIGE	P90337 crinia geor
78	2	13.3	11	1 BPPB_AGRHA	P01021 agkistrodon
79	2	13.3	11	1 BRK_MEGFL	P12797 megascolia
80	2	13.3	11	1 CX5A_CONAL	P58848 conus aulic
81	2	13.3	11	1 CXL1_CONNR	P58807 conus maruo
82	2	13.3	11	1 HS70_PINPS	P81672 pinus pinas
83	2	13.3	11	1 MHBT_KLEPN	P80580 klebsiella
84	2	13.3	11	1 MORN_HUMAN	P01163 homo sapien
85	2	13.3	11	1 RS30_ONCMY	P83328 oncorhynchu
86	2	13.3	11	1 TRN2_UPERU	P8616 uperoleia r
87	2	13.3	11	1 TKNA_GADMO	P28498 gadus morhu
88	2	13.3	11	1 TKNA_HORSE	P01290 equus cabal
89	2	13.3	11	1 TKNA_ONCMY	P28499 oncorhynchu
90	2	13.3	11	1 TKNA_RANCA	P22688 rana catesb
91	2	13.3	11	1 TKNA_RANR1	P29207 rana ridibu
92	2	13.3	11	1 TKNA_SCYCA	P41333 scyllorhinu
93	2	13.3	11	1 TKND_RANCA	P22691 rana catesb
94	2	13.3	11	1 UXB2_YEAST	P99013 saccharomyc
95	2	13.3	12	1 FAR7_PENMO	P83322 penaeus mon
96	2	13.3	12	1 NO40_SESKO	O24369 sesbania ro
97	2	13.3	12	1 PSP3_PHPVA	P80662 physcomitre
98	2	13.3	12	1 RF1_CONSP	P58805 conus spuri
99	2	13.3	12	1 RR16_GINBI	P36207 ginkgo bilo
100	2	13.3	12	1 RS19_ELYEP	Q47881 elm yellows

ALIGNMENTS

RESULT 1

```

COXA_ONCMY
ID COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Onchorynchus.
OX NCBI_TaxID=8022;
RN [1]
RN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund B., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 4 KVE 6

RESULT 2
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=75150968; PubMed=5539385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MM; L37220; -.
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.
SQ SEQUENCE 10 AA; 1004 MW; CFERC6AB02C3387D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 5 KVE 7

COXA_ONCMY
ID COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Onchorynchus.
OX NCBI_TaxID=8022;
RN [1]
RN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund B., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 4 KVE 6

RESULT 2
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=75150968; PubMed=5539385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MM; L37220; -.
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.
SQ SEQUENCE 10 AA; 1004 MW; CFERC6AB02C3387D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 5 KVE 7

PNEU_HUMAN
ID PNEU_HUMAN STANDARD; PRT; 10 AA.
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
DR PIR; B33143; B33143.
DR GO; GO:0030103; P:vasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 4 PKL 6

PNEU_RAT
ID PNEU_RAT STANDARD; PRT; 10 AA.
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 4 PKL 6

CSIS_BACSU
ID CSIS_BACSU STANDARD; PRT; 11 AA.

```

AC P81095;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).  
 OS Bacillus subtilis.  
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RN SEQUENCE.  
 RP STRAIN=168 / JH642;  
 RA Graumann P.L., Schmid R., Marahiel M.A.;  
 RL Submitted (OCT-1997) to the SWISS-PROT data bank.  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=168 / JH642; PubMed=8755892;  
 RX MEDLINE=96345629; Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
 RA "Cold shock stress-induced proteins in *Bacillus subtilis*.";  
 RT J. Bacteriol. 178:4611-4619(1996).  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -|- INDUCTION: In response to low temperature.  
 CC -|- CAUTION: Could not be found in the genome of *B. subtilis* 168.  
 FT NON\_TER 11  
 FT SEQUENCE 11 AA; 1360 MW; 15P6CEBE6322C330 CRC64;  
 SQ  
 Query Match 20.0%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KPF 4  
 DB 7 KPF 9  
 RESULT 6  
 Q20A COMTE STANDARD; PRT; 11 AA.  
 ID \_Q20A\_COMTE  
 AC P80464;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Quinolone 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Comamonas.  
 OX NCBI\_TaxID=285;  
 RN [1]  
 RN SEQUENCE.  
 RP STRAIN=63;  
 RX MEDLINE=96035899; PubMed=7556204;  
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
 RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from *Comamonas testosteroni* 63. The first two enzymes in quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995).  
 CC -|- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-1,2-DIHYDROQUINOLINE.  
 CC -|- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-1(2H)-one + reduced acceptor.  
 CC -|- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.  
 CC -|- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first step.  
 CC -|- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND TWO GAMMA CHAINS (PROBABLE).  
 CC PIR: S66606; S66606.  
 DR Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 11  
 FT SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;  
 SQ  
 Query Match 20.0%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3  
 DB 8 LKP 10  
 RESULT 7  
 IDHP RAT STANDARD; PRT; 13 AA.  
 AC P56574;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)  
 DE [Oxalosuccinate decarboxylase] (IDH) (NADP+-specific IDH) (IDP) (ICD-M) (Fragment).  
 GN IDH2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE.  
 RP STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -|- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).  
 CC -|- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2) + NADPH.  
 CC -|- SUBUNIT: Homodimer (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN (SPOT P8) IS: 9.0. ITS MW IS: 42 kDa.  
 CC -|- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.  
 DR InterPro; IPR001804; Isoch.  
 DR PROSITE; PS00470; IDH\_IMDH; PARTIAL.  
 KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle; Mitochondrion.  
 FT NON\_TER 13  
 FT SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;  
 SQ  
 Query Match 20.0%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 KVE 10  
 DB 6 KVE 8  
 RESULT 8  
 MAST\_VESBA STANDARD; PRT; 14 AA.  
 ID \_MAST\_VESBA  
 AC P21654;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan B.  
 OS Vespa basalis (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7444;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Venom;  
 RC MEDLINE=91174755; PubMed=2006909;  
 RA Lo C.-L., Hwang L.-L.;  
 RT "Structure and biological activities of a new mastoparan isolated

```
RT from the venom of the hornet Vespa basalis.";
```

```
RL Biochem. J. 274:453-456(1991).
```

```
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
```

```
CC that couple to phospholipase C.
```

```
DR PIR; S14336; S14336
```

```
KW Mast cell degranulation; Amidation.
```

```
FT MOD_RES 14 14 AMIDATION.
```

```
SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;
```

Query Match 20.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|||  
DB 2 KLK 4

RESULT 9

```
FGF1_CANFA STANDARD; PRT; 15 AA.
```

```
AC P18651;
```

```
DT 01-NOV-1990 (Rel. 16, Created)
```

```
DT 01-NOV-1990 (Rel. 16, Last sequence update)
```

```
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

```
DE Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
```

```
DE factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
```

```
GN FGF1 OR FGF-1.
```

```
OS Canis familiaris (Dog).
```

```
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
```

```
OX NCBI_TaxID=9615;
```

```
RN [1]
```

```
RP SEQUENCE.
```

```
RX MEDLINE=892311704; PubMed=2714282;
```

```
RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethke N.,
```

```
RA Sharma H.S., Schaper W.;
```

```
RT "Isolation of heparin-binding growth factors from bovine, porcine and
```

```
RT canine hearts."
```

```
RL Eur. J. Biochem. 181:67-73(1989).
```

```
CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
```

```
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
```

```
CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
```

```
CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
```

```
CC -!- SUBUNIT: Monomer.
```

```
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
```

```
CC THAN DOES BFGF.
```

```
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
```

```
DR PIR; S03955; S03955; IL1_HBGF.
```

```
DR InterPro; IPR002348; IL1_HBGF.
```

```
DR PROSITE; PS00247; HBGF_FGF; PARTIAL.
```

```
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
```

```
FT NON_TER 15 15
```

```
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;
```

Query Match 20.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7  
|||  
DB 5 PKL 7

RESULT 10

```
RM12_YEAST STANDARD; PRT; 15 AA.
```

```
AC P36522;
```

```
DT 01-JUN-1994 (Rel. 29, Created)
```

```
DT 01-JUN-1994 (Rel. 29, Last sequence update)
```

```
DT 01-JUN-1994 (Rel. 29, Last annotation update)
```

```
DE Mitochondrial 60S ribosomal protein L12 (YmL12) (Fragment).
```

```
GN MRPL12.
```

```
OS Saccharomyces cerevisiae (Baker's yeast).
```

```
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
```

```
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
```

```
OX NCBI_TaxID=4932;
```

```
RN [1]
```

```
RP SEQUENCE.
```

```
RX MEDLINE=91285106; PubMed=2060626;
```

```
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
```

```
RA Kitakawa M.;
```

```
RT "Extended N-terminal sequencing of proteins of the large ribosomal
```

```
RT subunit from yeast mitochondria.";
```

```
RL FEBS Lett. 284:51-56(1991).
```

```
DR SGD; L0002687; MRPL12.
```

```
KW Ribosomal protein; Mitochondrion.
```

```
FT NON_TER 15 15
```

```
SQ SEQUENCE 15 AA; 1851 MW; 74BCD9FEDDDB3900 CRC64;
```

Query Match 20.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11  
|||  
DB 7 VEV 9

RESULT 11

```
UBL1_MONDO STANDARD; PRT; 15 AA.
```

```
ID UBL1_MONDO
```

```
AC P50103;
```

```
DT 01-OCT-1996 (Rel. 34, Created)
```

```
DT 01-OCT-1996 (Rel. 34, Last sequence update)
```

```
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

```
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
```

```
DE L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
```

```
DE (PGP 9.5) (PGP9.5) (Fragment).
```

```
GN UCHL1.
```

```
OS Monodelphis domestica (Short-tailed grey opossum).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
```

```
OX NCBI_TaxID=13616;
```

```
RN [1]
```

```
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Liver;
```

```
RX MEDLINE=96102916; PubMed=8522974;
```

```
RA Mann D.A., Trowen A.R., Lavender F.B., Whittaker P.A.,
```

```
RA Thompson R.J.;
```

```
RT "Identification of evolutionary conserved regulatory sequences in the
```

```
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
```

```
RT hydrolase (PGP9.5) gene."
```

```
RL J. Neurochem. 66:35-46(1996).
```

```
CC -!- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
```

```
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
```

```
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
```

```
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
```

```
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
```

```
CC ubiquitin + a thiol.
```

```
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
```

```
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
```

-----

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```

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```
CC EMBL; U32208; AAA89059.1; -.
```

```
DR InterPro; IPR001578; UCH 1.
```

```
DR PROSITE; PS00140; UCH 1; PARTIAL.
```

```
KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
```

```
FT NON_TER 15 15
```

```
SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;
Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3
Db 3 LKP 5

RESULT 12
VORA_METTM STANDARD; PRT; 15 AA.
ID COX4_ONCMY STANDARD; PRT; 19 AA.
AC P80907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ketoisovalerate oxidoreductase subunit vora (EC 1.-.-.-) (VOR) (2-oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-ferredoxin oxidoreductase alpha subunit) (Fragment).
GN VORA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Testegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC -!- MISCELLANEOUS: As a pH optimum of 9.7 and an optimal temperature of 75 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531CA528F CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12
Db 13 EVF 15

RESULT 13
YALA_TRYBB STANDARD; PRT; 17 AA.
ID YALA_TRYBB STANDARD; PRT; 17 AA.
AC P17961;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 1.9 kDa protein in aldolase locus (ORFA).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RX MEDLINE=90272402; PubMed=2349093;
RA Vijayasarathy S., Ernest I., Itzhaki J., Sherman D., Mowatt M.R.,
RA Michels P.A.M., Clayton C.E.;
RT "The genes encoding fructose biphosphate aldolase in Trypanosoma brucei are interspersed with unrelated genes.";
RL Nucleic Acids Res. 18:2967-2975(1990).
CC -----
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CC -----
DR EMBL; X52586; CAA36821.1; -
DR PIR; S15064; S15064.
KW Hypothetical protein.
SQ SEQUENCE 17 AA; 1939 MW; 5FC2B9AF44AEF420 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEV 11
Db 5 VEV 7

RESULT 14
COX4_ONCMY STANDARD; PRT; 19 AA.
ID COX4_ONCMY STANDARD; PRT; 19 AA.
AC P80327;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) (Fragments).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE IV FAMILY.
DR PIR; S43624; S43624.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 9
FT NON_TER 10
FT NON_TER 19
SQ SEQUENCE 19 AA; 1963 MW; 9280E1D8EC77987E CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEV 11
Db 6 VEV 8

RESULT 15
COXA_THUOB STANDARD; PRT; 20 AA.
ID COXA_THUOB STANDARD; PRT; 20 AA.
AC P80972;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va-1 (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RT Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2404 MW; 7E82E43B7157355E CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 4 KVE 6

RESULT 16
JHBP_BOMMO
ID JHBP_BOMMO STANDARD; PRT; 20 AA.
AC P81627;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Juvenile hormone-binding protein (Fragment).
GN JHBP.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=Backokjam; TISSUE=Hemolymph;
RA Park C.-H., Kim H.R.;
RT "Characterization of high affinity juvenile hormone binding protein in
RT the hemolymph of Bombyx mori L.";
RL Tongmul Hakhoe Chi 37:495-503(1994).
RN [2]
RP IDENTIFICATION OF CYS-9.
RA Park C.-H.;
RL Submitted (DEC-1998) to the SWISS-PROT data bank.
CC -1- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROLYZED BY
CC GENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY.
CC -1- SUBCELLULAR LOCATION: Secreted.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2090 MW; B336332F08AE2FB8 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
DB 6 LKP 8

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RESULT 17
MI17_BOVIN
ID MI17_BOVIN STANDARD; PRT; 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the proteose peptone fraction of bovine milk.";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 10 PKL 12

RESULT 18
OM4V_VIBAL
ID OM4V_VIBAL STANDARD; PRT; 20 AA.
AC P83149;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein 40Va (Omp40Va) (Fragment).
OS Vibrio alginolyticus
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
RT alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.
KW Transmembrane; Porin; Outer membrane.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2229 MW; 4FA95CB24FEC3CDE CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
DB 2 EVF 4

RESULT 19

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OMPI_ACTAC
ID _OMPI_ACTAC STANDARD; PRT; 20 AA.
AC P20242;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE 39 kDa major outer membrane protein (Fragment)
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE.
RC STRAIN=Y4;
RA MEDLINE=91169244; PubMed=2004699;
RA Koikeguchi S., Kato K., Nishimura F., Kurihara H., Murayama Y.;
RT "Isolation and partial characterization of a 39 kDa major outer
membrane protein of Actinobacillus actinomycetemcomitans Y4.";
RL FEMS Microbiol. Lett. 61:85-89(1991).
DR PIR; A54538; A54538.
KW Outer membrane; Transmembrane; Porin.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2316 MW; A837A8C4764F527E CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 10 KVE 12

RESULT 20
TRYL_STREX
ID _TRYL_STREX STANDARD; PRT; 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin-like protease (EC 3.4.21.-) (Fragment)
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RA MEDLINE=95291424; PubMed=7773379;
RA Kim I.-S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
mycelium development of Streptomyces exfoliatus SMF13.";
RL Microbiology 141:1017-1025(1995).
CC -!- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -!- SIMILARITY: BELONGS TO PETIDASE FAMILY S2A.
DR MEOPS; S01.101; -.
DR InterPro; IPR001254; Ser_protease Try.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PFF 14
Db 12 PFF 14

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RESULT 21
TUFT_HUMAN
ID _TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
DR PIR; A02147; A02147.
DR MIM; 191150; -.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3
Db 2 KP 3

RESULT 22
PAP2_PARMA
ID _PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea mores sole (Pardachirus
marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
properties. Forms voltage-dependent, ion-permeable channels
in membranes. At high concentration causes cell membrane lysis.

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CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.  
KW Toxin.  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 4 PP 5

RESULT 23  
SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P1991;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Subesophageal ganglion pentapeptide.  
OS Acheta domesticus (House cricket).  
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
CC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
CC Acheta.  
OX NCBI\_TaxID=6997;  
RN [1]\_TaxID=6997;  
RP SEQUENCE.  
RA Wicker C., Wicker C.;  
RT "Isolation and structure of a peptide isolated from the  
RT subesophageal ganglion of Acheta domesticus (orthoptera).";  
RL Comp. Biochem. Physiol. 88C:185-187(1987).  
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
CC -!- GANGLIA.  
DR PIR; JS0319; JS0319.  
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4  
||  
Db 4 PP 5

RESULT 24  
UC22\_MAIZE STANDARD; PRT; 5 AA.  
AC P80628;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)  
DE (Fragment).  
OS Zea mays (Maize).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
CC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Fernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program."  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.

DR Maize-2DPAGE; P80628; COLEOPTILE.  
DR MaizedB; 123954; -.  
FT NON\_TER 1 1  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EV 11  
||  
Db 4 EV 5

RESULT 25  
OVM\_LEPDE STANDARD; PRT; 6 AA.  
AC P42985;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DB Oviductal motility stimulating peptide (Leb-OVM).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
CC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
CC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;  
CC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxID=7539;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=91271080; PubMed=2052497;  
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,  
RA Proost P., Torrekens S., de Loof A.;  
RT "Isolation, identification and synthesis of novel oviductal motility  
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa  
RT decemlineata.";  
RL Peptides 12:31-36(1991).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
CC OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3  
||  
Db 4 KP 5

RESULT 26  
CCF1\_ENTFA STANDARD; PRT; 7 AA.  
AC P20104;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone cCF10.  
OS Enterococcus faecalis (Streptococcus faecalis).  
CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=89008113; PubMed=3139658;  
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,  
RA Adsit J.C., Dunny G.M., Suzuki A.;  
RT "Structure of cCF10, a peptide sex pheromone which induces  
RT conjugative transfer of the Streptococcus faecalis tetracycline  
RT resistance plasmid, pCF10.";

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RL J. Biol. Chem. 263:14574-14578 (1988).
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR: A30812; A30812.
KW Phormone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VF 12
   ||
Db 5 VF 6

RESULT 27
FAR1_HELTI
ID FAR1_HELTI STANDARD; PRT; 7 AA.
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis";
RL Peptides 15:31-36 (1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76A810 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
   ||
Db 3 PF 4

RESULT 28
FAR4_PANRE
ID FAR4_PANRE STANDARD; PRT; 7 AA.
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF4 (KPNFIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
RA Thim L., Kubiak T.M., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of
RT KPNFIRFamide, a novel FMRamide-related peptide from the free-living

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RT nematode, Panagrellus redivivus.";
RL Peptides 16:87-93 (1995).
CC -!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
CC MUSCLE TENSION INCREASE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 1 KP 2

RESULT 29
TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactylophora (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactylophora tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT CDNA";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3 3
   HYDROXYLATION.
FT MOD RES 3 3
   AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 1 KP 2

RESULT 30
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE
RC  TISSUE=Fibroblast; PubMed=7523108;
RX  MEDLINE=95009907; Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RA  Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT  "Separation and sequencing of familial and novel murine proteins
RL  using preparative two-dimensional gel electrophoresis.";
RL  Electrophoresis 15:735-745(1994).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT  NON_TER 7
SQ  SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
DB 1 PK 2

RESULT 31
UN06 PINPS STANDARD; PRT; 7 AA.
ID UN06 PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle; PubMed=10344291;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 6 PF 7

RESULT 32
ANG2 BOTJA STANDARD; PRT; 8 AA.
ID ANG2 BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]

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RP SEQUENCE.
RC TISSUE=Plasma; PubMed=8829801;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 7 PF 8

RESULT 33
LPMS STAP STANDARD; PRT; 8 AA.
ID LPMS STAP STANDARD; PRT; 8 AA.
AC P23211;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Probable msra leader peptide.
OS Staphylococcus epidermidis.
OG Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=968; PubMed=2233255;
RX MEDLINE=91041730; PubMed=2233255;
RA Ross J.I., Bady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,
RA Wootton J.C.;
RT "Inducible erythromycin resistance in staphylococci is encoded by a
RT member of the ATP-binding transport super-gene family.";
RL Mol. Microbiol. 4:1207-1214(1990).
CC -1- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC PROTEIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52085; CAA36303.1; -.
CC PIR; S11157; LFSAME.
CC Leader peptide; Plasmid.
KW SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
DB 7 LK 8

RESULT 34
PPK2 PERAM STANDARD; PRT; 8 AA.
ID PPK2 PERAM STANDARD; PRT; 8 AA.
AC P82692;

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DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN TISSUE SPECIFICITY.  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYROKININ; FALSE NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
  
Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 PF 4  
Db 3 PF 4  
  
RESULT 35  
FPK3 PERAM  
ID \_PPK3\_PERAM STANDARD; PRT; 8 AA.  
AC P82618;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN TISSUE SPECIFICITY.  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RX MEDLINE=99212469; PubMed=10196736;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach.";  
RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN TISSUE SPECIFICITY.  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;  
  
Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 PF 4  
Db 3 PF 4  
  
RESULT 36  
RS7 MYCIT  
ID \_RS7\_MYCIT STANDARD; PRT; 8 AA.  
AC P33564;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 30S ribosomal protein S7 (Fragment).  
DE RPSG.  
GN RPSG.  
OS Mycobacterium intracellulare.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1767;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93197130; PubMed=8451173;  
RA Nair J., Rouse D.A., Morris S.L.;  
RT "Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare.";  
RL Nucleic Acids Res. 21:1039-1039(1993).  
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the head domain of the 30S subunit. Is located at the subunit interface close to the decoding center, probably blocks exit of the E-site tRNA (By similarity).  
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9 and S11 (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: L08171; AAA25376.1; -.  
DR PIR: S35538; S35538.  
DR HMAP; MF\_00480; -; 1.  
DR InterPro; IPR000235; Ribosomal S7.  
DR PROSITE; PS00052; RIBOSOMAL S7; PARTIAL.  
KW Ribosomal protein; rRNA-binding; rRNA-binding; tRNA-binding.  
FT INIT MET 0  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;  
  
Query Match 13.3%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 PK 6  
Db 7 PK 8

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RESULT 37
BUK_CLOPA          STANDARD;          PRT;          9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (BC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetate kinase family.
DR HAMAP: MF 00542; -!- 1.
DR InterPro: IPR000890; Acetate kin.
DR PROSITE: PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE: PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON TER          9
SQ SEQUENCE          9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match          13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 KL 7
DB          3 KL 4

RESULT 38
CCAP_CARMA
ID -CCAP_CARMA      STANDARD;          PRT;          9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
Tenebrio molitor (Yellow mealworm), and
Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunodea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangler J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
Schoolley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID          3          9
FT MOD_RES           9          9
SQ SEQUENCE          9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match          13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 PF 4
DB          1 PF 2

RESULT 39
CONO_CONGE
ID CONO_CONGE      STANDARD;          PRT;          9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824 (1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID          1          6
FT MOD_RES           9          9
SQ SEQUENCE          9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match          13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 PK 6
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Db          |||
            7 PK 8
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 40
COW_CONVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; D-amino acid.
FT DISULFID 3 5 5 D-TRYPTOPHAN.
FT MOD_RES 5 5 5
FT MOD_RES 9 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
|||
DB 6 KP 7

RESULT 41
FAR4_CALVO STANDARD; PRT; 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR FIR; D41978;
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
|||
DB 3 KP 4

RESULT 42
FAR5_ASCSU STANDARD; PRT; 9 AA.
AC P43170;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AFS.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
|||
DB 3 KP 4

RESULT 43
FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

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CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR; D24180; D24180. Fibrinogen C.  
DR InterPro; IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1 9  
FT NON TER 9 9 FIBRINOPEPTIDE B.  
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EV 11  
Db 3 EV 4

RESULT 44  
KML3\_BOMVA  
ID\_KML3\_BOMVA STANDARD; PRT; 9 AA.  
AC P83058;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE [Thr6]bradykinin.  
OS Bombina variegata (Yellow-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8348;  
RN [1]  
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
RC TISSUE-Skin secretion;  
RA Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.F., Shaw C.;  
RT "Cloning and post-translational processing of frog skin kininogens."  
RL Submitted (Jul-2001) to the SWISS-PROT data bank.  
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat  
CC arterial smooth muscle and constriction of intestinal smooth  
CC muscle.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
KW Amphibian defense peptide; Vasodilator; Bradykinin.  
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
Db 7 PF 8

RESULT 45  
LMT3\_LOCM1  
ID\_LMT3\_LOCM1 STANDARD; PRT; 9 AA.  
AC P41489;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamytropin 3 (LOM-MT-3).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,

de Loof A.;  
RT "Isolation, identification and synthesis of locustamytropin III and  
RT IV, two additional neuropeptides of Locusta migratoria: members of the  
RT locustamytropin peptide family.";  
RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; A61620; A61620.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
Db 4 PF 5

RESULT 46  
SAMP\_MUSCA  
ID\_SAMP\_MUSCA STANDARD; PRT; 9 AA.  
AC P19095;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serum amyloid P-component (SAP) (Fragment).  
OS Mustelus canis (Smooth dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;  
OC Mustelus.  
OX NCBI\_TaxID=7812;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83160932; PubMed=6403520;  
RA Robey P.A., Tanaka T., Liu T.-Y.;  
RT "Isolation and characterization of two major serum proteins from the  
RT dogfish, Mustelus canis, C-reactive protein and amyloid P  
RT component.";  
RL J. Biol. Chem. 258:3889-3894(1983).  
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID  
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
DR PIR; B20569; B20569.  
DR InterPro; IPR001759; Pentaxin.  
DR PROSITE; PS00289; PENTAXIN; PARTIAL.  
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
FT DOMAIN 1 >9 PENTAXIN.  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PF 5  
Db 2 PF 3

RESULT 47  
ULAK\_MOUSE  
ID\_ULAK\_MOUSE STANDARD; PRT; 9 AA.  
AC P99031;  
DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DE 13-DEC-1998 (Rel. 37, Last annotation update)  
DS Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RA Sanchez J.-C., Rouse V., Frutiger S., Hughes G.J., Van J.X.,  
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
RA Cowthorne M.;  
RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.  
DR SWISS-2DPAGE; P99031; MOUSE.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;  
  
Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KV 9  
Db 6 KV 7  
  
RESULT 48  
UPA3\_HUMAN  
ID UPA3\_HUMAN STANDARD; PRT; 9 AA.  
AC P30089;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RL "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.  
DR SWISS-2DPAGE; P30089; HUMAN.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
  
Query Match 13.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 FP 5  
Db 4 FP 5  
  
RESULT 49  
ANG1\_BOTJA  
ID ANG1\_BOTJA STANDARD; PRT; 10 AA.  
AC Q10581;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide I (Fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borghesei R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the  
RT plasma of the snake Bothrops jararaca."  
RL Comp. Biochem. Physiol. 113B:467-473(1996).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT NON\_TER 10  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;  
  
Query Match 13.3%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 PF 4  
Db 7 PF 8  
  
RESULT 50  
ANGT\_BOVIN  
ID ANGT\_BOVIN STANDARD; PRT; 10 AA.  
AC P01017;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-SEP-2003 (Rel. 42, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang  
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
DE (Fragment).  
GN AGT OR SERPIN8.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RA Elliott D.F., Peart W.S.;  
RT "The amino acid sequence in a hypertensin."  
RL Biochem. J. 65:246-254(1957).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the  
CC plasma.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR PIR; A90345; A90345.  
DR PDB; 3ER5; 15-JUL-92.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT PEPTIDE 2 8 ANGIOTENSIN III.  
FT NON\_TER 10  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;



RESULT 52  
BPP VIPAS

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KL 7 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 KL 10

Qy 2 KP 3  
 Db 4 KP 5

RESULT 54

COXQ\_RABIT  
 ID COXQ\_RABIT STANDARD; PRT; 10 AA.  
 AC P80336;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
 DE (Fragment).  
 GN COX8H.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferrocycochrome  
 CC c + 2 H(2)O.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3  
 Db 4 KP 5

RESULT 55

COXQ\_SHEEP  
 ID COXQ\_SHEEP STANDARD; PRT; 10 AA.  
 AC P80337;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
 DE (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferrocycochrome  
 CC c + 2 H(2)O.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3  
 Db 4 KP 5

RESULT 56

FAR6\_PANRE  
 ID FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82660;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRP-famide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OC NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND AMIDATION  
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of RMRFamide-related  
 RT peptides (fARPs) from free-living nematode, Panagrellus redivivus.";  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 10 10  
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4  
 Db 6 PF 7

RESULT 57

FARP\_LOCMI  
 ID FARP\_LOCMI STANDARD; PRT; 10 AA.  
 AC P38553;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Schistocerca gregaria (PVDHFLRF-amide) (Cardioexcitatory neuropeptide).  
 OS Locusta migratoria (Migratory locust), and  
 OS Schistocerca gregaria (Desert locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OC NCBI\_TaxID=7004, 7010;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=L.migratoria; TISSUE=Brain;  
 RX MEDLINE=93324430; PubMed=7687352;  
 RA Schoofs L., Holman G.M., Faemen L., Veelaert D., Amelincx M.,  
 RA de Loof A.;  
 RT "Isolation, identification, and synthesis of PVDHFLRFamide  
 RT (Schistocerca gregaria) in Locusta migratoria and its association with the  
 RT male accessory glands, the salivary glands, the heart, and the  
 RT oviduct.";  
 RL Peptides 14:409-421(1993).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;

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RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A32543; A32543..
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VF 12
   ||
Db 6 VF 7

RESULT 58
GONI CHEPR
ID -GONI CHEPR STANDARD; PRT; 10 AA.
AC P80677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
DE (Luliberin I).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
CX NCBI_TaxID=71177;
RN [1]
RP SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: GnRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
CC THE GONADUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC -!- MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR PROSITE; PS00473; GnRH; 1.
DR Pfam; PF00446; GnRH; 1.
KW Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5A85A3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 8 KP 9

RESULT 59
GONI PETMA
ID -GONI PETMA STANDARD; PRT; 10 AA.
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
DE (Luliberin I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
CX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey
RT brain.";
RL J. Biol. Chem. 261:4812-4819(1986).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A01412; RHLNGS.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 1B4B36237B1735AB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 8 KP 9

RESULT 60
GONI PETMA
ID -GONI PETMA STANDARD; PRT; 10 AA.
AC P30948;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III)
DE (Luliberin III).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
CX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=93178316; PubMed=8440174;
RA Sower S.A., Chiang Y.-C., Lovas S., Conlon J.M.;
RT "Primary structure and biological activity of a third gonadotropin-
RT releasing hormone from lamprey brain.";
RL Endocrinology 132:1125-1131(1993).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.

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DR PROSITE; PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1277 MW; 284B36237AA1F5A3 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 2 KP 3  
 Db 8 KP 9  
 RESULT 61  
 LCMS LEUMA  
 ID LCMS LEUMA STANDARD; PRT; 10 AA.  
 AC P21144; P41497;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucomyosuppressin (LMS) (LeM-MS).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 ON NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of leucomyosuppressin, an insect neuropeptide that inhibits spontaneous contractions of the cockroach hindgut."  
 RL Comp. Biochem. Physiol. 85C:329-333(1986).  
 CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH PROTODEUM (HINDGUT).  
 CC Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 11 VF 12  
 Db 6 VF 7  
 RESULT 62  
 MALE KLEPN  
 ID MALE KLEPN STANDARD; PRT; 10 AA.  
 AC Q05564;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Maltose-binding periplasmic protein (Maltodextrin-binding protein) (MBP) (Fragment).  
 DE (MBP) (Fragment).  
 GN MALE.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 ON NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1033-5PI4 / KAY2026;  
 RX MEDLINE=93211295; PubMed=8459773;  
 RA Bachellier S., Perrin D., Hofnung M., Gilson E.;  
 RT "Bacterial interspersed mosaic elements (BIMES) are present in the genome of Klebsiella.";

RL Mol. Microbiol. 7:537-544(1993).  
 CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND CHEMOTAXIS TOWARD MALTOLOGOSACCHARIDES.  
 CC -!- SUBCELLULAR LOCATION: Periplasmic.  
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 1.  
 CC  
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 CC  
 CC EMBL; X68329; CAA48406.1; -.  
 DR InterPro; IPR006061; SBP dom1.  
 DR PROSITE; PS01037; SBP\_BACTERIAL\_1; PARTIAL.  
 KW Transport; Sugar transport; Periplasmic.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDDA CRC64;  
 Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 QY 1 LK 2  
 Db 1 LK 2  
 RESULT 63  
 ODP2 BOVIN  
 ID ODP2 BOVIN STANDARD; PRT; 10 AA.  
 AC F11180;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihyrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2) (Fragment).  
 DE DLAT.  
 GN Bos taurus (Bovine).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88024154; PubMed=3117054;  
 RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;  
 RT "Primary structure around the lipate-attachment site on the E2 component of bovine heart pyruvate dehydrogenase complex.";  
 RL Biochem. J. 245:919-922(1987).  
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihyrolipoamide acetyltransferase (E2) and lipoaamide dehydrogenase (E3).  
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihyrolipoamide = CoA + S-acetyldihyrolipoamide.  
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL COFACTOR.  
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL SYMMETRY.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.  
 DR InterPro; IPR003016; Lipoyl.  
 DR PROSITE; PS00189; LIPOYL; PARTIAL.  
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;  
 KW Lipoyl  
 FT NON\_TER 1 1

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FT BINDING          5      5      LIPOYL.
FT NON_TER         10      10
SQ SEQUENCE        10 AA; 1066 MW; 889BECDA1ADD33AB1 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Pred.No. 1.4e+04; Indels 0; Gaps 0;

QY 9 VE 10
   ||
Db 1 VE 2

RESULT 64
PVK_LOCMI
ID PVK_LOCMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (Lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R.; Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal
perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005776; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Pred.No. 1.4e+04; Indels 0; Gaps 0;

QY 4 FP 5
   ||
Db 7 FP 8

RESULT 65
Q2OB_COMTE
ID Q2OB_COMTE STANDARD; PRT; 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Retznar S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
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RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-) QUINOLINE TO (3-METHYL-)2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1241 MW; C2E2C2SD9CDC769 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Pred.No. 1.4e+04; Indels 0; Gaps 0;

QY 4 FP 5
   ||
Db 3 FP 4

RESULT 66
RCA_PINPS
ID RCA_PINPS STANDARD; PRT; 10 AA.
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ribulose biphosphate carboxylase/oxygenase activase (RuBisCO
activase) (RA) (Water stress responsive protein 4) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE
CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CARBAMATE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; COA506D2C72B1EA6 CRC64;

Query Match
Best Local Similarity 13.3%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Pred.No. 1.4e+04; Indels 0; Gaps 0;

QY 11 VF 12
   ||
Db 7 VF 8
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CC      OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC      -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC      S-LAYER WITH OBLIQUE (P2) SYMMETRY.
CC      PIR; A60476; A60476.
KW      Cell wall; S-layer.
FT      NON_TER 10
SQ      SEQUENCE 10 AA; 1080 MW; 57AECACAB769DIA3 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PK 5
DB      ||
        5 PK 6

RESULT 69
SPI_HALRO
ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=96321313; PubMed=8759295;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RT "Purification and characterization of a 58,000-Da proteinase
RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia
RT roretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KV 9
DB      ||
        8 KV 9

RESULT 70
SYK_CAMUP
ID SYK_CAMUP STANDARD; PRT; 10 AA.
AC Q46164;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (BC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE (Fragment).
GN LYSS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OC NCBI_TaxID=28080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43954;

-----
CC      "Evolutionary relationships of a plant-pathogenic mycoplasma-like
CC      organism and Acholeplasma laidlawii deduced from two ribosomal protein
CC      gene sequences.";
CC      J. Bacteriol. 174:2606-2611(1992).
CC      -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC      LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
CC      (BY SIMILARITY).
CC      -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; M74771; AAA21914.1; -.
CC      PIR; F41839; F41839.
CC      InterPro; IPR000114; Ribosomal L16.
CC      PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
CC      PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
CC      Ribosomal protein; rRNA-binding.
FT      NON_TER 10
SQ      SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PK 6
DB      ||
        4 PK 5

RESULT 68
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. Gallieriae).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckeitch M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
```

RX MEDLINE=97149302; PubMed=8996110;  
 RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;  
 RT "Characterization of Campylobacter upsaliensis fur and its  
 RT localization in a highly conserved region of the Campylobacter  
 RT genome";  
 RL Gene 183:219-224(1996).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate  
 CC + L-lysyl-tRNA(Lys).  
 CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
 CC  
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 CC  
 CC EMBL: L77076; AAB41342.1; --  
 CC HAVAP: MF\_00252; 1  
 CC InterPro: IPR006195; tRNA\_Ligase\_II.  
 CC PROSITE: PS00862; AA\_TRNA\_LIGASE\_II; PARTIAL.  
 CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 CC Metal-binding; Magnesium.  
 CC NON TER 1  
 CC SEQUENCE 10 AA; 1218 MW; 9CER46AB13372B05 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2  
 ||  
 Db 1 LK 2

## RESULT 71

TEMK RANTE  
 ID TEMK RANTE STANDARD; PRT; 10 AA.  
 AC P36923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Temporin K.  
 OS Rana temporaria (European common frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 CC NCBI\_TaxID=8407;  
 CC [1]  
 CC SEQUENCE.  
 CC TISSUE=Skin secretion;  
 CC MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 RT temporaria";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 CC Amphibian defense peptide; Antibiotic; Amidation.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD RES 10 AMIDATION.  
 FT NON TER 10  
 CC SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2  
 ||  
 Db 6 LK 7

## RESULT 72

TKNB RANRI  
 ID TKNB RANRI STANDARD; PRT; 10 AA.  
 AC P29135;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Neurokinin A.  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 CC NCBI\_TaxID=8406;  
 CC [1]  
 CC SEQUENCE.  
 CC TISSUE=Intestine;  
 CC MEDLINE=93075037; PubMed=1332683;  
 RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,  
 RA Burcher E., Conlon J.M.;  
 RT "Primary structure and receptor-binding properties of a neurokinin A-  
 RT related peptide from frog gut";  
 RL Biochem. J. 287:827-832(1992).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 CC PIR; S27178; S27178.  
 CC InterPro: IPR002040; Tachykinin.  
 CC Pfam: PF02202; Tachykinin; 1.  
 CC PROSITE: PS00267; TACHYKININ; 1.  
 CC Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION.  
 CC SEQUENCE 10 AA; 1160 MW; 526B407059D5BAA7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LK 7  
 ||  
 Db 2 LK 3

## RESULT 73

UHA3 HUMAN  
 ID UHA3 HUMAN STANDARD; PRT; 10 AA.  
 AC P40930;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE.  
 CC TISSUE=Heart;  
 CC MEDLINE=95203287; PubMed=7895732;  
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
 RT "The human myocardial two-dimensional gel protein database: update  
 RT 1994";  
 RL Electrophoresis 15:1459-1465(1994).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.  
 CC NON TER 10  
 CC SEQUENCE 10 AA; 1049 MW; 6B8CDE41A041B76B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VE 10  
 ||  
 Db 2 VE 3

RESULT 74  
 UPAS\_HUMAN STANDARD; PRT; 10 AA.  
 ID UPAS\_HUMAN STANDARD; PRT; 10 AA.  
 AC P30031;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.  
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF  
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT  
 CC PROTEIN.  
 DR SWISS-2DPAGE; P30091; HUMAN.  
 FT NON\_TER 1 1 G->Y.  
 FT VARIANT 9 9 /FTID=VAR\_000002.  
 FT NON\_TER 10 10  
 FT SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6  
 ||  
 Db 4 PK 5

RESULT 75  
 URE3\_MORMO STANDARD; PRT; 10 AA.  
 ID URE3\_MORMO STANDARD; PRT; 10 AA.  
 AC P17339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea  
 DE amidohydrolase) (Fragment).  
 GN UREA.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences."  
 RL J. Bacteriol. 172:3073-3080(1990).

CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.  
 DR PIR; C35389; C35389.  
 KW Hydrolase.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EV 11  
 ||  
 Db 7 EV 8

Search completed: November 25, 2003, 18:17:28  
 Job time : 8.26064 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 36.1436 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKFPFKLKEVFFFP 15

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTRMBL 23: \*  
1: sp\_Archea: \*  
2: sp\_Bacteria: \*  
3: sp\_Fungi: \*  
4: sp\_Human: \*  
5: sp\_Invertebrate: \*  
6: sp\_Mammal: \*  
7: sp\_Mhc: \*  
8: sp\_Organelle: \*  
9: sp\_Phage: \*  
10: sp\_Plant: \*  
11: sp\_Rodent: \*  
12: sp\_Virus: \*  
13: sp\_Vertebrate: \*  
14: sp\_Unclassified: \*  
15: sp\_Virus: \*  
16: sp\_Bacteriaph: \*  
17: sp\_Archeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4	26.7	11	2	Q44090 acholeplasm
2	4	26.7	14	11	Q99PB8
3	4	26.7	15	8	Q9T2Q3
4	4	26.7	16	10	Q94F61
5	3	20.0	7	2	Q8GL00
6	3	20.0	8	4	Q9BY55
7	3	20.0	8	4	Q9UJ50
8	3	20.0	8	6	Q9BF93
9	3	20.0	8	6	Q9BFA0
10	3	20.0	8	6	Q9BF99
11	3	20.0	8	8	Q94909
12	3	20.0	9	4	Q16276
13	3	20.0	9	4	Q16605
14	3	20.0	10	2	Q9XBH3
15	3	20.0	10	6	Q9GKI5
16	3	20.0	10	6	Q9GKI4

17	3	20.0	10	8	Q8SL54
18	3	20.0	11	2	Q9RFZ2
19	3	20.0	11	5	P82700
20	3	20.0	12	4	Q8VLX8
21	3	20.0	12	4	Q9BR06
22	3	20.0	12	8	Q8SL49
23	3	20.0	12	8	Q9GI96
24	3	20.0	12	8	Q8SL40
25	3	20.0	12	8	Q8SL42
26	3	20.0	12	8	Q8SL28
27	3	20.0	12	10	Q41744
28	3	20.0	12	13	Q9PVC2
29	3	20.0	12	13	Q9PVC3
30	3	20.0	12	13	Q9PVC0
31	3	20.0	12	13	Q9PVC1
32	3	20.0	12	13	Q9PVB9
33	3	20.0	12	13	Q9PVC6
34	3	20.0	12	13	Q9PVB8
35	3	20.0	12	13	Q9PVB8
36	3	20.0	12	13	Q9PVC7
37	3	20.0	12	13	Q9PVC4
38	3	20.0	13	8	Q8SL43
39	3	20.0	13	8	Q8SL74
40	3	20.0	13	10	Q8S941
41	3	20.0	13	13	Q9PVA0
42	3	20.0	13	13	Q9PVB1
43	3	20.0	13	13	Q9PVB5
44	3	20.0	13	13	Q9PVA7
45	3	20.0	13	13	Q9PVB3
46	3	20.0	13	13	Q9PVB8
47	3	20.0	13	13	Q9PVB7
48	3	20.0	13	13	Q9PVB2
49	3	20.0	13	13	Q9PVA2
50	3	20.0	13	13	Q9PVB0
51	3	20.0	13	13	Q9PVB4
52	3	20.0	13	13	Q9PVB9
53	3	20.0	13	13	Q9PVA5
54	3	20.0	13	13	Q9PVA3
55	3	20.0	13	13	Q9PVA9
56	3	20.0	13	13	Q9PVC5
57	3	20.0	13	13	Q9PVA4
58	3	20.0	13	13	Q9PVA1
59	3	20.0	13	13	Q9PVB6
60	3	20.0	13	13	Q9PVB5
61	3	20.0	13	13	Q9PVB7
62	3	20.0	13	13	Q9PVB6
63	3	20.0	13	13	Q9PVA6
64	3	20.0	14	2	Q9R782
65	3	20.0	14	2	Q8KSE3
66	3	20.0	14	2	Q52636
67	3	20.0	14	2	Q54394
68	3	20.0	14	4	Q16232
69	3	20.0	14	4	Q96062
70	3	20.0	14	4	Q13022
71	3	20.0	14	9	O55249
72	3	20.0	14	11	Q9QVF3
73	3	20.0	14	12	Q84072
74	3	20.0	15	2	O54298
75	3	20.0	15	2	Q52304
76	3	20.0	15	2	Q9R4U7
77	3	20.0	15	2	Q9S0V1
78	3	20.0	15	4	Q9HCX8
79	3	20.0	15	8	Q9T2J9
80	3	20.0	15	8	Q8SM11
81	3	20.0	15	8	Q8SL26
82	3	20.0	15	8	Q8SL36
83	3	20.0	15	10	P82430
84	3	20.0	15	11	Q9QV76
85	3	20.0	16	2	Q44610
86	3	20.0	16	4	Q9UD41
87	3	20.0	16	4	Q9UCI8
88	3	20.0	16	6	Q9BGG8
89	3	20.0	16	8	Q8SL50

Q8SL54 aeonium haw  
Q9rfz2 mycoplasma  
P82700 leucophaea  
Q8vlx8 thermus the  
Q9br06 homo sapien  
Q8sl49 aeonium lan  
Q9gi96 sargassum p  
Q8sl40 aeonium urb  
Q8sl42 aeonium sim  
Q8sl28 aeonium hol  
Q41744 zea mays (m  
Q9pvc2 gadus morhu  
Q9pvc3 lampiris sp.  
Q9pvc0 mugil cepha  
Q9pvc1 lophius sp.  
Q9pvc6 oryzias lat  
Q9pvc6 plecoglossu  
Q9pvc8 hemiramphus  
Q9pvc7 esox lucius  
Q9pvc4 harpadon sp  
Q8sl43 aeonium spa  
Q8sl74 aichryson p  
Q8s941 beta vulgar  
Q9pva0 colisa laii  
Q9pva1 dendrochiru  
Q9pva5 mola mola (  
Q9pva7 dissostichu  
Q9pva3 hippocampus  
Q9pva8 psittodes s  
Q9pva7 balistes sp  
Q9pva2 mastacembel  
Q9pva0 thunnus sp.  
Q9pva0 dicentrarch  
Q9pva4 zeus faber  
Q9pva9 channa sp.  
Q9pva5 cryptocentr  
Q9pva3 acanthurus  
Q9pva9 epinephelus  
Q9pvc5 galaxias ma  
Q9pva4 siganus sp.  
Q9pva1 stromateus  
Q9pva5 ostracion s  
Q9pva5 sargocentro  
Q9pva7 fundulus he  
Q9pva6 poecilia la  
Q9pva6 salarias sp  
Q9r782 bacillus li  
Q8kes3 enterococcu  
Q52636 escherichia  
Q54394 streptomyce  
Q16232 homo sapien  
Q96062 homo sapien  
Q13022 homo sapien  
Q55249 bacterioph  
Q9qvf3 rattus sp.  
Q84072 influenza vi  
O54298 salmonella  
Q52304 escherichia  
Q9r4u7 acinetobact  
Q9s0v1 nitrogen fi  
Q9hcx8 homo sapien  
Q9t2j9 pisum sativ  
Q8sm11 lilium cand  
Q8sl26 aeonium vis  
Q8sl36 monanthes i  
P82430 nicotiana t  
Q9qv76 mus sp. pre  
Q44610 buchnera ap  
Q9ud41 homo sapien  
Q9uci8 homo sapien  
Q9bgg8 sorax arane  
Q8sl50 aeonium mas

90 Q8SL27 aeonium leu  
 91 Q8SL38 aichryson t  
 92 Q9BC18 rosa stella  
 93 Q8SL52 aeonium kor  
 94 Q8SL55 aeonium bal  
 95 Q8SL53 aeonium hie  
 96 Q8SL57 aeonium gom  
 97 O21922 streptococc  
 98 P83511 delonix reg  
 99 Q8CIS2 mus musculu  
 100 O89560 kaposi's sa

## ALIGNMENTS

## RESULT 1

Q44090 PRELIMINARY; PRT; 11 AA.  
 AC Q44090;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical export segment (Fragment).  
 OS Acholeplasma laidlawii.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Acholeplasma.  
 OX NCBI\_TaxID=2148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A-BF22;  
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;  
 RT "Sequence regions from Acholeplasma laidlawii which restore export of  
 RT beta-lactamase in Escherichia coli."  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 222875; CAA80495.1; --  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLVV 9

DB 3 KLVV 6

## RESULT 2

Q99PB8 PRELIMINARY; PRT; 14 AA.  
 AC Q99PB8;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Adenosine kinase (EC 2.7.1.20) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Singh B., Lin A., Wu Z.-C., Gupta R.S.;  
 RT "Gene Structure for Adenosine Kinase in Chinese Hamster and Human:  
 RT High Frequency Mutants of CHO cells involve deletions of several  
 RT introns and exons."  
 RL DNA Cell Biol. 0:0-0(2001).  
 DR EMBL; AF318953; AAK07186.1; --  
 KW Kinase; Transferase.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1526 MW; 27863376667D5A27 CRC64;

Query Match 26.7%; Score 4; DB 11; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLVV 9

DB 11 KLVV 14

## RESULT 3

Q9T2Q3 PRELIMINARY; PRT; 15 AA.  
 AC Q9T2Q3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE II-65 respiratory protein (Fragment).  
 OS Chlamydomonas reinhardtii.  
 OC Mitochondrion.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE.  
 EX MEDLINE=95079249; PubMed=7826432;  
 RA Atteia A.;  
 RT "Identification of mitochondrial respiratory proteins from the green  
 RT alga Chlamydomonas reinhardtii."  
 RL C. R. Acad. Sci., III, Sci. Vie 317:11-19(1994).  
 SQ SEQUENCE 15 AA; 1584 MW; 6E0B3B843E4379B6 CRC64;

Query Match 26.7%; Score 4; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10

DB 5 LKVE 8

## RESULT 4

Q94F61 PRELIMINARY; PRT; 16 AA.  
 AC Q94F61;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Prolamin-box binding factor (Fragment).  
 GN PBF.  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Cheyenne;  
 RA Chen Z., Fleming J., Zhi Y., Yi M.;  
 RT "Sequence of the prolamin-box binding factor (PBF) promoter sequence  
 RT from wheat."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF385139; AAK64285.1; --  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1770 MW; B406423B4FFEF76B CRC64;

Query Match 26.7%; Score 4; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVFP 13

DB 3 EVFP 6

```

RESULT 5
Q8GL00
ID Q8GL00 PRELIMINARY; PRT; 7 AA.
AC Q8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY142106; AN17857.1; -.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLV 8
DB 5 KLV 7

RESULT 6
Q9BY5
ID Q9BY5 PRELIMINARY; PRT; 8 AA.
AC Q9BY5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL: AY011664; AAG47575.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EBAB572A CRC64;

Query Match 20.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 6 KVE 8

RESULT 7
Q9UJ50
ID Q9UJ50 PRELIMINARY; PRT; 8 AA.
AC Q9UJ50;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE latrophilin-2 (Fragment).
GN LPHH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99153747; PubMed=10030676;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
RT latrophilin gene from a region of 1p31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20225451; PubMed=10760572;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Genomic structure and expression profile of LPHH1, a 7TM gene
RT variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92(2000).
DR EMBL: AJ244509; CAB60204.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1025 MW; 4D59D763344AAB0B CRC64;

Query Match 20.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4
DB 5 KPF 7

RESULT 8
Q9BF93
ID Q9BF93 PRELIMINARY; PRT; 8 AA.
AC Q9BF93;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balenopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL: AY011669; AAG47580.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 6 KVE 8

RESULT 9
Q9BFA0
ID Q9BFA0 PRELIMINARY; PRT; 8 AA.

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AC Q9BFA0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011661; AAG47572.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331BEAB572A CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 6 KVE 8

RESULT 10
ID Q9BF99 PRELIMINARY; PRT; 8 AA.
AC Q9BF99;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OC NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011662; AAG47573.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331BEAB572A CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 6 KVE 8

RESULT 11
ID Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).

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OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Geilissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URF-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -.
RN Mitochondrion.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLK 8
Db 5 KLK 7

RESULT 12
ID Q16276 PRELIMINARY; PRT; 9 AA.
AC Q16276;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Neurofibromatosis type 2 (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95038750; PubMed=7951241;
RA Arai E., Ikeuchi T., Nakamura Y.;
RT "Characterization of the translocation breakpoint on chromosome
RT 22q12.2 in a patient with neurofibromatosis type 2 (NF2).";
RL Hum. Mol. Genet. 3:937-939(1994).
DR EMBL; S75841; AAD14190.2; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1044 MW; 1E4CDD337232404 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLK 8
Db 4 KLK 6

RESULT 13
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;

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RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88330756; PubMed=3138230;  
 RA "Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;  
 RT "Human glutathione S-transferases. The Ha multigene family encodes  
 RT products of different but overlapping substrate specificities.";  
 RL J. Biol. Chem. 263:12797-12800(1988).  
 DR EMBL; M21867; AAA52617.1; -.  
 DR EMBL; M21866; AAA52618.1; -.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;  
  
 Query Match 20.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 PKL 7  
 Db |||  
 5 PKL 7  
  
 RESULT 14  
 Q9XBH3 PRELIMINARY; PRT; 10 AA.  
 ID Q9XBH3  
 AC Q9XBH3;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Celf-like protein (Fragment).  
 GN CELF.  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ATCC 10987;  
 RX MEDLINE=99231848; PubMed=10217496;  
 RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;  
 RT "Genome organisation is not conserved between Bacillus cereus and  
 RT Bacillus subtilis.";  
 RL Microbiology 145:621-631(1999).  
 DR EMBL; AJ000394; CAB40625.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1264 MW; D3757EC33339C9D6 CRC64;  
  
 Query Match 20.0%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 8 KVE 10  
 Db |||  
 7 KVE 9  
  
 RESULT 15  
 Q9GKI5 PRELIMINARY; PRT; 10 AA.  
 ID Q9GKI5  
 AC Q9GKI5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Fragile X mental retardation 1 protein (Fragment).  
 GN FMR1.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21264938; PubMed=11058604;  
 RA Kumari D., Usdin K.;  
 RT "Interaction of the transcription factors USF1, USF2, and alpha-  
 RT Pal/Nrf-1 with the FMR1 promoter. Implications for fragile x mental

RT retardation syndrome.";  
 RL J. Biol. Chem. 276:4357-4364(2001).  
 DR EMBL; AF251349; AAG44598.1; -.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1160 MW; 7C2A2BCB02D2C72B CRC64;  
  
 Query Match 20.0%; Score 3; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 9 VEV 11  
 Db |||  
 6 VEV 8  
  
 RESULT 16  
 Q9GKI4 PRELIMINARY; PRT; 10 AA.  
 ID Q9GKI4  
 AC Q9GKI4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Fragile X mental retardation 1 protein (Fragment).  
 GN FMR1.  
 OS Macaca arctoides (Stump-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9540;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21264938; PubMed=11058604;  
 RA Kumari D., Usdin K.;  
 RT "Interaction of the transcription factors USF1, USF2, and alpha-  
 RT Pal/Nrf-1 with the FMR1 promoter. Implications for fragile x mental  
 RT retardation syndrome.";  
 RL J. Biol. Chem. 276:4357-4364(2001).  
 DR EMBL; AF251350; AAG44599.1; -.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1160 MW; 7C2A2BCB02D2C72B CRC64;  
  
 Query Match 20.0%; Score 3; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 9 VEV 11  
 Db |||  
 6 VEV 8  
  
 RESULT 17  
 Q8SL54 PRELIMINARY; PRT; 10 AA.  
 ID Q8SL54  
 AC Q8SL54;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE FsbA (Fragment).  
 GN PSBA.  
 OS Aeonium haworthii.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Saxifragales; Crassulaceae; Aeonium.  
 OX NCBI\_TaxID=35950;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;  
 RT "Evolution and diversification of the Macaronesian clade of  
 RT Crassulaceae.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY082203; AM13947.1; -.  
 KW Chloroplast.

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FT  NON TER      1      1
SQ  SEQUENCE 10 AA; 988 MW;  COED9F45A772CB02 CRC64;

Query Match      20.0%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  9 VEV 11
    |||
Db  3 VEV 5

RESULT 18
Q9RFZ2
AC  Q9RFZ2      PRELIMINARY;      PRT;      11 AA.
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Fructose biphosphate aldolase (Fragment).
GN  FBA.
OS  Mycoplasma mycoides subsp. capri.
OC  Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC  Entomoplasmataceae.
OX  NCBI_TaxID=40477;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PG3;
RX  MEDLINE=20193983; PubMed=10727835;
RA  Thaucourt F., Lorenzon S., David A., Breard A.;
RT  "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT  of a putative membrane protein gene.";
RL  Vet. Microbiol. 72:251-268(2000).
DR  EMBL; AF162998; AAF15255.1; -.
FT  NON TER      11
SQ  SEQUENCE 11 AA; 1371 MW;  50B0881A3331FB57 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 PKL 7
    |||
Db  2 PKL 4

RESULT 19
P82700
ID  P82700      PRELIMINARY;      PRT;      11 AA.
AC  P82700;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  Periviscerokinin-3 (UEM-PVK-3).
OS  Leucophaea maderae (Madeira cockroach),
OS  Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS  Blaberus craniifer,
OS  Blaptica dubia (Argentinian wood cockroach), and
OS  Gromphadorina portentos (Cockroach).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC  Blaberidae; Leucophaea.
OX  NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN  [1]
RP  SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC  TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX  MEDLINE=20307624; PubMed=10849006;
RA  Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT  "Identification of novel periviscerokinin from single neurohaemal
RT  release sites in insects. MS/MS fragmentation complemented by Edman
RT  degradation.";
RL  Eur. J. Biochem. 267:3869-3873(2000).
CC  -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

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CC  (MYOTROPIC ACTIVITY).
KW  -!- MASS SPECTROMETRY; MW=1146.6; METHOD=MALDI.
KW  Neuropeptide; Amidation.
FT  MOD RES      11
SQ  SEQUENCE 11 AA; 1147 MW;  2F4D9FF2D7605698 CRC64;

Query Match      20.0%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 PFP 5
    |||
Db  7 PFP 9

RESULT 20
Q8VLX8
ID  Q8VLX8      PRELIMINARY;      PRT;      12 AA.
AC  Q8VLX8;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Lysyl-tRNA synthetase (Fragment).
GN  LYS.
OS  Thermus thermophilus.
OC  Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC  Thermus.
OX  NCBI_TaxID=274;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=KT8;
RA  Spada S., Pembroke J.T., Wall J.G.;
RT  "Cloning and characterisation of the czrB metal cation efflux protein
RT  from T. thermophilus.";
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ307316; CAC83721.1; -.
KW  Aminoacyl-tRNA synthetase.
FT  NON TER      1
SQ  SEQUENCE 12 AA; 1327 MW;  5D2A33E27ECDD813 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LKP 3
    |||
Db  1 LKP 3

RESULT 21
Q9BR06
ID  Q9BR06      PRELIMINARY;      PRT;      12 AA.
AC  Q9BR06;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  DJ343K2.3 (Novel protein) (Fragment).
GN  DJ621N11.4.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Laird G.;
RL  Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AL031659; CAC34516.1; -.
FT  NON TER      12
SQ  SEQUENCE 12 AA; 1422 MW;  DC7PBF1578B2C9D2 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      10 EVF 12
Db      4 EVF 6

RESULT 22
Q8SL49
ID Q8SL49 PRELIMINARY; PRT; 12 AA.
AC Q8SL49;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Psba (Fragment).
GN PSBA.
OS Aeonium lancelottense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=111152;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082208; AAM13952.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 12 AA; 1291 MW; COEDC9DC3D72CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEV 11
Db      5 VEV 7

RESULT 23
Q9GI96
ID Q9GI96 PRELIMINARY; PRT; 12 AA.
AC Q9GI96;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN RBCS.
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillips N.E.;
RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998), University of Hawaii.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=nepi27;
RA Phillips N.E., Smith C.M., Morden C.W.;
RT "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 12 AA; 1200 MW; C0FB1B6DF372CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEV 11
Db      5 VEV 7

RESULT 24
Q8SL40
ID Q8SL40 PRELIMINARY; PRT; 12 AA.
AC Q8SL40;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Psba (Fragment).
GN PSBA.
OS Aeonium urbicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=111161;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082217; AAM13961.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 12 AA; 1291 MW; COEDC9DC3D72CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEV 11
Db      5 VEV 7

RESULT 25
Q8SL42
ID Q8SL42 PRELIMINARY; PRT; 12 AA.
AC Q8SL42;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Psba (Fragment).
GN PSBA.
OS Aeonium simsii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=35955;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082215; AAM13959.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 12 AA; 1200 MW; C0FB1B6DF372CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11  
|  
|  
|  
Db 5 VEV 7

## RESULT 26

Q8SL28 ID Q8SL28 PRELIMINARY; PRT; 12 AA.  
AC Q8SL28;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE PSBA (Fragment).  
GN PSBA.  
OS Aeonium holochrysum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Crassulaceae; Aeonium.  
OX NCBI\_TaxID=35951;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;  
RT "Evolution and diversification of the Macaronesian clade of  
RT Crassulaceae inferred from the chloroplast and nuclear data."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY022283; AAM13973.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1200 MW; CQF1B6DF372CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;

Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11  
|  
|  
|  
Db 5 VEV 7

## RESULT 27

Q41744 ID Q41744 PRELIMINARY; PRT; 12 AA.  
AC Q41744;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Alcohol dehydrogenase (Fragment).  
GN ADH1.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TRANSPOSOM=Mu3;  
RX MEDLINE=87277357; PubMed=3038674;  
RA Chen C.H., Oishi K.K., Kloeckner-Gruissem B., Freeling M.;  
RT "Organ-specific expression of maize Adh1 is altered after a Mu  
RT transposon insertion."  
RL Genetics 116:469-477(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TRANSPOSOM=Mu3;  
RA Freeling M.;  
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U19613; AAC48978.1; -.  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1217 MW; 233663790942C338 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 12;

Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8  
|  
|  
|  
Db 9 KLK 11

## RESULT 28

Q9PVC2 ID Q9PVC2 PRELIMINARY; PRT; 12 AA.  
AC Q9PVC2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Gadus morhua (Atlantic cod).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
OX NCBI\_TaxID=8049;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aCod;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134603; AAD54088.1; -.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31B69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;

Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10  
|  
|  
|  
Db 8 KVE 10

## RESULT 29

Q9PVC3 ID Q9PVC3 PRELIMINARY; PRT; 12 AA.  
AC Q9PVC3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Lampris sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Lampridiformes; Lampridae; Lampris.  
OX NCBI\_TaxID=94303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aLamp;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134602; AAD54087.1; -.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.



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FT NON_TER      1
FT NON_TER      12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 30
Q9PVC0
ID Q9PVC0      PRELIMINARY;      PRT;      12 AA.
AC Q9PVC0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Mugil cephalus (Flathead mullet) (Mugil japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Mugil.
OX NCBI_TaxID=48193;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aMullet;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134605; AAD54090.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER      1
FT NON_TER      12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 31
Q9PVC1
ID Q9PVC1      PRELIMINARY;      PRT;      12 AA.
AC Q9PVC1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Lophius sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=30791;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aAngler;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."

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RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134604; AAD54089.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER      1
FT NON_TER      12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 32
Q9PVB9
ID Q9PVB9      PRELIMINARY;      PRT;      12 AA.
AC Q9PVB9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aMedaka;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134606; AAD54091.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER      1
FT NON_TER      12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 33
Q9PVC6
ID Q9PVC6      PRELIMINARY;      PRT;      12 AA.
AC Q9PVC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Plecoglossus altivelis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.
OX NCBI_TaxID=61084;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aAyu;

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RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134598; AAD54084.1; --
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 34
Q9PVB8 PRELIMINARY; PRT; 12 AA.
AC Q9PVB8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Hemirhamphus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Hemirhamphidae; Hemiramphus.
OX NCBI_TaxID=94223;
RN [1]_TaxID=94223;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aHalifbeak;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134607; AAD54092.1; --
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 35
Q9PVA8 PRELIMINARY; PRT; 12 AA.
AC Q9PVA8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Mullus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciiformes; Percoidae;

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OC Mullidae; Mullus.
OX NCBI_TaxID=94224;
RN [1]_TaxID=94224;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aGoatfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134617; AAD54102.1; --
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 36
Q9PVC7 PRELIMINARY; PRT; 12 AA.
AC Q9PVC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Esoc lucius (Northern pike).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC Esocidae; Esoc.
OX NCBI_TaxID=8010;
RN [1]_TaxID=8010;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aPike;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134598; AAD54083.1; --
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 37
Q9PVC4 PRELIMINARY; PRT; 12 AA.
AC Q9PVC4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.

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OS Harpadon sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Aulipiformes; Synodontidae; Harpadontinae; Harpadon.  
OX NCBI\_TaxID=94310;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh49abduck; PubMed=10468597;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134601; AAD54086.1; --  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone.1.  
FT NON\_TER 1  
FT NON\_TER 12  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1529 MW; 97BESAE4C31B69A CRC64;  
Query Match 20.0%; Score 3; DB 13; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 KVE 10  
Db 8 KVE 10  
RESULT 38  
Q8SL43  
ID Q8SL43 PRELIMINARY; PRT; 13 AA.  
AC Q8SL43  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE beta-2 polypeptide (Pyrrophosphate-ENERGIZED) inorganic pyrophosphatase  
DE PsaA (Fragment).  
DE PsaA.  
GN PSBA.  
OS Aeonium spatulatum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Crassulaceae; Aeonium.  
OX NCBI\_TaxID=35956;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;  
RT "Evolution and diversification of the Macaronesian clade of  
Crassulaceae.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY082214; AAM13958.1; --  
KW Chloroplast.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 13 AA; 1313 MW; C0FB1B6DAD0ECB02 CRC64;  
Query Match 20.0%; Score 3; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 VEV 11  
Db 6 VEV 8  
RESULT 39  
Q8SL74  
ID Q8SL74 PRELIMINARY; PRT; 13 AA.  
AC Q8SL74;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE PsaA (Fragment).  
DE PsaA.  
GN PSBA.

OS Aichryson porphyrogenetos.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Saxifragales; Crassulaceae; Aichryson.  
OX NCBI\_TaxID=190205;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;  
RT "Evolution and diversification of the Macaronesian clade of  
Crassulaceae.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY082183; AAM13927.1; --  
KW Chloroplast.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 13 AA; 1313 MW; C0FB1B6DAD0ECB02 CRC64;  
Query Match 20.0%; Score 3; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 VEV 11  
Db 6 VEV 8  
RESULT 40  
Q9S941  
ID Q9S941 PRELIMINARY; PRT; 13 AA.  
AC Q9S941;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 23, Last annotation update)  
DE H(+)-translocating (pyrophosphate-ENERGIZED) inorganic pyrophosphatase  
DE beta-2 polypeptide (HC 3.6.1.1) (Fragment).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.  
OX NCBI\_TaxID=161934;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92179265; PubMed=1311852;  
RA Sarafian V., Kim Y., Poole R.J., Rea P.A.;  
RT "Molecular cloning and sequence of cDNA encoding the pyrophosphate-  
energized vacuolar membrane proton pump of Arabidopsis thaliana.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).  
SQ SEQUENCE 13 AA; 1243 MW; C9DB193C37C22AAD CRC64;  
Query Match 20.0%; Score 3; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 KVE 10  
Db 11 KVE 13  
RESULT 41  
Q9PVA0  
ID Q9PVA0 PRELIMINARY; PRT; 13 AA.  
AC Q9PVA0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Colisa lalia (dwarf gourami).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Anabantoidae; Belontiidae; Colisa.  
OX NCBI\_TaxID=50373;

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RN SEQUENCE FROM N.A.
RP STRAIN=Gh4aGouramy;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134625; AAD54110.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31B6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 42
Q9PVB1 ID Q9PVB1 PRELIMINARY; PRT; 13 AA.
AC Q9PVB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Dendrochirus zebra (zebra turkeyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Scorpaenoidae; Scorpaenidae; Dendrochirus.
OX NCBI_TaxID=94308;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aGouramy;
RA MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134614; AAD54099.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31B6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 43
Q9PV95 ID Q9PV95 PRELIMINARY; PRT; 13 AA.
AC Q9PV95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Mola mola (ocean sunfish).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Molidae; Mola.
OX NCBI_TaxID=94237;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aSunfish;
RA MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134630; AAD54115.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 44
Q9PVA7 ID Q9PVA7 PRELIMINARY; PRT; 13 AA.
AC Q9PVA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Growth hormone (fragment).
GN GH.
OS Dissostichus mawsoni (Antarctic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Dissostichus.
OX NCBI_TaxID=36200;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aTooth;
RA MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134618; AAD54103.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 45
Q9PVB3 ID Q9PVB3 PRELIMINARY; PRT; 13 AA.
AC Q9PVB3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
GN GH.
OS Hippocampus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Syngnathidae; Hippocampus.
OX NCBI_TaxID=72047;
RN [1]_TaxID=72047;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aseahorse;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134612; AAD54097.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

RESULT 46
Q9PV98
ID Q9PV98 PRELIMINARY; PRT; 13 AA.
AC Q9PV98;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Psettoodes sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Psettoidei; Psettoidae; Psettoodes.
OX NCBI_TaxID=94241;
RN [1]_TaxID=94241;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aFlatfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134627; AAD54112.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

RESULT 47
Q9PV97
ID Q9PV97 PRELIMINARY; PRT; 13 AA.
AC Q9PV97;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Balistes sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Balistidae; Balistes.
OX NCBI_TaxID=94230;
RN [1]_TaxID=94230;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aTrigger;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134628; AAD54113.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

RESULT 48
Q9PV92
ID Q9PV92 PRELIMINARY; PRT; 13 AA.
AC Q9PV92;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OC Mastacembelus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Mastacembelidae; Mastacembelus.
OX NCBI_TaxID=94235;
RN [1]_TaxID=94235;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aMasta;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134613; AAD54098.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

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QY      8 KVE 10
Db      8 KVE 10

RESULT 49
Q9PVA2 PRELIMINARY; PRT; 13 AA.
AC Q9PVA2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Thunnus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aTuna;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
    evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134623; AAD54100.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8B4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 50
Q9PVB0 PRELIMINARY; PRT; 13 AA.
AC Q9PVB0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Dicentrarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Dicentrarchus.
OX NCBI_TaxID=13489;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aseabass;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
    evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134615; AAD54100.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8B4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 51
Q9PVB4 PRELIMINARY; PRT; 13 AA.
AC Q9PVB4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Zeus faber (John Dory).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.
OX NCBI_TaxID=64108;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aDories;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
    evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134611; AAD54096.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8B4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 52
Q9PV99 PRELIMINARY; PRT; 13 AA.
AC Q9PV99;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Channa sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Channoidae;
OC Channidae; Channa.
OX NCBI_TaxID=94222;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4amurrel;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
    evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134626; AAD54111.1; -.
DR InterPro; IPR001400; Somatotropin.

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DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      |||
        8 KVE 10

RESULT 53
Q9PVA5 PRELIMINARY; PRT; 13 AA.
AC Q9PVA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Cryptocentrus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Gobioidae;
OC Gobiidae; Cryptocentrus.
OX NCBI_TaxID=94314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4ablenny;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134620; AAD54105.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      |||
        8 KVE 10

RESULT 54
Q9PVA3 PRELIMINARY; PRT; 13 AA.
AC Q9PVA3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Acanthurus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes;
OC Acanthuroidei; Acanthuridae; Acanthurus.
OX NCBI_TaxID=94220;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4asurgon;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;

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RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134622; AAD54107.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      |||
        8 KVE 10

RESULT 55
Q9PVA9 PRELIMINARY; PRT; 13 AA.
AC Q9PVA9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Epinephelus coioides (Orange-spotted grouper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percioidae;
OC Serranidae; Epinephelus.
OX NCBI_TaxID=94232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4Agrouper;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134616; AAD54101.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      |||
        8 KVE 10

RESULT 56
Q9PVC5 PRELIMINARY; PRT; 13 AA.
AC Q9PVC5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aGag1;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134620; AAD54085.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 8 KVE 10

RESULT 57
Q9PVA4
ID Q9PVA4 PRELIMINARY; PRT; 13 AA.
AC Q9PVA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Siganus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes;
OC Acanthuroidei; Siganidae; Siganus.
OX NCBI_TaxID=94227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aRabbitfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134621; AAD54106.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 8 KVE 10

RESULT 58
Q9PVA1
ID Q9PVA1 PRELIMINARY; PRT; 13 AA.
AC Q9PVA1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Stromateus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes;
OC Stromateoidei; Stromateidae; Stromateus.
OX NCBI_TaxID=94245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aPomfret;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134624; AAD54109.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 8 KVE 10

RESULT 59
Q9PV96
ID Q9PV96 PRELIMINARY; PRT; 13 AA.
AC Q9PV96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Ostracion sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Ostraciidae; Ostracion.
OX NCBI_TaxID=94239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aBoxfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134629; AAD54114.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 8 KVE 10

RESULT 60
Q9PVB5
ID Q9PVB5 PRELIMINARY; PRT; 13 AA.
AC Q9PVB5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Sargocentron sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;  
OC Sargocentron.  
OX NCBI\_TaxID=94226;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aFundulus;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134610; AAD54095.1; -.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;  
Query Match 20.0%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KVE 10  
Db 8 KVE 10

RESULT 61  
Q9PVB7  
ID Q9PVB7 PRELIMINARY; PRT; 13 AA.  
AC Q9PVB7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Fundulus heteroclitus (Killifish) (Mummichog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Cyprinodontiformes; Fundulidae; Fundulus.  
OX NCBI\_TaxID=8078;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aFundulus;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134608; AAD54093.1; -.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;  
Query Match 20.0%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KVE 10  
Db 8 KVE 10

RESULT 62

Q9PVB6  
ID Q9PVB6 PRELIMINARY; PRT; 13 AA.  
AC Q9PVB6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Poecilia latipinna.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Cyprinodontiformes; Poeciliidae; Poecilia.  
OX NCBI\_TaxID=48699;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aMolly;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134609; AAD54094.1; -.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;  
Query Match 20.0%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KVE 10  
Db 8 KVE 10

RESULT 63  
Q9PVA6  
ID Q9PVA6 PRELIMINARY; PRT; 13 AA.  
AC Q9PVA6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Salarias sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Blennioidei;  
OC Blennioidei; Salarias.  
OX NCBI\_TaxID=94312;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gh4aGoby;  
RX MEDLINE=99398697; PubMed=10468597;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF134619; AAD54104.1; -.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; hormone; 1.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;  
Query Match 20.0%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 KVE 10



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DE NF2 protein (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94348501; PubMed=8069299;
RA Arakawa H., Hayashi N., Nagase H., Ogawa M., Nakamura Y.;
RT "Alternative splicing of the NF2 gene and its mutation analysis of
RT breast and colorectal cancers.";
RL Hum. Mol. Genet. 3:565-568(1994).
DR EMBL; S73855; AAD14139.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1513 MW; 82766855653CBB2A CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
DB 1 LKP 3

RESULT 69
Q96Q62 PRELIMINARY; PRT; 14 AA.
ID Q96Q62
AC Q96Q62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial ribosomal protein S11 (Fragment).
GN MRPS11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429115; PubMed=11543634;
RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
RA Watanabe K., Tanaka T.;
RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
RT to the chromosomes and implications for human disorders.";
RL Genomics 77:65-70(2001).
DR EMBL; AB051349; BAB54939.2; -.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1585 MW; C07121F2234438DD CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 2 KVE 4

RESULT 70
Q13022 PRELIMINARY; PRT; 14 AA.
ID Q13022
AC Q13022;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Prohibitin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17179; AAA86691.1; -.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1586 MW; EFA1DA48DB1B3BC1 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
DB 8 VEV 10

RESULT 71
O55249 PRELIMINARY; PRT; 14 AA.
ID O55249
AC O55249;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RegB protein (Fragment).
GN REGB.
OS Bacteriophage T6.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
ON NCBI_TaxID=10656;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T6;
RX MEDLINE=94357192; PubMed=8076614;
RA Repoila F., Tetaert F., Bouet J., Krusch H.M.;
RT "Genomic polymorphism in the T-even bacteriophages.";
RL EMBO J. 13:4181-4192(1994).
DR EMBL; Z35074; CAA84449.1; -.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1735 MW; DC726CF8795B60D2 CRC64;

Query Match 20.0%; Score 3; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
DB 6 EVF 8

RESULT 72
Q9QVF3 PRELIMINARY; PRT; 14 AA.
ID Q9QVF3
AC Q9QVF3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRANSFERRIN-PEPTIDE 35 (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-

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RT  metastasizing tumor cells: identification as transferrin." ;
RL  J. Cell. Biochem. 47:261-271(1991).
DR  InterPro; IPR001156; Transferrin.
DR  Pfam; PF00405; transferrin; 1.
FT  NON_TER 1
FT  NON_TER 14 14
SQ  SEQUENCE 14 AA; 1499 MW; 01AE8289E54E3224 CRC64;

Query Match      20.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LKP 3
Db  8 LKP 10

RESULT 73
Q84072      PRELIMINARY; PRT; 14 AA.
ID  Q84072
AC  Q84072;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Influenza A/fpv/rostock/34 (H7n1), polymerase 1 (Seg 2), 3' end of
DE  vrna (Initiator region for protein coding) (Fragment).
OS  Influenzavirus A.
OC  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC  Influenza A viruses.
OX  NCBI_TaxID=197911;
RN  [1]
RP  SEQUENCE FROM N.A. PubMed=493121;
RX  MEDLINE=80034428; PubMed=493121;
RA  Robertson J.S.;
RT  "5' and 3' terminal nucleotide sequences of the rna genome segments of
RL  influenza virus.";
RL  Nucleic Acids Res. 6:3745-3757(1979).
DR  EMBL; J02119; AAA43580.1; -.
DR  InterPro; IPR001407; Flu_Pbl.
DR  Pfam; PF00602; Flu_Pbl; 1.
FT  NON_TER 14 14
SQ  SEQUENCE 14 AA; 1558 MW; 41863E77ED22FE27 CRC64;

Query Match      20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  7 LKV 9
Db  10 LKV 12

RESULT 74
O54298      PRELIMINARY; PRT; 15 AA.
ID  O54298
AC  O54298;
DT  01-JUN-1998 (TrEMBLrel. 06, Created)
DT  01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  RNA polymerase alpha subunit (Fragment).
GN  RPOA.
OS  Salmonella typhimurium.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Salmonella.
OX  NCBI_TaxID=602;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=LT2;
RX  MEDLINE=98188310; PubMed=9520473;
RA  Bjorkman J., Hughes D., Andersson D.;
RT  "Virulence of antibiotic resistant Salmonella typhimurium.";
RL  Proc. Natl. Acad. Sci. U.S.A. 95:3949-3953(1998).
DR  EMBL; AJ223236; CAA11204.1; -.

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ET  NON_TER 15 15
SQ  SEQUENCE 15 AA; 1720 MW; D1E381FC9FBC3D10 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LKP 3
Db  9 LKP 11

RESULT 75
Q52304      PRELIMINARY; PRT; 15 AA.
ID  Q52304
AC  Q52304; Q52634;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE  TRAL protein (Fragment).
OS  Escherichia coli.
OC  Plasmid IncFII R1, and Plasmid IncFII R1-19 (R1 drd-19).
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86059219; PubMed=2999074;
RA  Frost L.S., Finlay B.B., Opgenorth A., Paranchych W., Lee J.S.;
RT  "Characterization and sequence analysis of pilin from F-like
RT  plasmids";
RL  J. Bacteriol. 164:1238-1247(1985).
DR  EMBL; M19710; AAA92660.1; -.
DR  EMBL; K03091; AAA92757.1; -.
KW  Plasmid.
FT  NON_TER 15 15
SQ  SEQUENCE 15 AA; 1844 MW; 5CCA91188EB3511A CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6 KLK 8
Db  8 KLK 10

Search completed: November 25, 2003, 18:25:25
Job time : 38.1936 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 48.5904 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-8  
Perfect score: 15  
Sequence: 1 LKPPFKLKEVFPFP 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Colostrinin derive
2	15	100.0	15	22	Colostrinin peptid
3	15	100.0	15	22	Colostrinin peptid
4	15	100.0	15	22	Ewe colostrinin pe
5	15	100.0	15	23	Colostrinin consti
6	15	100.0	15	23	Colostrinin consti
7	15	100.0	15	23	Neural cell regula
8	15	100.0	16	22	Ewe colostrinin pe
9	7	46.7	10	22	Colostrinin peptid

11	22	AAE07198	Modified colostrin
9	21	AAE07257	Peptide encoded by
9	23	ABJ01751	158PID7 related HL
9	23	ABJ01752	158PID7 related HL
9	23	ABJ01851	158PID7 related HL
9	23	ABJ01855	158PID7 related HL
9	23	ABJ01996	158PID7 related HL
10	23	ABJ01366	158PID7 related HL
10	23	ABJ01907	158PID7 related HL
10	23	ABJ01929	158PID7 related HL
11	19	AAW48881	Cyclic peptide gra
16	21	AAW59323	Tyrosine phosphata
16	24	ABP82437	G protein-coupled
17	24	ABP82437	G protein-coupled
17	24	ABP83371	G protein-coupled
19	24	ABP83371	G protein-coupled
5	19	AAW65794	Polypolyol inhibit
6	23	AAE22869	Carrot red leaf lu
7	20	AAW49731	Compact structure
7	23	ABG32211	Sheep colostrinin
7	23	ABB77133	Classical swine fe
7	23	ABB07085	Hepatitis C virus
8	15	AAE59968	Peptide signal seq
9	17	AAW07412	Antibacterial/anti
9	17	AAW07413	Antibacterial/anti
9	17	AAW07414	Antibacterial/anti
9	17	AAW07415	Antibacterial/anti
9	22	ABB14478	Human C35 peptide
9	22	AAE91625	Opioind peptide SEQ
9	22	AAE76273	Influenza virus im
9	23	AAE31250	Human mace9 peptid
9	23	ABJ01633	158PID7 related HL
9	23	ABB79424	Human MMP-2 PEX pe
10	17	AAE91324	Dynorphin A analog
10	22	AAW43031	Mycoplasma genital
10	22	AAE83581	Arabidopsis thalia
10	22	AAE84280	Arabidopsis thalia
10	22	AAE85870	Saccharomyces cere
10	22	AAE88260	Saccharomyces cere
10	22	AAE88261	Saccharomyces cere
10	22	AAE88262	Saccharomyces cere
10	22	AAE88263	Saccharomyces cere
10	22	AAE91622	Opioind peptide SEQ
10	23	ABG63388	Vascular response-
10	23	ABG63566	Human CRPI tryptic
10	23	ABJ01599	158PID7 related HL
10	23	ABJ01656	158PID7 related HL
10	24	ABR47212	Staphylococcus aur
10	24	ABR47212	Staphylococcus aur
10	24	ABR47279	Staphylococcus aur
10	24	ABR47286	Staphylococcus aur
10	24	ABR47290	Staphylococcus aur
11	15	AAE45216	Des-Tyr Dynorphin
11	17	AAE91341	Dynorphin A analog
11	17	AAE91323	Dynorphin A analog
11	19	AAE65968	Des-Tyr-Gly dynorp
11	21	AAE15261	Specific factor VI
11	21	AAE15262	Specific factor VI
11	21	AAE15263	Specific factor VI
11	21	AAE15264	Specific factor VI
11	21	AAE15266	Specific factor VI
11	22	AAE02349	Caenorhabditis ele
11	22	AAE91600	Opioind peptide SEQ
11	22	AAE91619	Opioind peptide SEQ
11	22	AAE91621	Opioind peptide SEQ
12	2	AAE10402	Analgesic peptide.
12	15	AAE45205	des-Tyr Dynorphin
12	15	AAE45215	des-Tyr Dynorphin
12	17	AAE91340	Dynorphin A analog
12	17	AAE91331	Dynorphin A analog
12	17	AAE91322	Dynorphin A analog
12	19	AAE65958	Des-Tyr dynorphin
12	19	AAE65957	Des-Tyr-Gly dynorp
12	20	AAE02595	Dynorphin analogue
12	21	AAE30277	CD4+ T-cell activa

83 Human chemokine de  
84 Opioid peptide SEQ  
85 Opioid peptide SEQ  
86 Opioid peptide SEQ  
87 Opioid peptide SEQ  
88 Opioid peptide SEQ  
89 Protease Cleavage  
90 Tumour necrosis fa  
91 Tumour necrosis fa  
92 Analgesic peptide.  
93 Analgesic peptide.  
94 Sequence of dynorp  
95 des-Tyr Dynorphin  
96 des-Tyr Dynorphin  
97 Dynorphin A(1-13)  
98 Dynorphin-A. Synt  
99 Dynorphin A analog  
100 Dynorphin A analog

ALIGNMENTS

RESULT 1  
AAB72253  
ID AAB72253 standard; peptide; 15 AA.  
XX  
AC AAB72253;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 8.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
FN WO20011937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22818.  
XX  
PR 17-AUG-1999; 99US-0149311.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGG-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2001-202804/20.  
XX  
PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX  
PS Claim 1; Page 34; 50pp; English.  
XX  
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;  
Query Match 100.0%; Score 15; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LKPPPKLKVEVFPFP 15  
Db 1 LKPPPKLKVEVFPFP 15  
RESULT 2  
AAB72507  
ID AAB72507 standard; Peptide; 15 AA.  
XX  
AC AAB72507;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #8.  
XX  
KW Dermatological; oxidative stress regulator; colostrinin.  
XX  
OS Unidentified.  
XX  
FN WO200112650-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22665.  
XX  
PR 17-AUG-1999; 99US-0149310.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2001-218342/22.  
XX  
PT Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX  
PS Claim 6; Page 25; 48pp; English.  
XX  
CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 15; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LKPPPKLKVEVFPFP 15  
Db 1 LKPPPKLKVEVFPFP 15  
RESULT 3  
AAB72539  
ID AAB72539 standard; Peptide; 15 AA.  
XX  
AC AAB72539;  
XX  
DT 09-MAY-2001 (first entry)  
XX

DE Colostrinin peptide #8.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US222774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 PT  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKPPFKLKVEVFPFP 15  
 DB 1 LKPPFKLKVEVFPFP 15  
 1 LKPPFKLKVEVFPFP 15  
 1 LKPPFKLKVEVFPFP 15  
 RESULT 4  
 AAB59313  
 ID AAB59313 standard; Peptide; 15 AA.  
 XX  
 AC AAB59313;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment A-4.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 XX WO200075173-A2.  
 PN  
 XX 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REG-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKPPFKLKVEVFPFP 15  
 DB 1 LKPPFKLKVEVFPFP 15  
 1 LKPPFKLKVEVFPFP 15  
 1 LKPPFKLKVEVFPFP 15  
 RESULT 5  
 AAE20235  
 ID AAE20235 standard; peptide; 15 AA.  
 XX  
 AC AAE20235;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #8.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22776.  
 XX  
 PR 17-AUG-2000; 2000WO-US22776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPPKLKVEVFPP 15  
 |||||  
 Db 1 LKPPPKLKVEVFPP 15

RESULT 6  
 AAM51043  
 ID AAM51043 standard; Peptide: 15 AA.

XX AC AAM51043;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide.

XX DE Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 15 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX PD 21-FEB-2002.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patient. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-6 and interleukin-10.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPPKLKVEVFPP 15  
 |||||  
 Db 1 LKPPPKLKVEVFPP 15

RESULT 7  
 AAO14584

ID AAO14584 standard; peptide; 15 AA.

XX AC AAO14584;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 8.

XX DE Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 15 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX PD 21-FEB-2002.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid



CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPPKLKVEVFPFP 15  
 |||||  
 Db 1 LKPPPKLKVEVFPFP 15

RESULT 8  
 AAB59344  
 ID AAB59344 standard; Peptide; 16 AA.  
 XX AC AAB59344;  
 XX DT 21-MAR-2001 (first entry)  
 XX DE Ewe colostrinin peptide fragment derived sequence #4.  
 XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX OS Ovis sp.  
 XX PN WO200075173-A2.  
 XX PD 14-DEC-2000.  
 XX PF 02-JUN-2000; 200WO-GB02128.  
 XX PR 02-JUN-1999; 99GB-0012852.  
 XX PA (REG-) REGEN THERAPEUTICS PLC.  
 XX PI Georgiades JA;  
 XX DR WPI; 2001-071058/08.  
 XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX Claim 8; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

SQ Sequence 16 AA;

Query Match 100.0%; Score 15; DB 22; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPPKLKVEVFPFP 15  
 |||||  
 Db 2 LKPPPKLKVEVFPFP 16

RESULT 9  
 AAE07188  
 ID AAE07188 standard; peptide; 10 AA.

XX AAE07188;  
 XX 06-NOV-2001 (first entry)  
 XX Colostrinin peptide 4.  
 XX Colostrinin; nontropic; neuroprotective; immunomodulatory; antibacterial;  
 XX Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 XX KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 XX antiviral.  
 XX Unidentified.  
 OS WO200155199-A1.  
 XX PN 02-AUG-2001.  
 XX PD 26-JAN-2001; 2001WO-GB00329.  
 XX PF 26-JAN-2000; 2000GB-0001825.  
 XX PR (REG-) REGEN THERAPEUTICS PLC.  
 XX PA Georgiades JA;  
 XX PI WPI; 2001-488775/53.  
 XX DR Peptide useful as an inter alia in the treatment of e.g. disorders of  
 XX the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -  
 XX Claim 1; Page 15; 40pp; English.

CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the developmental of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 4 related to the invention.

SQ Sequence 10 AA;

Query Match 46.7%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PCLKVEV 11  
 |||||  
 Db 1 PCLKVEV 7

RESULT 10  
 AAE07198  
 ID AAE07198 standard; peptide; 11 AA.  
 XX AC AAE07198;

XX 06-NOV-2001 (first entry)  
 XX Modified colostrinin cyclic peptide #4.  
 XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 XX Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 XX central nervous system disorder; neurodegenerative disorder; weight loss;  
 XX beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 XX acquired immunological deficiency; neurological disorder; dementia;  
 XX antiviral; cyclic.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX Modified-site 1  
 XX /note= "N-terminal acetyl"; this residue forms a cyclic  
 XX linkage with Pro found at the C-terminal end"  
 XX WO200155199-A1.  
 XX 02-AUG-2001.  
 XX 26-JAN-2001; 2001WO-GB00329.  
 XX 26-JAN-2000; 2000GB-0001825.  
 XX (REG- ) REGEN THERAPEUTICS PLC.  
 XX Georgiades JA;  
 XX WPI; 2001-486775/53.  
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 XX the immune system and the central nervous system comprises ten  
 XX amino-terminal amino acid sequence derived from peptides present in  
 XX colostrinin -  
 XX Example 2; Page 8; 40pp; English.  
 XX The invention relates to colostrinin peptide fragments which are useful,  
 XX inter alia, in the treatment of chronic disorders of the immune system  
 XX and the central nervous system. Colostrinin peptides are used as a  
 XX medicament in the treatment of neurological disorders e.g., dementia,  
 XX neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 XX disease e.g., Parkinson's disease, mental disorders e.g., psychosis and  
 XX neurosis, in acquired immunological deficiencies, chronic bacterial and  
 XX viral infections and diseases characterised by the presence of beta-  
 XX amyloid plaques and as a dietary supplement for babies, small children,  
 XX adults and senile persons, who have been subjected to chemotherapy or  
 XX have suffered from cachexia or weight loss due to the chronic disease.  
 XX Colostrinin peptides are also used as food additives and as an auxiliary  
 XX withdrawal treatment for drug addicts, after a period of detoxification  
 XX and in persons dependent on stimulants. Colostrinin peptides are used to  
 XX prepare antibodies and to treat emotional disturbances, e.g. emotional  
 XX disturbances of psychiatric patients in a state of depression. These  
 XX colostrinin peptides improves the development of immune system in a new  
 XX born child and to correct the immunological deficiencies in a child.  
 XX The present sequence is modified colostrinin cyclic peptide #4 related to  
 XX the invention.  
 XX Sequence 11 AA;  
 XX  
 XX Query Match 46.7%; Score 7; DB 22; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 0.54;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 5 PKLKVEV 11  
 XX | | | | |  
 XX Db 2 PKLKVEV 8  
 XX  
 XX RESULT 11

AAV70257  
 ID AAV70257 standard; peptide; 9 AA.  
 XX  
 AC AAV70257;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Peptide encoded by forward primer-2 for human Fc-Angiostatin immunofusin.  
 XX  
 KW Human; immunoglobulin gamma Fc fragment; angiostatin; immunofusin;  
 KW angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic;  
 KW antipsoriatic; antidiabetic; ophthalmological; immunosuppressant;  
 KW vasotropic; vulnery; treatment; antiarteriosclerosis; tumour;  
 KW metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;  
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;  
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;  
 KW wound granulation; keloid scar; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200011033-A2.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 25-AUG-1999; 99WO-US19329.  
 XX  
 PR 25-AUG-1998; 98US-0097883.  
 XX  
 PA (LEXI-) LEXINGEN PHARM CORP.  
 XX  
 PI Lo K, Li Y, Gillies SD;  
 XX  
 DR WPI; 2000-237616/20.  
 XX  
 DR N-PSDB; AA251297.  
 XX  
 PT Novel fusion protein of angiostatin or endostatin and an immunoglobulin  
 XX FC region, useful for treating conditions mediated by angiogenesis,  
 XX such as rheumatoid arthritis, tumors and macular degeneration -  
 XX  
 PS Example 4; Page 47; 68pp; English.  
 XX  
 CC The patent discloses a DNA molecule encoding a fusion protein comprising  
 CC a signal sequence, an immunoglobulin Fc region, and an angiogenesis  
 CC inhibitor selected from angiostatin, endostatin, a plasminogen fragment  
 CC having angiostatin activity, a collagen XVIII fragment having endostatin  
 CC activity, or combinations of them. The fusion protein (immunofusin) is  
 CC used to inhibit angiogenesis and to treat diseases or conditions mediated  
 CC by angiogenesis. Conditions that may be treated include solid tumours,  
 CC blood born tumours, tumour metastasis, benign tumours including  
 CC haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic  
 CC granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases  
 CC degeneration, corneal graft rejection, neovascular glaucoma, retrolental  
 CC fibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis,  
 CC plaque neovascularisation, telangiectasia, haemophilic joints,  
 CC angiofibroma, wound granulation, and excessive or abnormal stimulation of  
 CC endothelial cells, intestinal cells, atherosclerosis, scleroderma and  
 CC hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in  
 CC gene therapy. The present sequence is a peptide encoded by forward primer  
 CC used in the construction of immunofusin comprising human immunoglobulin  
 CC gamma (IgG) Fc fragment and human angiostatin (Fc-Angio fusion protein).  
 XX  
 SQ Sequence 9 AA;  
 XX  
 XX Query Match 33.3%; Score 5; DB 21; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 5 PKLKV 9  
 XX | | | | |  
 XX Db 1 PKLKV 5

```

RESULT 12'
ABJ01751
ID  ABOJ1751 standard; Peptide; 9 AA.
XX
AC  ABOJ1751;
XX
DT  19-SEP-2002 (first entry)
XX
DE  158P1D7 related HLA peptide SEQ ID No 451.
XX
KW  Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW  HLA.
XX
OS  Homo sapiens.
XX
PN  WO200216593-A2.
XX
PD  28-FEB-2002.
XX
PF  22-AUG-2001; 2001WO-US26276.
XX
PR  22-AUG-2000; 2000US-227098P.
XX
PT  10-APR-2001; 2001US-282739P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI  Challita-eid PM, Jakobovits A;
XX
DR  WPI; 2002-425659/45.
XX
PT  New compositions comprising a gene (designated 158P1D7), its encoded
PT  protein or their modulators, useful for treating or diagnosing cancers,
PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT  or humans)
XX
PS  Disclosure; Page 142; 181pp; English.
XX
CC  The invention relates to a novel nucleic acid, designated 158P1D7. The
CC  compositions are useful for treating or diagnosing cancers, particularly
CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC  horses or humans). The compositions are also useful for monitoring
CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC  of the invention can be used in gene therapy to treat the said disorders.
CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
CC  to the 158P1D7 protein of the invention.
XX
SQ  Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  5 PRLKV 9
Db  4 PRLKV 8

RESULT 13
ABJ01752
ID  ABOJ1752 standard; Peptide; 9 AA.
XX
AC  ABOJ1752;
XX
DT  19-SEP-2002 (first entry)
XX
DE  158P1D7 related HLA peptide SEQ ID No 452.
XX
KW  Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW  HLA.
XX
PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;

```

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OS  Homo sapiens.
XX
PN  WO200216593-A2.
XX
PD  28-FEB-2002.
XX
PF  22-AUG-2001; 2001WO-US26276.
XX
PR  22-AUG-2000; 2000US-227098P.
XX
PT  10-APR-2001; 2001US-282739P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI  Challita-eid PM, Jakobovits A;
XX
DR  WPI; 2002-425659/45.
XX
PT  New compositions comprising a gene (designated 158P1D7), its encoded
PT  protein or their modulators, useful for treating or diagnosing cancers,
PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT  or humans)
XX
PS  Disclosure; Page 142; 181pp; English.
XX
CC  The invention relates to a novel nucleic acid, designated 158P1D7. The
CC  compositions are useful for treating or diagnosing cancers, particularly
CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC  horses or humans). The compositions are also useful for monitoring
CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC  of the invention can be used in gene therapy to treat the said disorders.
CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
CC  to the 158P1D7 protein of the invention.
XX
SQ  Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  5 PRLKV 9
Db  2 PRLKV 6

RESULT 14
ABJ01851
ID  ABOJ1851 standard; Peptide; 9 AA.
XX
AC  ABOJ1851;
XX
DT  19-SEP-2002 (first entry)
XX
DE  158P1D7 related HLA peptide SEQ ID No 551.
XX
KW  Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW  HLA.
XX
OS  Homo sapiens.
XX
PN  WO200216593-A2.
XX
PD  28-FEB-2002.
XX
PF  22-AUG-2001; 2001WO-US26276.
XX
PR  22-AUG-2000; 2000US-227098P.
XX
PT  10-APR-2001; 2001US-282739P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;

```

```

PI Challita-eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT or humans)
XX
PS Disclosure; Page 146; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6
|||||

RESULT 15
ABJ01855
ID ABJ01855 standard; Peptide; 9 AA.
XX
AC ABJ01855;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide SEQ ID No 555.
XX
DE Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26276.
XX
PR 22-AUG-2000; 2000US-227098P.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
XX Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid PM, Jakobovits A;
XX WPI; 2002-425659/45.
XX
XX New compositions comprising a gene (designated 158PID7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans)
XX
PS Disclosure; Page 146; 181pp; English.
XX
XX The invention relates to a novel nucleic acid, designated 158PID7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6
|||||

RESULT 16
ABJ01996
ID ABJ01996 standard; Peptide; 9 AA.
XX
AC ABJ01996;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide #37.
XX
DE Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26276.
XX
PR 22-AUG-2000; 2000US-227098P.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
XX Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid PM, Jakobovits A;
XX WPI; 2002-425659/45.
XX
XX New compositions comprising a gene (designated 158PID7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans)
XX
PS Disclosure; Page 140; 181pp; English.
XX
XX The invention relates to a novel nucleic acid, designated 158PID7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
|||||

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```

CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 4 PKLKV 8
|||||

RESULT 16
ABJ01996
ID ABJ01996 standard; Peptide; 9 AA.
XX
AC ABJ01996;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide #37.
XX
DE Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26276.
XX
PR 22-AUG-2000; 2000US-227098P.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
XX Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid PM, Jakobovits A;
XX WPI; 2002-425659/45.
XX
XX New compositions comprising a gene (designated 158PID7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans)
XX
PS Disclosure; Page 140; 181pp; English.
XX
XX The invention relates to a novel nucleic acid, designated 158PID7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
|||||

```

```

Db      .      4 PKLKV 8

RESULT 17
ABJ01366
ID  ABJ01366 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01366;
XX
XX  DT  19-SEP-2002 (first entry)
XX
XX  DE  158PID7 related HLA peptide SEQ ID No 66.
XX
XX  KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200216593-A2.
XX
XX  PD  28-FEB-2002.
XX
XX  PF  22-AUG-2001; 2001WO-US26276.
XX
XX  PR  22-AUG-2000; 2000US-227098P.
XX
XX  PR  10-APR-2001; 2001US-282739P.
XX
XX  PA  (AGEN-) AGENSYS INC.
XX
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX  PI  Challita-eid PM, Jakobovits A;
XX
XX  DR  WPI; 2002-425659/45.
XX
XX  PT  New compositions comprising a gene (designated 158PID7), its encoded
XX  PT  protein or their modulators, useful for treating or diagnosing cancers,
XX  PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX  PS  or humans) -
XX
XX  PS  Disclosure; Page 147; 181pp; English.
XX
XX  CC  The invention relates to a novel nucleic acid, designated 158PID7. The
XX  CC  compositions are useful for treating or diagnosing cancers, particularly
XX  CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX  CC  horses or humans). The compositions are also useful for monitoring
XX  CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX  CC  of the invention can be used in gene therapy to treat the said disorders.
XX  CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
XX  CC  to the 158PID7 protein of the invention.
XX
XX  SQ  Sequence 10 AA;

Query Match      33.3%; Score 5; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      |||||
        4 PKLKV 8

RESULT 19
ABJ01929
ID  ABJ01929 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01929;
XX
XX  DT  19-SEP-2002 (first entry)
XX
XX  DE  158PID7 related HLA peptide SEQ ID No 629.
XX
XX  KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200216593-A2.
XX
XX  PD  28-FEB-2002.
XX
XX  PF  22-AUG-2001; 2001WO-US26276.
XX
XX  PR  22-AUG-2000; 2000US-227098P.
XX
XX  PR  10-APR-2001; 2001US-282739P.
XX
XX
XX

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CC islet-cell transplant to alleviate their pre-existing diabetes. The  
 CC peptides can be used therapeutically to protect against or ameliorate the  
 CC symptoms associated with type 1 diabetes. The vaccines can be used for  
 CC raising an immune response against Rotavirus. T-cell epitopes in  
 CC autoantigens have potential diagnostic and therapeutic applications and  
 CC may hold clues to environmental agents that could trigger or exacerbate  
 CC autoimmune diseases. The present invention identified T-cell epitopes  
 CC that may provide such clues.

XX Sequence 16 AA;

Query Match 33.3%; Score 5; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLVKE 10  
 |||||

Db 8 KLVKE 12

RESULT 22

ABP82437

ID ABP82437 standard; Peptide; 16 AA.

XX

AC ABP82437;

XX

DT 04-MAR-2003 (first entry)

XX

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1110.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US50107.

XX

PR 19-DEC-2000; 2000US-257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases

XX

PS Claim 1; Fig 2; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific

CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.

SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 24; Length 16;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPFPK 6

|||||

Db 9 KPFPK 13

RESULT 23

AAB30278

ID AAB30278 standard; Peptide; 17 AA.

XX

AC AAB30278;

XX

DT 12-FEB-2001 (first entry)

XX

DE CD4+ T-cell activation methods peptide ligand #40.

XX

KW CD4+ T-cell activation; peptide epitope; autoimmune disease;  
 KW infectious disease; cancer; immunological mass fingerprinting.

XX

OS Synthetic.

XX

PN WO200063702-A1.

XX

PD 26-OCT-2000.

XX

PF 20-APR-2000; 2000WO-US10888.

XX

PR 21-APR-1999; 99US-0130355.

XX

PR 21-APR-1999; 99US-0295868.

XX

PA (ZYCO-) ZYCOS INC.

XX

PA (UNLO) KINGS COLLEGE LONDON.

XX

PI Peakman M, Chicx RM;

XX

DR WPI; 2000-665270/64.

XX

PT Identifying a class II major histocompatibility complex-binding fragment-

XX

PT of a polypeptide useful for diagnosing and protecting against diabetes  
 PT comprises contacting a ligand, a polypeptide and a mammalian antigen  
 PT presenting cell

XX

PS Claim 35; Page 96; 118pp; English.

XX

CC The present invention is concerned with a method, designated  
 CC immunological mass fingerprinting, which enables the identification of  
 CC peptide epitopes that activate CD4+ T-cells. Peptides of this kind are  
 CC also given. CD4+ cells are involved in the pathogenesis of disease, and  
 CC the peptides can be used in the prevention and treatment of autoimmune  
 CC diseases such as diabetes, multiple sclerosis, rheumatoid arthritis,





CC disorder leading to neurodegeneration, notably Alzheimer's and  
CC Parkinson's diseases, or anyotropic lateral sclerosis. The neurotrophic  
CC compounds avoid the side effects of immunosuppressant drugs, including  
CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,  
CC involuntary tremors, headaches, and hypertension. They are also free from  
CC the difficulties in delivery and bioavailability of large molecular  
CC weight proteins. The present sequence represents a specifically claimed  
CC neurotrophic compound.  
XX  
SQ Sequence 5 AA;  
  
Query Match 26.7%; Score 4; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 PFPK 6  
Db 2 PFPK 5  
|||||  
  
RESULT 26  
AAE22869  
ID AAE22869 standard; peptide; 6 AA.  
AC AAE22869;  
XX  
XX 09-AUG-2002 (first entry)  
XX  
XX Carrot red leaf luteovirus (CRLV) peptide motif #2.  
XX  
XX Carrot red leaf luteovirus; CRLV; potato leaf roll polerovirus; PLRV;  
KW barley yellow dwarf virus; BYDV; beet Western yellow virus; BWVY;  
KW luteovirus detection.  
XX  
XX Carrot red leaf luteovirus.  
XX  
XX WO200222868-A2.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-GB04053.  
XX  
XX 14-SEP-2000; 2000GB-0022505.  
XX  
XX (NATU-) NATURAL ENVIRONMENT RES COUNCIL.  
XX  
XX Cooper JI, Naylor M;  
XX  
XX WPI; 2002-393973/42.  
XX  
XX  
XX Primer useful in diagnosing the presence of luteovirus sequences in  
XX plant tissue, is capable of hybridizing to conserved regions of nucleic  
XX acid for e.g. carrot red leaf luteovirus and barley yellow dwarf virus  
XX  
XX  
XX Claim 7; Page 17; 29pp; English.  
XX  
XX The invention relates to a method for detecting luteoviruses and primers  
XX capable of hybridizing to conserved regions of nucleic acids of  
XX carrot red leaf luteovirus (CRLV), potato leaf roll polerovirus (PLRV),  
XX barley yellow dwarf virus (BYDV) and beet Western yellow virus (BWVY).  
XX These primers are useful for diagnosing the presence of a luteovirus  
XX sequence in a plant tissue nucleic acid sample. The method comprises  
XX treating the nucleic acid with a first polymerase chain reaction (PCR)  
XX primer, preferably CL2, to obtain a DNA product, treating the DNA  
XX product with one or more second PCR primers, preferably a mixture of  
XX CL1 and CL2 to obtain a PCR product, and comparing the nucleotide  
XX sequence or corresponding amino acid sequence of the PCR product with  
XX a known nucleotide sequence or corresponding amino acid sequence  
XX characteristics of the luteovirus. The primers of the invention are  
XX also useful for diagnosing the presence of CRLV or PLRV sequences in  
XX a plant tissue, where the second PCR primers used are CL1 and CL3.  
XX The present sequence is CRLV peptide motif.

XX  
SQ Sequence 6 AA;  
  
Query Match 26.7%; Score 4; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KVEV 11  
Db 3 KVEV 6  
|||||  
  
RESULT 27  
AAV49731  
ID AAV49731 standard; peptide; 7 AA.  
XX  
XX AAV49731;  
XX  
XX 19-JAN-2000 (first entry)  
XX  
XX Compact structure forming exemplification peptide #24.  
XX  
XX Compact structure forming peptide; dimerisation; stability; scaffold;  
KW library screening; drug screening; gene therapy.  
KW  
XX Synthetic.  
XX  
XX WO9951625-A2.  
XX  
XX 14-OCT-1999.  
XX  
XX 02-APR-1999; 99WO-US07374.  
XX  
XX 02-APR-1998; 98US-0080444.  
XX  
XX (RIGE-) RIGEL PHARM INC.  
XX  
XX Anderson D;  
XX  
XX WPI; 1999-620191/53.  
XX  
XX Novel dimerization peptides which self-associate are used with other  
XX proteins to effect the formation of compact structures -  
XX  
XX Disclosure; Page 8; 75pp; English.  
XX  
XX The present invention describes peptides which have a moderate or high  
XX affinity for each other, when added as extensions to both the N-terminus  
XX and C-terminus of a protein, can be used to help fold the protein into  
XX a compact structure. This compact structure is more stable to proteases.  
XX A composition (A) comprises at least a first dimerisation peptide (I)  
XX comprising the sequence (S1) that is no more than 8 amino acids long,  
XX where the composition optionally comprises a second dimerisation peptide  
XX (II): NH2-X1-X2-X3-X4-X5-COOH (S1) where X1 to X4 = Ala, Val, Ile, Leu,  
XX Trp, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu;  
XX NH2-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are  
XX displayed intracellularly or extracellularly and are useful to identify  
XX binding proteins and molecules, and to modulate intracellular signalling  
XX pathways. A library of constrained proteins may be evaluated in vivo for  
XX its bioactive potential. The invention can be used to access molecules  
XX or targets within living cells, and then provide for the isolation of  
XX the constrained protein which has a phenotypic effect on the living  
XX cells. The methods are also useful to identify in vitro binding partners  
XX of the constrained protein. The compositions of the invention are useful  
XX as a scaffold for gene therapy and for potential use as a therapeutic  
XX in physiological fluids. The present sequence is used in the  
XX exemplification of the present invention.  
XX  
SQ Sequence 7 AA;  
  
Query Match 26.7%; Score 4; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      6 KLKV 9
      |||||
Db      2 KLKV 5

RESULT 28
ID      ABG32211 standard; peptide; 7 AA.
XX
AC      ABG32211;
XX
DT      05-NOV-2002 (first entry)
XX
DE      Sheep colostrinin derived peptide #5.
XX
KW      Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;
KW      central nervous system disorder; neurological disorder; neurosis;
KW      mental disorder; psychosis; neurodegenerative disorder;
KW      Alzheimer's disease; motor neuron disease; immune system disorder;
KW      acquired immunological deficiency; bacterial infection; viral infection;
KW      amyloid plaque; dietary supplement; cachexia; weight loss;
KW      senile dementia; Parkinson's disease; emotional disturbance; depression;
KW      drug addiction; drug withdrawal.
XX
OS      Ovis aries.
XX
PN      WO200246211-A2.
XX
PD      13-JUN-2002.
XX
PF      05-DEC-2001; 2001WO-GB05376.
XX
PR      06-DEC-2000; 2000GB-0029777.
XX
PA      (REGE-) REGEN THERAPEUTICS PLC.
XX
PI      Georgiades JA;
XX
WPI; 2002-619016/66.
XX
Novel peptides isolated from colostrinin polypeptide, useful for
treating viral and bacterial infections, disorders of immune system and
central nervous system e.g., Alzheimer's disease, dementia, and as food
additive -
XX
Claim 1; Page 8; 16pp; English.
XX
The invention relates to a peptide derived from colostrinin (a colostrum
protein known to be a cytokine inducer) substantially entirely consists
of the peptide sequences appearing as ABG32207-ABG32223. Also included
are a composition comprising two or more of the peptides in combination
with a carrier, a dietary supplement comprising an orally ingestible
combination of the peptide in combination with a carrier and an antibody
which binds to the peptide, and which is obtainable by using peptide as
an antigen. The peptide is useful as a medicament for treating chronic
disorders of central nervous system e.g., neurological disorders and/or
mental disorders such as psychosis and/or neurosis, dementia,
neurodegenerative disorders such as Alzheimer's disease, motor
neuron disease, chronic disorders of immune system, diseases
with bacterial and viral etiology, acquired immunological deficiencies,
chronic bacterial, viral infections. The peptide is also useful for
treating diseases characterised by presence of amyloid plaque. The
peptide is also useful as a dietary supplement for babies, small
children, adults who have been subjected to chemotherapy and/or
adults who have suffered from cachexia or weight loss due to chronic
disease. The peptide is also useful for treating senile dementia,
Parkinson's disease, emotional disturbances and depression. The peptides
may also be used as an auxiliary withdrawal treatment for drug addicts,
after a period of detoxification, and in persons dependent on stimulants.
The present sequence is a colostrinin derived peptide of the invention.
XX
Sequence: 7 AA;
SQ

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Query Match      26.7%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPKK 6
      |||||
Db      3 PPKK 6

RESULT 29
ID      ABB77133 standard; peptide; 7 AA.
XX
AC      ABB77133;
XX
DT      15-JUL-2002 (first entry)
XX
DE      Classical swine fever virus envelope protein E2 epitope #5.
XX
KW      Classical swine fever virus; envelope protein; E2; vaccine; virucide;
KW      pig.
XX
OS      Classical swine fever virus.
XX
PN      WO200220048-A1.
XX
PD      14-MAR-2002.
XX
PF      20-JUL-2001; 2001WO-CN01189.
XX
PR      10-AUG-2000; 2000CN-0121292.
XX
PA      (UYQI ) UNIV TSINGHUA.
PA      (BEIJ-) BEIJING FEIKAI BIOTECH CO LTD.
XX
PI      Chen Y, Dong X, Xiao Y;
XX
WPI; 2002-292232/33.
XX
Production of classical swine fever virus epitope vaccines containing
conjugated epitope peptides, useful in treating mutation of classical
swine fever virus particularly applicable in pig farming -
XX
Claim 4; Page 7; 13pp; Chinese.
XX
The sequence represents an epitope of the classical swine fever virus
envelope protein E2. The invention relates to a novel classical swine
fever virus vaccine comprising at least 1 epitope peptide conjugated to a
carrier protein or peptide and each having mono-epitopes repeated at
least once or multi-epitopes repeated at least once, in which the
epitopes are chosen from neutralizing epitope on envelope protein E2 of
classical swine fever virus and mutation epitope. The vaccine of the
invention has virucide activity. The vaccines are useful in treating
mutation of classical swine fever virus and curing the fever, and are
particularly applicable in pig farming.
XX
Sequence 7 AA;
SQ

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---

```

Query Match      26.7%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KPFP 5
      |||||
Db      3 KPFP 6

RESULT 30
ID      ABB07085 standard; peptide; 7 AA.
XX
AC      ABB07085;
XX
Sequence: 7 AA;
SQ

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XX 25-JUN-2002 (first entry)
DT Hepatitis C virus NS3-serine protease inhibitor related peptide #9.
DE Hepatitis C virus; HCV; NS3-serine protease inhibitor; hepatitis;
KW HCV protease inhibitor; infection; virucide; hepatotropic.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 6
FT Modified-site /note= "nVal-(CO)"
XX
PN WO200208256-A2.
XX
XX 31-JAN-2002.
PD
XX 19-JUL-2001; 2001WO-US22826.
XX
XX 21-JUL-2000; 2000US-220109P.
XX
XX (SCHE ) SCHERING CORP.
PA (CORV-) CORVAS INT INC.
XX
XX Sakkena AK, Girijavallabhan VM, Lovey RG, Jao EE, Bennett F;
PI McCormick J, Wang H, Pike RE, Bogen SL, Liu Y, Arasappan A;
PI Parekh T, Pinto FA, Njoroge FG, Ganguly AK, Brunck TK, Kemp SJ;
PI Levy OE, Lim-Wilby M;
XX
XX WPI; 2002-361644/39.
XX
XX Novel peptide inhibitor compounds of hepatitis virus NS3/NS4a serine
PT protease, useful for treating hepatitis C virus disorders -
XX
XX Example 1; Page 107; 196pp; English.
XX
XX The present invention describes a peptide compound (I) exhibiting
CC hepatitis C virus (HCV) protease inhibitory activity, including
CC enantiomers, stereoisomers, rotomers and tautomers, pharmaceutically
CC acceptable salts, solvates or derivatives. Also described are: (I) a
CC pharmaceutical composition (II) comprising (I); and (2) preparing (II)
CC for treating disorders associated with HCV protease involving bringing
CC into intimate contact (I) and a carrier. (I) has virucide and
CC hepatotropic activities and can be used as HCV NS3/NS4a serine protease
CC inhibitors. (I) is useful for manufacturing a medicament to treat
CC disorders associated with HCV protease. (I) can be used for modulating
CC activity of HCV protease preferably, HCV NS3/NS4a protease and for
CC modulating the processing of HCV polypeptide. (II) is useful for
CC treating disorders associated with HCV and for treating disorders
CC associated with HCV protease. (I) is useful for treating hepatitis
CC caused by HCV. The present sequence represents a peptide given in an
XX example from the present invention.
XX
XX Sequence 7 AA;
XX
Query Match 26.7%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 10 EVFP 13
DB 2 EVFP 5
XX
RESULT 31
AAR59968
ID AAR59968 standard; peptide; 8 AA.
XX
AC AAR59968;
XX

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DT 25-MAR-2003 (updated)
DT 14-FEB-1995 (first entry)
XX
DE Peptide signal sequence of platelet derived growth factor A.
XX
KW Therapeutic; metabolic interactions; PSS; analogues.
XX
OS Synthetic.
XX
XX WO9416328-A1.
XX
XX 21-JUL-1994.
XX
XX 30-DEC-1993; 93WO-US12679.
XX
XX 30-DEC-1992; 92US-0997727.
XX
XX (RATH/) RATH M.
XX
XX Rath M;
XX
XX WPI; 1994-249399/30.
XX
XX Identifying peptide signal sequences in a protein - and use of
PT their synthetic analogues for treating or preventing, e.g.
PT cardiovascular and auto-immune disease, infections and cancer.
XX
XX Claim 38; Page 17; 28pp; English.
XX
XX The sequence is that of a signal sequence analogous to that of
CC platelet derived growth factor chain A.
CC See also AAR59944-83.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 8 AA;
XX
Query Match 26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 PKLK 8
DB 4 PKLK 7
XX
RESULT 32
AAR07412
ID AAR07412 standard; peptide; 9 AA.
XX
AC AAR07412;
XX
XX 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
DE Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 9 /note= "opt. amidated"
XX
XX JP08134096-A.
XX
XX 28-MAY-1996.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX

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XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 KLKV 9
XX 1 KLKV 4
XX
XX RESULT 33
XX AAW07413
XX ID AAW07413 standard; peptide; 9 AA.
XX AC
XX AC AAW07413;
XX
XX 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
XX
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "opt. amidated"
XX
XX JF08134096-A.
XX
XX 28-MAY-1996.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 KLKV 9
XX 1 KLKV 4
XX
XX RESULT 33
XX AAW07413
XX ID AAW07413 standard; peptide; 9 AA.
XX AC
XX AC AAW07413;
XX
XX 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
XX
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "opt. amidated"
XX
XX JF08134096-A.
XX
XX 28-MAY-1996.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an

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CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 KLKV 9
XX 1 KLKV 4
XX
XX RESULT 34
XX AAW07414
XX ID AAW07414 standard; peptide; 9 AA.
XX AC
XX AC AAW07414;
XX
XX 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
XX
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "opt. amidated"
XX
XX JF08134096-A.
XX
XX 28-MAY-1996.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX 01-NOV-1994; 94JP-0268723.
XX
XX (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 6 KLKV 9
XX 1 KLKV 4
XX
XX RESULT 35
XX AAW07415
XX ID AAW07415 standard; peptide; 9 AA.

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XX AC AAW07415;
XX DT 20-JAN-1997 (first entry)
XX DE Antibacterial/antifungal, synthetic peptide.
XX KW Antimicrobial; food additive; preservative; low toxicity; fungus;
XX KW bacterium; treatment; inhibitory.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 9
XX FT /note= "opt. amidated"
XX PN JP08134096-A.
XX PD 28-MAY-1996.
XX PF 01-NOV-1994; 94JP-0268723.
XX PR 01-NOV-1994; 94JP-0268723.
XX PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX DR WPI; 1996-306572/31.
XX PT New antimicrobial nona;peptide(s) - useful for treating bacterial
XX PT and fungal diseases and as preservatives for food and feedstuffs
XX PS Example 4; Page 8; 10pp; Japanese.
XX CC AAW07406-W07418 are peptides which have both antifungal and
XX CC antibacterial properties. The peptides can be synthesised by solid phase
XX CC synthesis or chemical synthesis in large amounts at a low cost. The
XX CC peptides are specific examples of a generic peptide KXXXXXXX (see
XX CC AAW07405) and can be used as microbial additives for foods and animal
XX CC feeds. The peptides were shown to have minimum inhibitory concns. of
XX CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
XX CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
XX CC amidated N-terminus are preferred).
XX SQ Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 KLKV 9
XX DB ||||
XX 1 KLKV 4
XX
XX RESULT 36
XX ABB14478
XX ID ABB14478 standard; Peptide; 9 AA.
XX AC ABB14478;
XX DT 22-JAN-2002 (first entry)
XX DE Human C35 peptide epitope #1982.
XX KW Human; C35; cytostatic; gene therapy; vaccine; tumour antigen;
XX KW breast cancer; bladder cancer; tumour immunotherapy; epitope;
XX KW major histocompatibility complex binding peptide; MHC.
XX OS Homo sapiens.
XX PN WO200174859-A2.
XX XX 11-OCT-2001.

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XX 04-APR-2001; 2001WO-US10855.
XX 04-APR-2000; 2000US-194463P.
XX (UYRP ) UNIV ROCHESTER.
XX Zauderer M, Evans EE, Borrello MA;
XX WPI; 2001-626383/72.
XX Novel C35 polypeptides and C35 genes useful in immunogenic compositions
XX and vaccines, for inducing antibody and cell-mediated immunity against
XX target cells, such as tumor cells that express C35 gene
XX Disclosure; Page 166; 331pp; English.
XX The present invention relates to human C35 (see AAG78997). C35 is a novel
XX tumour antigen that is overexpressed in human breast and bladder
XX carcinoma. C35 is thought to be a promising candidate for tumour
XX immunotherapy, in immunogenic compositions and vaccines, to induce
XX antibody and cell-mediated immunity against target cells, such as tumour
XX cells that express C35 genes. The present sequence is a C35 peptide
XX epitope. This peptide is predicted to be a major histocompatibility
XX complex (MHC) binding peptide.
XX SQ Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 FPKL 7
XX DB ||||
XX 1 FPKL 4
XX
XX RESULT 37
XX AAB91625
XX ID AAB91625 standard; Peptide; 9 AA.
XX AC AAB91625;
XX DT 22-JUN-2001 (first entry)
XX DE Opioid peptide SEQ ID NO:801.
XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX KW blood component; modification; succinimidy; maleimido group; amino;
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2000069900-A2.
XX DT 23-NOV-2000.
XX DE 17-MAY-2000; 2000WO-US13576.
XX PR 17-MAY-1999; 99US-0134406.
XX PR 10-SEP-1999; 99US-0153406.
XX PR 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity

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XX Disclosure; Page 457; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidease stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CC exemplification of the present invention.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
| | | |  
Db 2 PKLK 5

RESULT 38  
AAB76273  
ID AAB76273 standard; Peptide; 9 AA.  
XX AC  
XX AAB76273;  
DT 10-APR-2001 (first entry)  
XX DE  
DE Influenza virus immunogenic peptide.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC; cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
KW human immunodeficiency virus; protozoicide; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV; cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
KW renal carcinoma; cervical carcinoma; lymphoma; malaria; condyloma acuminatum.  
XX  
OS Influenza virus.  
XX  
PN WO200100225-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 28-JUN-2000; 2000WO-US17842.  
XX  
PR 29-JUN-1999; 99US-0141422.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S;  
XX  
DR WPI; 2001-112389/12.  
XX  
PT Composition comprising human leukocyte antigen binding peptide which comprises isolated, prepared epitope useful for treating viral  
PT infections such as acquired immunodeficiency syndrome, and cancer -  
XX  
PS Claim 1; Page 51; 58pp; English.

XX The present invention describes a composition (I) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 8-11 residue amino acid sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic, virucide, hepatotropic, antiinflammatory, anti-HIV (human immunodeficiency virus) and protozoicide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response. (I) is useful for inducing a cytotoxic T cell response against a preslected antigen in a patient expressing a specific major histocompatibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer, hepatitis B, hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma acuminatum.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
| | | |  
Db 2 PKLK 5

RESULT 39  
AAE31250  
ID AAE31250 standard; peptide; 9 AA.  
XX AC  
XX AAE31250;  
XX DT 24-FEB-2003 (first entry)  
XX DE  
DE Human mage9 peptide #3.  
KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200272627-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 11-MAR-2002; 2002WO-EP02666.  
XX  
PR 09-MAR-2001; 2001US-274250P.  
PR 14-MAY-2001; 2001US-290353P.  
PR 18-MAY-2001; 2001US-291610P.  
XX  
PA (CALL-) CALLISTOGEN AG.  
XX  
PI Wrede P, Walden P, Eichler-Mertens M, Filter M;  
XX  
DR WPI; 2002-759836/82.  
XX  
PT Providing, identifying or optimizing peptides for inducing cytotoxic T-lymphocytes and for treating cancer, comprises selecting conserved PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the protein -  
PT  
XX  
PS Disclosure; Page 10; 32pp; English.  
XX  
XX The invention relates to a method for providing, identifying or/and CC optimising peptides which induce cytotoxic T-lymphocytes and to the CC uses of the obtained peptides for vaccination. The method is useful for providing, identifying and/or optimising peptides that are useful CC in manufacturing a pharmaceutical composition for the induction of CC cytotoxic T-lymphocytes, and for the prevention, treatment or diagnosis CC of cancer or viral infections. The invention is also used in gene CC

CC	therapy. The present sequence is human mage9 peptide used to illustrate	
XX	the method of the invention.	
XX		
SQ	Sequence 9 AA;	
	Query Match 26.7%; Score 4; DB 23; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	6 KLKV 9	
Db	3 KLKV 6	
RESULT 40		
ABJ01633	ID ABJ01633 standard; Peptide; 9 AA.	
XX	AC ABJ01633;	
XX	DT 19-SEP-2002 (first entry)	
XX	DE 158PID7 related HLA peptide SEQ ID No 333.	
XX	KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;	
KW	cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;	
KW	HLA.	
XX	XX Homo sapiens.	
XX	OS WO200216593-A2.	
XX	PN 28-FEB-2002.	
XX	PD 22-AUG-2001; 2001WO-US26276.	
XX	PF 22-AUG-2000; 2000US-227098P.	
PR	10-APR-2001; 2001US-282739P.	
XX	XX (AGEN-) AGENSYS INC.	
PA	PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;	
XX	PI Challita-eid PM, Jakobovits A;	
XX	DR WPI; 2002-425659/45.	
XX	XX New compositions comprising a gene (designated 158PID7), its encoded	
PT	protein or their modulators, useful for treating or diagnosing cancers,	
PT	particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses	
PT	or humans)	
XX	PS Disclosure; Page 137; 181pp; English.	
XX	XX The invention relates to a novel nucleic acid, designated 158PID7. The	
CC	compositions are useful for treating or diagnosing cancers, particularly	
CC	bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,	
CC	horses or humans). The compositions are also useful for monitoring	
CC	genetic abnormalities and in preparing cancer vaccines. The nucleic acid	
CC	of the invention can be used in gene therapy to treat the said disorders.	
CC	This sequence represents a human leukocyte antigen (HLA) peptide relating	
CC	to the 158PID7 protein of the invention.	
XX		
SQ	Sequence 9 AA;	
	Query Match 26.7%; Score 4; DB 23; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	5 PKLK 8	
Db	6 PKLK 9	
RESULT 41		
ABJ79424	ID ABB79424 standard; peptide; 9 AA.	
XX	XX ABB79424;	
XX	DT 08-JUL-2002 (first entry)	
XX	DE Human MMP-2 PEX peptide 8.	
XX	XX Human; matrix metalloproteinase-2; MMP-2; enzyme; thrombolytic;	
KW	anticoagulant; cardiant; antiarteriosclerotic; cytostatic; osteopathic;	
KW	antiinflammatory; antibacterial; virucide; fungicide; anipisoriatic;	
KW	vulnary; cerebroprotective; antiangular; ophthalmological;	
KW	antirheumatic; antiarthritic; antiulcer; vasotropic; nephrotropic;	
KW	alpha-v-beta-3 integrin receptor; thrombosis; tumour; osteoporosis;	
KW	infection; veterinary medicine; rheumatoid arthritis; Crohn's disease;	
KW	antimicrobial; antiseptic.	
XX	XX Homo sapiens.	
OS	OS Synthetic.	
XX	XX WO200220566-A2.	
XX	PD 14-MAR-2002.	
XX	PF 28-AUG-2001; 2001WO-EP09899.	
XX	PR 07-SEP-2000; 2000DE-1044325.	
XX	XX (MERE ) MERCK PATENT GMBH.	
XX	XX Jonczyk A, Diefenbach B, Groth U, Zischinsky G;	
PI	WPI; 2002-329868/36.	
DR	XX New matrix metalloproteinase-2 derivative peptides, are alpha-v-beta-3	
PT	integrin receptor inhibitors useful e.g. for treating thrombosis,	
PT	cardiac infarction, tumors, osteoporosis, inflammation or infections	
XX	XX Examples; Page 24; 35pp; German.	
XX	XX The invention relates to peptides (ABB79414-ABB79426) derived from the	
CC	C-terminal fragment PEX of matrix metalloproteinase-2 (MMP-2). Matrix MMP-2	
CC	derivatives of formula X-Y-Z (I) and their salts and solvates are	
CC	described.	
CC	X = H, 1-10C alkanoyl or peptide fragment consisting of 1-20 naturally	
CC	occurring amino acid residues;	
CC	Y = peptide fragment selected from the sequence region 466-660 of human	
CC	Pro-MMP-2; and	
CC	Z = OH, NH 2, NH-1-10C alkyl N(1-10C alkyl) 2 or peptide fragment	
CC	consisting of 1-20 naturally occurring amino acid residues.	
CC	Primary amino groups are optionally protected conventionally. The	
CC	peptides and MMP-2 derivatives are used for combating diseases involving	
CC	interaction of ligands (specifically MMP-2) with the alpha-v-beta-3	
CC	integrin receptor, especially pathological processes supported or	
CC	propagated by angiogenesis, thrombosis, cardiac infarction, coronary	
CC	heart disease, arteriosclerosis, tumours, osteoporosis, fibrosis,	
CC	inflammation, infections, psoriasis or wound healing deficiency. More	
CC	generally the peptides and MMP-2 derivatives are useful in human and	
CC	veterinary medicine for the treatment and/or prophylaxis of thrombosis,	
CC	myocardial infarction, apoplexy, angina pectoris, tumour diseases,	
CC	osteolytic diseases (e.g. osteoporosis or hypercalcaemia), pathological	
CC	angiogenic diseases (e.g. inflammation), ophthalmological diseases (e.g.	
CC	diabetic retinopathy, macular degeneration, myopia, ocular histioplasmosis	
CC	or rubecotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative	
CC	colitis, Crohn's disease, atherosclerosis, psoriasis, restenosis after	
CC	angioplasty, viral, bacterial or fungal infections, acute renal failure	
CC	or wound healing deficiency; as antimicrobial/antiseptic agents in	
CC	operations involving biomaterials, implants, catheters or cardiac	
CC	pacemakers); or as diagnostic agents or reagents. The present sequence is	
CC	that of a human MMP-2 PEX peptide useful in examples of the invention.	
XX		

SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPKL 7  
 ||||  
 Db 3 FPKL 6

RESULT 42

AAR91324  
 ID AAR91324 standard; peptide; 10 AA.

XX AC AAR91324;

XX DT 10-OCT-1996 (first entry)

XX DE Dynorphin A analogue Dyn A (4-13).

XX KW Analogue; dynorphin A; endogenous opioid; proenkephalin B; truncation;  
 KW receptor; binding; nociceptive; analgesic; pain-killer; resistance; burn;  
 KW neuropathic; neurogenic; allodynia; post-operative pain; side effect;  
 KW drowsiness; addiction.

XX OS Synthetic.

XX PN W09606626-A1.

XX PD 07-MAR-1996.

XX PF 26-AUG-1994; 94WO-US09563.

XX PR 26-AUG-1994; 94WO-US09563.

XX PA (GOLD/) GOLDSTEIN A.

XX FA (LEEN/) LEE N M.

XX FI Goldstein A, Lee NM;

XX WPI; 1996-160138/16.

XX PT N-terminally truncated dynorphin A analogues - useful for treating  
 XX pain, esp. for pain resistant to opioid analgesics

XX PS Claim 13; Page 17; 22pp; English.

XX CC The peptides AAR91320-45 represent analogues of dynorphin A, a member of  
 CC the dynorphin group of endogenous opioids derived from proenkephalin B.  
 CC The novel peptides contain N- and C-terminal truncations as compared to  
 CC the 17 amino acid natural dynorphin A. The peptides AAR91320-7 have a  
 CC truncation of the N-terminal Tyr-Gly-Gly amino acids and serial  
 CC deletions of the C-terminal amino acids. It has been shown that  
 CC dynorphin A analogues having the N-terminal Tyr residue deleted do not  
 CC bind to mu, delta or kappa opioid receptors. The peptides presented here  
 CC are analogues that do not bind to opioid receptors but retain an  
 CC anti-nociceptive (i.e. analgesic) activity. The peptides can be used to  
 CC treat pain which is resistant to opioid analgesics e.g. neuropathic or  
 CC neurogenic pain, allodynia, post-operative pain or burns. Since the  
 CC peptides do not interact with the opioid receptors, side effects  
 CC associated with opioid analgesics, e.g. drowsiness or addiction are  
 CC avoided.

XX SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 17; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
 ||||  
 Db 7 PKLK 10

RESULT 43

AAM43031

ID AAM43031 standard; Peptide; 10 AA.

XX AC AAM43031;

XX DT 22-OCT-2001 (first entry)

XX DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 340.

XX KW Mycoplasma genitalium; complementary peptide; ligand;  
 KW protein-protein interaction; drug design; intermolecular;  
 KW intramolecular.

XX OS Mycoplasma genitalium.

XX PN W0200142278-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04778.

XX PR 13-DEC-1999; 99GB-0029466.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX DR WPI; 2001-514238/56.

XX CC Complementary peptide ligands as reagents and drugs for drug discovery

XX PT programs and as lead ligands to facilitate drug design and development,  
 XX are generated from microbial genome sequences -

XX PS Example 2; Page 96; 161pp; English.

XX CC The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or agonising specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intermolecular (between proteins) and intermolecular (within a  
 CC protein) sequences.

XX SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPKL 7  
 ||||  
 Db 5 FPKL 8

RESULT 44

AAG83581

ID AAG83581 standard; Peptide; 10 AA.

XX AC AAG83581;

XX XX



DT 11-SEP-2001 (first entry)  
XX Arabidopsis thaliana peptide ligand #221.  
DE Plant; peptide pesticide; peptide herbicide; agricultural research.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX WO200142279-A2.  
XX 14-JUN-2001.  
XX 13-DEC-2000; 2000WO-GB04781.  
XX 13-DEC-1999; 99GB-0029469.  
XX (PROT-) PROTEOM LTD.  
XX Roberts GW, Heal JR;  
XX WPI; 2001-381629/40.  
XX A set of peptide ligands for agricultural research and development of  
PT therapeutic agents comprise specific complementary peptides to proteins  
PT encoded by genes of plant genomes -  
XX Example 4; Page 61; 201pp; English.  
XX The present invention relates to a set of peptide ligands consisting of  
CC specific complementary peptides to proteins encoded by genes of plant  
CC genomes. The present sequence is one such peptide from Arabidopsis  
CC thaliana. The peptides of the present invention are useful in an assay to  
CC identify a peptide, especially a peptide pesticide or herbicide. The  
CC peptides are also useful for tools for agricultural research and  
XX development.  
XX Sequence 10 AA;  
XX  
XX Query Match 26.7%; Score 4; DB 22; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 10 EVFP 13  
XX ||||  
XX 4 EVFP 7  
XX  
XX DB  
XX  
XX RESULT 45  
XX AAG84280  
XX ID AAG84280 standard; Peptide; 10 AA.  
XX AC AAG84280;  
XX DT 11-SEP-2001 (first entry)  
XX Arabidopsis thaliana peptide ligand #920.  
DE Plant; peptide pesticide; peptide herbicide; agricultural research.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX WO200142279-A2.  
XX 14-JUN-2001.  
XX 13-DEC-2000; 2000WO-GB04781.  
XX 13-DEC-1999; 99GB-0029469.  
XX (PROT-) PROTEOM LTD.  
XX Roberts GW, Heal JR;  
XX WPI; 2001-381629/40.  
XX A set of peptide ligands for agricultural research and development of  
PT therapeutic agents comprise specific complementary peptides to proteins  
PT encoded by genes of plant genomes -  
XX Example 4; Page 61; 201pp; English.  
XX The present invention relates to a set of peptide ligands consisting of  
CC specific complementary peptides to proteins encoded by genes of plant  
CC genomes. The present sequence is one such peptide from Arabidopsis  
CC thaliana. The peptides of the present invention are useful in an assay to  
CC identify a peptide, especially a peptide pesticide or herbicide. The  
CC peptides are also useful for tools for agricultural research and  
XX development.  
XX Sequence 10 AA;  
XX  
XX Query Match 26.7%; Score 4; DB 22; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 10 EVFP 13  
XX ||||  
XX 4 EVFP 7  
XX  
XX DB  
XX  
XX RESULT 46  
XX AAG85870  
XX ID AAG85870 standard; Peptide; 10 AA.  
XX AC AAG85870;  
XX DT 11-SEP-2001 (first entry)  
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 819.  
DE Saccharomyces cerevisiae;  
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.  
XX Saccharomyces cerevisiae.  
XX WO200142276-A1.  
XX 14-JUN-2001.  
XX 13-DEC-2000; 2000WO-GB04773.  
XX 13-DEC-1999; 99GB-0029471.  
XX (PROT-) PROTEOM LTD.  
XX Roberts GW, Heal JR;  
XX WPI; 2001-367863/38.  
XX Identifying complementary peptides by analysis of protein and  
PT nucleotide sequence databases, useful in drug design -  
XX Example 3; Page 143; 488pp; English.  
XX The invention relates to the identification of complementary peptides  
CC by analysis of protein and nucleotide sequence databases from higher  
CC eukaryotic genomes, excluding human and plants. The specific  
CC complementary peptides interact with their relevant target proteins  
CC encoded in the eukaryote genome. The peptides may be used as reagents  
CC and drugs for drug discovery and as lead ligands for drug design and  
CC development. The present sequence is a complementary peptide from  
XX Saccharomyces cerevisiae.  
XX Sequence 10 AA;  
XX  
XX Query Match 26.7%; Score 4; DB 22; Length 10;

DR WPI; 2001-381629/40.  
XX A set of peptide ligands for agricultural research and development of  
PT therapeutic agents comprise specific complementary peptides to proteins  
PT encoded by genes of plant genomes -  
XX Example 4; Page 159; 201pp; English.  
XX The present invention relates to a set of peptide ligands consisting of  
CC specific complementary peptides to proteins encoded by genes of plant  
CC genomes. The present sequence is one such peptide from Arabidopsis  
CC thaliana. The peptides of the present invention are useful in an assay to  
CC identify a peptide, especially a peptide pesticide or herbicide. The  
CC peptides are also useful for tools for agricultural research and  
XX development.  
XX Sequence 10 AA;  
XX  
XX Query Match 26.7%; Score 4; DB 22; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 9 VEVF 12  
XX ||||  
XX 7 VEVF 10  
XX  
XX DB  
XX  
XX RESULT 46  
XX AAG85870  
XX ID AAG85870 standard; Peptide; 10 AA.  
XX AC AAG85870;  
XX DT 11-SEP-2001 (first entry)  
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 819.  
DE Saccharomyces cerevisiae;  
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.  
XX Saccharomyces cerevisiae.  
XX WO200142276-A1.  
XX 14-JUN-2001.  
XX 13-DEC-2000; 2000WO-GB04773.  
XX 13-DEC-1999; 99GB-0029471.  
XX (PROT-) PROTEOM LTD.  
XX Roberts GW, Heal JR;  
XX WPI; 2001-367863/38.  
XX Identifying complementary peptides by analysis of protein and  
PT nucleotide sequence databases, useful in drug design -  
XX Example 3; Page 143; 488pp; English.  
XX The invention relates to the identification of complementary peptides  
CC by analysis of protein and nucleotide sequence databases from higher  
CC eukaryotic genomes, excluding human and plants. The specific  
CC complementary peptides interact with their relevant target proteins  
CC encoded in the eukaryote genome. The peptides may be used as reagents  
CC and drugs for drug discovery and as lead ligands for drug design and  
CC development. The present sequence is a complementary peptide from  
XX Saccharomyces cerevisiae.  
XX Sequence 10 AA;  
XX  
XX Query Match 26.7%; Score 4; DB 22; Length 10;

```
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12
Db 1 VEVF 4

RESULT 47
AAG88260
ID AAG88260 standard; Peptide; 10 AA.
XX
AC AAG88260;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3209.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 5; Page 472; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
Db 5 LKVE 8

RESULT 48
AAG88261
ID AAG88261 standard; Peptide; 10 AA.
XX
AC AAG88261;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3210.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
```

```
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 5; Page 472; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
Db 5 LKVE 8

RESULT 49
AAG88262
ID AAG88262 standard; Peptide; 10 AA.
XX
AC AAG88262;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3211.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
```

PT nucleotide sequence databases, useful in drug design -  
XX  
PS Example 5; Page 472; 488pp; English.  
XX

CC The invention relates to the identification of complementary peptides  
CC by analysis of protein and nucleotide sequence databases from higher  
CC eukaryotic genomes, excluding human and plants. The specific  
CC complementary peptides interact with their relevant target proteins  
CC encoded in the eukaryote genome. The peptides may be used as reagents  
CC and drugs for drug discovery and as lead ligands for drug design and  
CC development. The present sequence is a complementary peptide from  
CC Saccharomyces cerevisiae.  
XX  
XX

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10  
| | | |  
Db 4 LKVE 7

RESULT 50  
AAG88263  
ID AAG88263 standard; Peptide; 10 AA.

XX AC AAG88263;

XX DT 11-SEP-2001 (first entry)

XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3212.

XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.

XX OS Saccharomyces cerevisiae.

XX PN WO200142276-A1.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04773.

XX PR 13-DEC-1999; 99GB-0029471.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX DR WPI; 2001-367863/38.

XX PT Identifying complementary peptides by analysis of protein and  
XX nucleotide sequence databases, useful in drug design -

XX PS Example 5; Page 473; 488pp; English.

XX CC The invention relates to the identification of complementary peptides  
CC by analysis of protein and nucleotide sequence databases from higher  
CC eukaryotic genomes, excluding human and plants. The specific  
CC complementary peptides interact with their relevant target proteins  
CC encoded in the eukaryote genome. The peptides may be used as reagents  
CC and drugs for drug discovery and as lead ligands for drug design and  
CC development. The present sequence is a complementary peptide from  
CC Saccharomyces cerevisiae.  
XX  
XX

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10  
| | | |  
Db 6 LKVE 9

RESULT 51

AAB91622  
ID AAB91622 standard; Peptide; 10 AA.

XX AC AAB91622;

XX DT 22-JUN-2001 (first entry)

XX DE Opioid peptide SEQ ID NO: 798.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
XX blood component; modification; succinimide; maleimido group; amino;  
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents  
XX peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 456; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.

XX SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
| | | |  
Db 3 PKLK 6

RESULT 52  
ABG69388  
ID ABG69388 standard; peptide; 10 AA.  
XX AC ABG69388;  
XX DT 21-OCT-2002 (first entry)  
XX Vascular response-associated protein isoform tryptic digest peptide #19.  
XX DE Vascular response; VR; vascular response-associated feature; VRP;  
XX KW vascular response-associated protein isoform; VRPI; blood; serum;  
XX KW plasma; aneurysm; stenosis; atherosclerosis; congestion; oedema;  
XX KW haemorrhage; shock; stroke; varicose vein; vasculitis; angilitis;  
XX KW VRPI tryptic digest peptide; antiatherosclerotic; haemostatic;  
XX KW cerebroprotective; antiinflammatory; vasotropic.  
XX OS Unidentified.  
XX PN WO200254080-A2.  
XX PD 11-JUL-2002.  
XX PF 24-DEC-2001; 2001WO-GB05774.  
XX PR 29-DEC-2000; 2000US-260387P.  
XX PR 24-OCT-2001; 2001US-0260387.  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Herman EH, Holt GD, Sistare FD, Zhang J;  
XX DR WPI; 2002-583636/62.  
XX PT Screening, diagnosis or prognosis of vascular response including shock,  
PT stroke, in subject, by detecting vascular response-associated features  
PT or vascular response-associated protein isoforms in body fluid from  
PT subject -  
XX PS Disclosure; Page 35; 156pp; English.  
XX CC The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of vascular response (VR) in a  
CC subject. The method comprises analysing a test sample of body fluid  
CC from the subject by two-dimensional electrophoresis to generate a 2D  
CC array of vascular response-associated features (VRPs), whose relative  
CC abundance correlates with presence, absence, stage or severity of VR  
CC and comparing the abundance of each feature with the abundance of that  
CC chosen feature in body fluid from persons free from VR. The invention  
CC also describes vascular response-associated protein isoforms (VRPIs)  
CC detectable in blood, serum or plasma. The methods and compositions of  
CC the invention are useful for the screening, diagnosis or prognosis of  
CC VR in a subject, for determining the stage or severity of VR in a  
CC subject, for identifying a subject at risk of developing VR, or for  
CC monitoring the effect of therapy administered to a subject having VR.  
CC Antibodies capable of binding to VRPIs are useful for treating or  
CC preventing VR. An agent that modulates the activity of VRPI is useful  
CC in the manufacture of a medicament for the treatment or prevention of  
CC VR in a subject. The vascular response includes aneurysm, stenosis,  
CC atherosclerosis, congestion, oedema, haemorrhage, shock, stroke,  
CC varicose veins, and vasculitis (angilitis). ABG69370-ABG69449 represent  
CC VRPI tryptic digest peptides.

XX SQ Sequence 10 AA;  
Query Match 26.7%; Score 4; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12  
| | | |  
Db 6 VEVF 9

RESULT 53  
ABG69566  
ID ABG69566 standard; Peptide; 10 AA.  
XX AC ABG69566;  
XX DT 21-OCT-2002 (first entry)  
XX DE Human CRPI tryptic digest peptide #47.  
XX KW Human; cardiac response; CR; cardiac response-associated protein isoform;  
XX KW CRPI; aneurysm; angina; arrhythmia; cardiomyopathy; cardiac arrest;  
XX KW myocardial infarction; coronary; atherosclerosis; oedema; endocarditis;  
XX KW haemorrhage; stenosis; shock; tryptic digest peptide.  
XX OS Homo sapiens.  
XX PN WO200254079-A2.  
XX PD 11-JUL-2002.  
XX PF 24-DEC-2001; 2001WO-GB05763.  
XX PR 29-DEC-2000; 2000US-260389P.  
XX PR 24-OCT-2001; 2001US-0260389.  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Herman EH, Holt GD, Sistare FD, Zhang J;  
XX DR WPI; 2002-583635/62.  
XX PT Screening, diagnosis or prognosis of cardiac response in a subject, by  
PT detecting cardiac response-associated features or cardiac  
PT response-associated protein isoforms in body fluid or tissue from the  
PT subject -  
XX PS Disclosure; Page 30; 138pp; English.

XX CC The present invention relates to a new method for screening, diagnosis or  
CC prognosis of cardiac response (CR) in a subject. The method of the  
CC invention involves analysing a test sample of body fluid or tissue from  
CC subject by 2D electrophoresis to generate a 2D array of features, whose  
CC relative abundance correlates with the presence, absence, stage or  
CC severity of CR and comparing abundance of each feature with the abundance  
CC of that chosen feature in body fluid from persons free from CR. The  
CC method is useful for screening, diagnosis or prognosis of CR in a  
CC subject, for determining the stage or severity of CR in a subject, for  
CC identifying a subject at risk of developing CR, or for monitoring the  
CC effect of therapy administered to a subject with CR. The method is also  
CC useful for screening agents that interact with one or more of the CRPIs  
CC (cardiac response-associated protein isoforms). The invention is useful  
CC for diagnosis or to determine the efficacy of a given treatment regimen.  
CC The cardiac response includes aneurysm, angina, arrhythmia,  
CC cardiomyopathy, cardiac arrest (myocardial infarction), coronary  
CC atherosclerosis, oedema, endocarditis, haemorrhage, stenosis, and shock.  
CC The present amino acid sequence represents one of a collection (ABG69520-  
CC ABG69591) of human CRPI tryptic digest peptides, as described in the  
CC specification.

XX SQ Sequence 10 AA;  
Query Match 26.7%; Score 4; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12  
| | | |  
Db 6 VEVF 9

```

RESULT 54
ABJ01569
ID  ABJ01569 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01569;
XX
XX  DT  19-SEP-2002 (first entry)
XX
XX  DE  158PID7 related HLA peptide SEQ ID No 269.
XX
XX  KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  HLA.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200216593-A2.
XX
XX  PD  28-FEB-2002.
XX
XX  PF  22-AUG-2000; 2001WO-US26276.
XX
XX  PR  22-AUG-2000; 2000US-227098P.
XX
XX  PR  10-APR-2001; 2001US-282739P.
XX
XX  PA  (AGEN-) AGENSYS INC.
XX
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX  PI  Challita-eid PM, Jakobovits A;
XX
XX  DR  WPI; 2002-425659/45.
XX
XX  PT  New compositions comprising a gene (designated 158PID7), its encoded
XX  PT  protein or their modulators, useful for treating or diagnosing cancers,
XX  PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX  PT  or humans)
XX
XX  PS  Disclosure; Page 135; 181pp; English.
XX
XX  CC  The invention relates to a novel nucleic acid, designated 158PID7. The
XX  CC  compositions are useful for treating or diagnosing cancers, particularly
XX  CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX  CC  horses or humans). The compositions are also useful for monitoring
XX  CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX  CC  of the invention can be used in gene therapy to treat the said disorders.
XX  CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
XX  CC  to the 158PID7 protein of the invention.
XX
XX  SQ  Sequence 10 AA;

Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db ||||
7 PKLK 10

RESULT 55
ABJ01656
ID  ABJ01656 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01656;
XX
XX  DT  19-SEP-2002 (first entry)
XX
XX  DE  158PID7 related HLA peptide SEQ ID No 356.
XX
XX  KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  HLA.

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XX OS Homo sapiens.
XX PN WO200216593-A2.
XX PD 28-FEB-2002.
XX PF 22-AUG-2001; 2001WO-US26276.
XX PR 22-AUG-2000; 2000US-227098P.
XX PR 10-APR-2001; 2001US-282739P.
XX PA (AGEN-) AGENSYS INC.
XX PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX PI Challita-eid PM, Jakobovits A;
XX DR WPI; 2002-425659/45.
XX PT New compositions comprising a gene (designated 158PID7), its encoded
XX PT protein or their modulators, useful for treating or diagnosing cancers,
XX PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX PT or humans)
XX PS Disclosure; Page 138; 181pp; English.
XX CC The invention relates to a novel nucleic acid, designated 158PID7. The
XX CC compositions are useful for treating or diagnosing cancers, particularly
XX CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX CC horses or humans). The compositions are also useful for monitoring
XX CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX CC of the invention can be used in gene therapy to treat the said disorders.
XX CC This sequence represents a human leukocyte antigen (HLA) peptide relating
XX CC to the 158PID7 protein of the invention.
XX SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db ||||
7 PKLK 10

RESULT 56
ABR47212
ID  ABR47212 standard; Peptide; 10 AA.
XX
XX  AC  ABR47212;
XX
XX  DT  10-JUN-2003 (first entry)
XX
XX  DE  Staphylococcus aureus CHIPS-related peptide #2401.
XX
XX  KW  CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;
XX  KW  formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
XX  KW  inflammation; cardiovascular disease; central nervous system disease;
XX  KW  gastrointestinal disease; skin disease; genitourinary disease;
XX  KW  joint disease; respiratory disease; HIV infection; antiinflammatory;
XX  KW  cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
XX  KW  gynecological; immunosuppressive; anti-HIV.
XX
XX  OS  Staphylococcus aureus.
XX
XX  PN  Synthetic.
XX
XX  PN  WO2003006048-A1.
XX
XX  PD  23-JAN-2003.
XX
XX  PF  11-JUL-2001; 2001WO-EP08004.
XX

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PR 11-JUL-2001; 2001WO-EP08004.
XX (JARI-) JARI PHARM BV.
XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX WPI; 2003-247783/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 55; 89pp; English.
XX
XX The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
XX Sequence 10 AA;
SQ
Query Match 26.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPK 6
Db 5 PPK 8
|||||
|||||
RESULT 57
ABR47279
ID ABR47279 standard; Peptide; 10 AA.
XX
XX ABR47279;
XX
XX 10-JUN-2003 (first entry)
DT
DE Staphylococcus aureus CHIPS-related peptide #2458.
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
OS Synthetic.
XX
XX WO2003006048-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 11-JUL-2001; 2001WO-EP08004.
PF
XX
XX 11-JUL-2001; 2001WO-EP08004.
PR
XX
XX (JARI-) JARI PHARM BV.
PA
XX
XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-247783/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 56; 89pp; English.
XX
XX The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
XX Sequence 10 AA;
SQ
Query Match 26.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EVFP 13
Db 4 EVFP 7
|||||
|||||
RESULT 58
ABR47286
ID ABR47286 standard; Peptide; 10 AA.
XX
XX ABR47286;
XX
XX 10-JUN-2003 (first entry)
DT
DE Staphylococcus aureus CHIPS-related peptide #2475.
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
OS Synthetic.
XX
XX WO2003006048-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 11-JUL-2001; 2001WO-EP08004.
PF
XX
XX 11-JUL-2001; 2001WO-EP08004.
PR
XX
XX (JARI-) JARI PHARM BV.
PA
XX
XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-247783/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 56; 89pp; English.
XX
XX

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CC The present invention relates to peptides (ABR44811-ABR47162 and  
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)  
CC from Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the  
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or  
CC neutrophils, monocytes and endothelial cells or involving acute or  
CC chronic inflammation reactions. The diseases or disorders include  
CC cardiovascular diseases, disease of the central nervous system,  
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint  
CC diseases, respiratory diseases and HIV infection.  
XX  
XX  
SQ Sequence 10 AA;  
  
Query Match 26.7%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 12 FPPF 15  
Db 4 FPPF 7  
  
RESULT 59  
ABR47290  
ID ABR47290 standard; Peptide; 10 AA.  
XX  
XX ABR47290;  
XX  
DT 10-JUN-2003 (first entry)  
DE Staphylococcus aureus CHIPS-related peptide #2479.  
XX  
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
XX Staphylococcus aureus.  
OS Synthetic.  
XX  
XX WO2003006048-A1.  
PN  
XX  
PD 23-JAN-2003.  
XX  
XX 11-JUL-2001; 2001WO-EP08004.  
PF  
XX 11-JUL-2001; 2001WO-EP08004.  
PR  
XX (JARI-) JARI PHARM BV.  
PA  
XX  
XX  
PI Van Kessel CPM, Gosselaar-de Haas CUC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
XX WPI; 2003-247783/25.  
DR  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases -  
PT  
XX  
XX Example 1; Page 56; 89pp; English.  
PS  
XX  
XX The present invention relates to peptides (ABR44811-ABR47162 and  
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)  
CC from Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the  
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or  
CC neutrophils, monocytes and endothelial cells or involving acute or  
CC chronic inflammation reactions. The diseases or disorders include  
CC cardiovascular diseases, disease of the central nervous system,

CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint  
CC diseases, respiratory diseases and HIV infection.  
XX  
SQ Sequence 10 AA;  
  
Query Match 26.7%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 KPFP 5  
Db 4 KPFP 7  
  
RESULT 60  
AAR45216  
ID AAR45216 standard; Protein; 11 AA.  
XX  
XX AAR45216;  
XX  
DT 25-MAR-2003 (updated)  
DT 01-JAN-1980 (first entry)  
XX  
XX des-Tyr Dynorphin A (1-17) analogue #14.  
XX  
XX Analogue; dynorphin; dynorphin A (1-17); des-Tyr; cerebral; spinal;  
KW ischemia; respiratory depression; gastroenteric spasm;  
KW narcotic analgesic; anti-inflammation; immune system.  
XX  
XX Homo sapiens.  
XX  
XX WO9325217-A1.  
PN  
XX  
PD 23-DEC-1993.  
XX  
XX 01-JUN-1993; 93WO-US05161.  
PF  
XX 12-JUN-1992; 92US-0897920.  
PR  
XX (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (TAKE/) TAKEMORI A E.  
XX  
XX Lee NM, Loh HH, Takemori AE;  
PI WPI; 1994-007185/01.  
DR  
XX  
XX Des-Tyr dynorphin analogues - potentiate activity of narcotic  
PT analgesics and/or block withdrawal symptoms; are more stable in  
PT vivo than native dynorphin  
XX  
XX Claim 2; Page 8; 24pp; English.  
PS  
XX  
XX The sequences given in AAR45202-21 are analogues of dynorphins based  
CC on the sequence given in AAR45211. This sequence represents the first  
CC of the dynorphins to be isolated and is designated "dynorphin A (1-  
CC 17)". The claimed peptides of the invention have at least six amino  
CC acids, but are des-Tyr with respect to dynorphin A (1-17). These  
CC peptides may be used to reverse at least some neurological deficit  
CC in treating cerebral and spinal ischemia, in inhibiting respiratory  
CC depression or gastroenteric spasms produced by narcotic analgesics  
CC to a naive host, as an adjunct for anti-inflammatory medication, and  
CC in blocking narcotic-induced impairment in a host whose immune  
CC system has been damaged by narcotic analgesics.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX  
SQ Sequence 11 AA;  
  
Query Match 26.7%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 PKLK 8

```

Db      8 PKLK 11
|||||
RESULT 61
AAR91341
ID   AAR91341 standard; peptide; 11 AA.
XX   AC      AAR91341;
XX   DT      10-OCT-1996 (first entry)
XX   DE      Dynorphin A analogue Dyn A (3-13).
XX   KW      Analogue; dynorphin A; endogenous opioid; proenkephalin B; truncation;
XX   KW      receptor; binding; nociceptive; analgesic; pain-killer; resistance; burn;
XX   KW      neuropathic; neurogenic; allodynia; post-operative pain; side effect;
XX   KW      drowsiness; addiction.
XX   OS      Synthetic.
XX   PN      WO9606626-A1.
XX   PD      07-MAR-1996.
XX   PF      26-AUG-1994; 94WO-US09563.
XX   PR      26-AUG-1994; 94WO-US09563.
XX   PS      (GOLD/) GOLDSTEIN A.
XX   PT      (LEEN/) LEE N M.
XX   PI      Goldstein A, Lee NM;
XX   DR      WPI; 1996-160138/16.
XX   CC      The peptides AAR91320-45 represent analogues of dynorphin A, a member of
XX   CC      the dynorphin group of endogenous opioids derived from proenkephalin B.
XX   CC      The novel peptides contain N- and C-terminal truncations as compared to
XX   CC      the 17 amino acid natural dynorphin A. The peptides AAR91337-45 have a
XX   CC      truncation of the N-terminal Tyr-Gly amino acids and serial deletions of
XX   CC      the C-terminal amino acids. It has been shown that dynorphin A
XX   CC      analogues having the N-terminal Tyr residue deleted do not bind to mu,
XX   CC      delta or kappa opioid receptors. The peptides presented here are
XX   CC      analogues that do not bind to opioid receptors but retain an
XX   CC      anti-nociceptive (i.e. analgesic) activity. The peptides can be used to
XX   CC      treat pain which is resistant to opioid analgesics e.g. neuropathic or
XX   CC      neurogenic pain, allodynia, post-operative pain or burns. Since the
XX   CC      peptides do not interact with the opioid receptors, side effects
XX   CC      associated with opioid analgesics, e.g. drowsiness or addiction, are
XX   CC      avoided.
XX   SQ      Sequence 11 AA;
XX   Query Match 26.7%; Score 4; DB 17; Length 11;
XX   Best Local Similarity 100.0%; Pred. No. 7e+02;
XX   Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
Db      8 PKLK 11
|||||
RESULT 62
AAR91323
ID   AAR91323 standard; peptide; 11 AA.
XX   AC      AAR91323;
XX   DT      12-NOV-1998 (first entry)
XX   DE      Des-Tyr-Gly dynorphin analogue #17.
XX   KW      dynorphin A; narcotic; analgesic; withdrawal symptoms; opiate addict;
XX   KW      morphine; pain.
XX   OS      Synthetic.
XX   PN      WO9606626-A1.
XX   PD      07-MAR-1996.
XX   PF      26-AUG-1994; 94WO-US09563.
XX   PR      26-AUG-1994; 94WO-US09563.
XX   PS      (GOLD/) GOLDSTEIN A.
XX   PT      (LEEN/) LEE N M.
XX   PI      Goldstein A, Lee NM;
XX   DR      WPI; 1996-160138/16.
XX   CC      The peptides AAR91320-45 represent analogues of dynorphin A, a member of
XX   CC      the dynorphin group of endogenous opioids derived from proenkephalin B.
XX   CC      The novel peptides contain N- and C-terminal truncations as compared to
XX   CC      the 17 amino acid natural dynorphin A. The peptides AAR91337-45 have a
XX   CC      truncation of the N-terminal Tyr-Gly amino acids and serial deletions of
XX   CC      the C-terminal amino acids. It has been shown that dynorphin A
XX   CC      analogues having the N-terminal Tyr residue deleted do not bind to mu,
XX   CC      delta or kappa opioid receptors. The peptides presented here are
XX   CC      analogues that do not bind to opioid receptors but retain an
XX   CC      anti-nociceptive (i.e. analgesic) activity. The peptides can be used to
XX   CC      treat pain which is resistant to opioid analgesics e.g. neuropathic or
XX   CC      neurogenic pain, allodynia, post-operative pain or burns. Since the
XX   CC      peptides do not interact with the opioid receptors, side effects
XX   CC      associated with opioid analgesics, e.g. drowsiness or addiction, are
XX   CC      avoided.
XX   SQ      Sequence 11 AA;
XX   Query Match 26.7%; Score 4; DB 17; Length 11;
XX   Best Local Similarity 100.0%; Pred. No. 7e+02;
XX   Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
Db      7 PKLK 10
|||||
RESULT 63
AAR65968
ID   AAR65968 standard; peptide; 11 AA.
XX   AC      AAR65968;
XX   DT      12-NOV-1998 (first entry)
XX   DE      Des-Tyr-Gly dynorphin analogue #17.
XX   KW      dynorphin A; narcotic; analgesic; withdrawal symptoms; opiate addict;
XX   KW      morphine; pain.
XX   OS      Synthetic.

```



OS Homo sapiens.  
PN US5807827-A.  
XX  
XX 15-SEP-1998.  
XX  
XX 14-MAY-1997; 97US-0856053.  
XX  
XX 27-SEP-1993; 93US-0127132.  
PR 12-JUN-1992; 92US-0897920.  
PR 20-DEC-1995; 95US-0581479.  
PR 14-MAY-1997; 97US-0856053.  
XX  
PA (DST-) DES-TYR DYNORPHIN PARTNERSHIP.  
XX  
PI Lee NM, Loh HH, Takemori AE;  
XX  
XX WPI; 1998-520169/44.  
XX  
XX Treatment of narcotic analgesic tolerance with dynorphin analogues -  
PT useful for treating narcotics addicts and allowing the use of lower  
PT doses of e.g. morphine to treat chronic pain  
XX  
XX Example 1; Column 4; 12pp; English.  
XX  
XX The invention relates to the treatment of narcotic analgesic tolerance.  
CC It comprises administering a dynorphin analogue that is des-tyr or des-  
CC Tyr-Glu at the N terminus and which has at least 7 amino acid residues.  
CC The dynorphin analogue, which potentiates analgesic actions, is useful  
CC when administered in a solution in conjunction with a narcotic analgesic  
CC for: (a) blocking withdrawal symptoms in e.g. opiate addicts, and (b)  
CC allowing lower doses of e.g. morphine to be used in treating chronic  
CC pain. The present sequence represents a dynorphin analogue, which is  
CC without the N-terminal tyrosine-glycine residues (des-Tyr-Gly) with  
CC respect to endogenous dynorphin.  
XX  
XX Sequence 11 AA;  
SQ  
Query Match 26.7%; Score 4; DB 19; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PKLK 8  
Db 8 PKLK 11  
RESULT 64  
AAB15261  
ID AAB15261 standard; peptide; 11 AA.  
XX  
AC AAB15261;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Specific factor VIII binding peptide #24.  
XX  
KW Factor VIII binding peptide; factor VIII purification; haemophilia.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 2..10  
XX  
PN WO200040602-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 03-JAN-2000; 2000WO-US00043.  
XX  
PR 04-JAN-1999; 99US-0224785.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;  
XX  
XX WPI; 2000-475816/41.  
XX  
XX New polypeptides which bind Factor VIII and/or Factor VIII-like  
PT polypeptides, useful for the detection and purification of human Factor  
PT VIII and/or Factor VIII-like polypeptides -  
XX  
XX Claim 2; Page 28; 57pp; English.  
XX  
XX The present sequence is the sequence of a peptide which can  
CC be used to bind Factor VIII and Factor VIII-like proteins. The two  
CC cysteine residues present cause it to form a disulphide bond, thus  
CC creating a stable loop structure. The Factor VIII isolated by this  
CC peptide can then be used in the treatment of Haemophilia A.  
XX  
XX Sequence 11 AA;  
SQ

XX Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;  
PI WPI; 2000-475816/41.  
XX  
XX New polypeptides which bind Factor VIII and/or Factor VIII-like  
PT polypeptides, useful for the detection and purification of human Factor  
PT VIII and/or Factor VIII-like polypeptides -  
XX  
XX Claim 2; Page 28; 57pp; English.  
XX  
XX The present sequence is the sequence of a peptide which can  
CC be used to bind Factor VIII and Factor VIII-like proteins. The two  
CC cysteine residues present cause it to form a disulphide bond, thus  
CC creating a stable loop structure. The Factor VIII isolated by this  
CC peptide can then be used in the treatment of Haemophilia A.  
XX  
XX Sequence 11 AA;  
SQ  
Query Match 26.7%; Score 4; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 VFPF 14  
Db 4 VFPF 7  
RESULT 65  
AAB15262  
ID AAB15262 standard; peptide; 11 AA.  
XX  
AC AAB15262;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Specific factor VIII binding peptide #25.  
XX  
KW Factor VIII binding peptide; factor VIII purification; haemophilia.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 2..10  
XX  
PN WO200040602-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 03-JAN-2000; 2000WO-US00043.  
XX  
PR 04-JAN-1999; 99US-0224785.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;  
XX  
XX WPI; 2000-475816/41.  
XX  
XX New polypeptides which bind Factor VIII and/or Factor VIII-like  
PT polypeptides, useful for the detection and purification of human Factor  
PT VIII and/or Factor VIII-like polypeptides -  
XX  
XX Claim 2; Page 28; 57pp; English.  
XX  
XX The present sequence is the sequence of a peptide which can  
CC be used to bind Factor VIII and Factor VIII-like proteins. The two  
CC cysteine residues present cause it to form a disulphide bond, thus  
CC creating a stable loop structure. The Factor VIII isolated by this  
CC peptide can then be used in the treatment of Haemophilia A.  
XX  
XX Sequence 11 AA;  
SQ

Query Match 26.7%; Score 4; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
    ||||  
Db 4 VFPF 7

RESULT 66  
AAB15263  
ID AAB15263 standard; peptide; 11 AA.  
XX  
AC AAB15263;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Specific factor VIII binding peptide #26.  
XX  
KW Factor VIII binding peptide; factor VIII purification; haemophilia.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 2..10  
XX  
PN WO200040602-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 03-JAN-2000; 2000WO-US00043.  
XX  
PR 04-JAN-1999; 99US-0224785.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;  
XX  
DR WPI; 2000-475816/41.  
XX  
PN New polypeptides which bind Factor VIII and/or Factor VIII-like  
PT polypeptides, useful for the detection and purification of human Factor  
FT VIII and/or Factor VIII-like polypeptides -  
XX  
PS Claim 2; Page 28; 57pp; English.  
XX  
CC The present sequence is the sequence of a peptide which can  
CC be used to bind Factor VIII and Factor VIII-like proteins. The two  
CC cysteine residues present cause it to form a disulphide bond, thus  
CC creating a stable loop structure. The Factor VIII isolated by this  
CC peptide can then be used in the treatment of Haemophilia A.

XX  
SQ Sequence 11 AA;  
    Query Match 26.7%; Score 4; DB 21; Length 11;  
    Best Local Similarity 100.0%; Pred. No. 7e+02; 0; Indels 0; Gaps 0;  
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
    ||||  
Db 4 VFPF 7

RESULT 67  
AAB15264  
ID AAB15264 standard; peptide; 11 AA.  
XX  
AC AAB15264;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Specific factor VIII binding peptide #27.

KW Factor VIII binding peptide; factor VIII purification; haemophilia.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 2..10  
XX  
PN WO200040602-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 03-JAN-2000; 2000WO-US00043.  
XX  
PR 04-JAN-1999; 99US-0224785.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;  
XX  
DR WPI; 2000-475816/41.  
XX  
PN New polypeptides which bind Factor VIII and/or Factor VIII-like  
PT polypeptides, useful for the detection and purification of human Factor  
FT VIII and/or Factor VIII-like polypeptides -  
XX  
PS Claim 2; Page 28; 57pp; English.  
XX  
CC The present sequence is the sequence of a peptide which can  
CC be used to bind Factor VIII and Factor VIII-like proteins. The two  
CC cysteine residues present cause it to form a disulphide bond, thus  
CC creating a stable loop structure. The Factor VIII isolated by this  
CC peptide can then be used in the treatment of Haemophilia A.

XX  
SQ Sequence 11 AA;  
    Query Match 26.7%; Score 4; DB 21; Length 11;  
    Best Local Similarity 100.0%; Pred. No. 7e+02; 0; Indels 0; Gaps 0;  
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
    ||||  
Db 4 VFPF 7

RESULT 68  
AAB15266  
ID AAB15266 standard; peptide; 11 AA.  
XX  
AC AAB15266;  
XX  
DT 19-DEC-2000 (first entry)  
XX  
DE Specific factor VIII binding peptide #29.  
XX  
KW Factor VIII binding peptide; factor VIII purification; haemophilia.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 2..10  
XX  
PN WO200040602-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 03-JAN-2000; 2000WO-US00043.  
XX  
PR 04-JAN-1999; 99US-0224785.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;  
XX

DR WPI; 2000-475816/41.  
XX  
PT New polypeptides which bind Factor VIII and/or Factor VIII-like  
PT polypeptides, useful for the detection and purification of human Factor  
PT VIII and/or Factor VIII-like polypeptides -  
XX  
PS Claim 2; Page 28; 57pp; English.  
XX  
XX  
CC The present sequence is the sequence of an example of a peptide which can  
CC be used to bind Factor VIII and Factor VIII-like proteins. The two  
CC cysteine residues present cause it to form a disulphide bond, thus  
CC creating a stable loop structure. The Factor VIII isolated by this  
CC peptide can then be used in the treatment of Haemophilia A.  
XX  
SQ Sequence 11 AA;  
  
Query Match 26.7%; Score 4; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 VFPF 14  
Db 4 VFPF 7  
  
RESULT 69  
AAE02349  
ID AAE02349 standard; Protein; 11 AA.  
XX  
AC AAE02349;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Caenorhabditis elegans Ras suppressor SUR-5 AMP binding motif #2.  
XX  
XX  
KW Ras suppressor; SUR-5; cytostatic; Ras signalling; gene therapy;  
KW cell growth; differentiation; proliferation; transgenic animal;  
KW cancer; nematode; AMP binding motif.  
XX  
OS Caenorhabditis elegans.  
XX  
FN US6225456-B1.  
XX  
PD 01-MAY-2001.  
XX  
PF 06-MAY-1999; 99US-0307265.  
XX  
PR 07-MAY-1998; 98US-0084590.  
XX  
PA (UYTE-) UNIV TECHNOLOGY CORP.  
XX  
PI Gu T, Orita S, Han M;  
XX  
XX WPI; 2001-342417/36.  
XX  
XX Novel Ras suppressor SUR-5 polynucleotides from human, murine,  
PT Caenorhabditis elegans, for treating Ras-mediated effects, especially  
PT cancer and producing SUR-5 polypeptides for screening drugs altering  
PT Ras signaling -  
XX  
XX Example 12; Column 71; 50pp; English.  
XX  
XX  
CC The invention relates to Ras suppressor sur-5 polynucleotides and  
CC polypeptides (SUR-5) from human, murine and Caenorhabditis elegans  
CC (nematode). SUR-5 polynucleotides are useful for producing poly-  
CC peptides by recombinant techniques, which are useful as targets for  
CC screening drugs that alter Ras signalling and the physiological  
CC effects of Ras such as effects on cell growth, differentiation and  
CC proliferation. SUR-5 genes are useful in gene therapy for treating  
CC diseases or altering physiological states characterised by unwanted  
CC proliferation of cells or other Ras-mediated effects, especially  
CC cancer. The invention also provides methods of producing transgenic  
CC animals expressing SUR-5.

CC The present sequence is C. elegans Ras suppressor SUR-5 AMP  
CC binding motif.  
XX  
SQ Sequence 11 AA;  
  
Query Match 26.7%; Score 4; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 KVEV 11  
Db 8 KVEV 11  
  
RESULT 70  
AAB91600  
ID AAB91600 standard; Peptide; 11 AA.  
XX  
AC AAB91600;  
XX  
DT 22-JUN-2001 (first entry)  
XX  
DE Opioid peptide SEQ ID NO:776.  
XX  
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200069900-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 17-MAY-2000; 2000WO-US13576.  
XX  
PR 17-MAY-1999; 99US-0134406.  
PR 10-SEP-1999; 99US-0153406.  
PR 15-OCT-1999; 99US-0159783.  
XX  
PA (CONJ-) CONJUCHEM INC.  
XX  
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
XX  
XX WPI; 2001-112059/12.  
XX  
XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity  
PT -  
XX  
XX Disclosure; Page 449; 733pp; English.  
XX  
XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
 ||||  
 DB 8 PKLK 11

RESULT 71  
 AAB91619  
 ID AAB91619 standard; Peptide; 11 AA.  
 XX  
 AC AAB91619;

XX 22-JUN-2001 (first entry)

DE Opioid peptide SEQ ID NO:795.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 455; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CC exemplification of the present invention.

SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8

DB 8 PKLK 11  
 ||||

RESULT 72  
 AAB91621  
 ID AAB91621 standard; Peptide; 11 AA.  
 XX  
 AC AAB91621;

XX 22-JUN-2001 (first entry)

DE Opioid peptide SEQ ID NO:797.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 456; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CC exemplification of the present invention.

SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8

DB 4 PKLK 7

RESULT 73

AAP10402  
 ID AAP10402 standard; peptide; 12 AA.  
 XX  
 AC AAP10402;  
 XX  
 DT 16-DEC-1992 (first entry)  
 XX  
 DE Analgesic peptide.  
 XX  
 KW Dynorphin; enkephalin; endorphin; opioid receptor; neurotransmitter;  
 KW radioimmunoassay; mood altering; muscle relaxing; regulatory.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 2  
 FT /label= D-form  
 FT Modified-site 12  
 FT /label= amidated  
 FT  
 XX EP29300-A.  
 PN  
 XX 27-MAY-1981.  
 PD  
 XX 20-OCT-1980; 80EP-0303698.  
 PF  
 XX 05-NOV-1979; 79US-0091615.  
 PR  
 XX (ADDI ) ADDI-COLOR AG.  
 PA  
 XX Goldstein A;  
 PI  
 XX WPI; 1981-40572D/23 (40572D).  
 XX  
 DR Oligopeptide contg. alternating basic hydrophilic and hydrophobic  
 PT unit - useful e.g. as analgesics and for raising antisera  
 PT  
 XX Claim 5; Page 20; 4lpp; English.  
 PS  
 XX The synthetic peptide is an example of an extremely generic  
 CC oligopeptide having a chain of at least 5 amino acids with  
 CC alternating basic hydrophilic and hydrophobic amino acids. The  
 CC peptide is a dynorphin analogue, having greater potency than leu-  
 CC enkephalin and beta-endorphin. The peptide is an intermediate for  
 CC an analgesic, an analgesic itself, and an opioid antagonist which is  
 CC useful for studying the structure of opioid binding sites. By  
 CC interaction with opioid receptor sites, they provide analgesic, mood  
 CC altering, muscle relaxing and blood-flow regulating effects.  
 CC See also AAP10403-5.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 26.7%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 PKLK 8  
 Db |||||  
 9 PKLK 12  
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 AAR45205  
 ID AAR45205 standard; Protein; 12 AA.  
 XX  
 AC AAR45205;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 01-JAN-1980 (first entry)  
 XX  
 DE des-Tyr Dynorphin A (1-17) analogue #4.  
 XX  
 KW Analogue; dynorphin; dynorphin A (1-17); des-Tyr; cerebral; spinal;  
 XX

KW ischemia; respiratory depression; gastroenteric spasm;  
 KW narcotic analgesic; anti-inflammation; immune system.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9325217-A1.  
 XX  
 PD 23-DEC-1993.  
 XX  
 PF 01-JUN-1993; 93WO-US05161.  
 XX  
 PR 12-JUN-1992; 92US-0897920.  
 XX  
 PA (LEEN/) LEE N M.  
 PA (LOHH/) LOH H H.  
 PA (TAKE/) TAKEMORI A E.  
 XX  
 PI Lee NM, Loh HH, Takemori AE;  
 XX WPI; 1994-007185/01.  
 DR  
 XX Des-Tyr dynorphin analogues - potentiate activity of narcotic  
 PT analgesics and/or block withdrawal symptoms; are more stable in  
 PT vivo than native dynorphin  
 XX  
 PS Claim 1; Page 7; 24pp; English.  
 XX  
 CC The sequences given in AAR45202-21 are analogues of dynorphins based  
 CC on the sequence given in AAR45211. This sequence represents the first  
 CC of the dynorphins to be isolated and is designated "dynorphin A (1-  
 CC 17)". The claimed peptides of the invention have at least six amino  
 CC acids, but are des-Tyr with respect to dynorphin A (1-17). These  
 CC peptides may be used to reverse at least some neurological deficit  
 CC in treating cerebral and spinal ischemia, in inhibiting respiratory  
 CC depression or gastroenteric spasms produced by narcotic analgesics  
 CC to a naive host, as an adjunct for anti-inflammatory medication, and  
 CC in blocking narcotic-induced impairment in a host whose immune  
 CC system has been damaged by narcotic analgesics.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 12 AA;  
 Query Match 26.7%; Score 4; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 PKLK 8  
 Db |||||  
 9 PKLK 12  
 RESULT 75  
 AAR45215  
 ID AAR45215 standard; Protein; 12 AA.  
 XX  
 AC AAR45215;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 01-JAN-1980 (first entry)  
 XX  
 DE des-Tyr Dynorphin A (1-17) analogue #13.  
 XX  
 KW Analogue; dynorphin; dynorphin A (1-17); des-Tyr; cerebral; spinal;  
 KW ischemia; respiratory depression; gastroenteric spasm;  
 KW narcotic analgesic; anti-inflammation; immune system.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9325217-A1.  
 XX  
 PD 23-DEC-1993.  
 XX  
 PF 01-JUN-1993; 93WO-US05161.  
 XX

XX  
PR 12-JUN-1992; 92US-0897920.  
XX  
PA (LEEN/) LEE N M.  
PA (LOHH/) LOH H H.  
PA (TAKE/) TAKEMORI A E.  
XX  
PI Lee NM, Loh HH, Takemori AE;  
XX WPI; 1994-007185/01.  
XX  
PT Des-Tyr dynorphin analogues - potentiate activity of narcotic  
PT analgesics and/or block withdrawal symptoms; are more stable in  
PT vivo than native dynorphin  
XX  
PS Claim 2; Page 8; 24pp; English.  
XX  
CC The sequences given in AAR45202-21 are analogues of dynorphins based  
CC on the sequence given in AAR45211. This sequence represents the first  
CC of the dynorphins to be isolated and is designated "dynorphin A (1-  
CC 17)". The claimed peptides of the invention have at least six amino  
CC acids, but are des-tyr with respect to dynorphin A (1-17). These  
CC peptides may be used to reverse at least some neurological deficit  
CC in treating cerebral and spinal ischemia, in inhibiting respiratory  
CC depression or gastroenteric spasms produced by narcotic analgesics  
CC to a naive host, as an adjunct for anti-inflammatory medication, and  
CC in blocking narcotic-induced impairment in a host whose immune  
CC system has been damaged by narcotic analgesics.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 12 AA;  
XX  
Query Match 26.7%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PKLK 8  
Db 8 PKLK 11  
Search completed: November 25, 2003, 18:15:49  
Job time : 49.5904 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 29.8404 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPFKLKVVEVFPFP 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:\*

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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	15	100.0	15	US-10-281-652-8	Sequence 8, Appli
2	5	33.3	9	US-10-292-418-15	Sequence 15, Appli
3	5	33.3	9	US-10-277-292-451	Sequence 41, App
4	5	33.3	9	US-10-277-292-452	Sequence 452, App
5	5	33.3	9	US-10-277-292-551	Sequence 551, App
6	5	33.3	9	US-10-277-292-555	Sequence 555, App
7	5	33.3	9	US-10-280-340-451	Sequence 451, App
8	5	33.3	9	US-10-280-340-452	Sequence 452, App
9	5	33.3	9	US-10-280-340-551	Sequence 551, App
10	5	33.3	9	US-10-280-340-555	Sequence 555, App
11	5	33.3	10	US-10-277-292-66	Sequence 66, Appl
12	5	33.3	10	US-10-277-292-607	Sequence 607, App
13	5	33.3	10	US-10-277-292-629	Sequence 629, App
14	5	33.3	10	US-10-280-340-66	Sequence 66, Appl
15	5	33.3	10	US-10-280-340-607	Sequence 607, App

16	5	33.3	10	US-10-280-340-629	Sequence 629, App
17	5	33.3	16	US-10-225-567A-1110	Sequence 1110, Ap
18	5	33.3	19	US-10-225-567A-2044	Sequence 2044, Ap
19	4	26.7	4	US-09-750-736-4	Sequence 4, Appli
20	4	26.7	5	US-09-992-124A-7	Sequence 7, Appli
21	4	26.7	7	US-09-909-062-13	Sequence 13, Appli
22	4	26.7	7	US-10-293-371-15	Sequence 15, Appli
23	4	26.7	7	US-10-293-371-30	Sequence 30, Appli
24	4	26.7	7	US-10-293-371-32	Sequence 32, Appli
25	4	26.7	7	US-10-293-371-40	Sequence 40, Appli
26	4	26.7	7	US-10-293-371-41	Sequence 41, Appli
27	4	26.7	7	US-10-293-371-42	Sequence 42, Appli
28	4	26.7	9	US-09-393-634-91	Sequence 91, Appli
29	4	26.7	9	US-09-824-787B-124	Sequence 124, App
30	4	26.7	9	US-10-383-982-91	Sequence 91, Appli
31	4	26.7	9	US-10-277-292-333	Sequence 333, App
32	4	26.7	9	US-10-280-340-333	Sequence 333, App
33	4	26.7	10	US-09-572-270A-221	Sequence 221, App
34	4	26.7	10	US-09-572-270A-920	Sequence 920, App
35	4	26.7	10	US-09-573-822C-340	Sequence 340, App
36	4	26.7	10	US-10-277-292-269	Sequence 269, App
37	4	26.7	10	US-10-277-292-356	Sequence 356, App
38	4	26.7	10	US-10-280-340-269	Sequence 269, App
39	4	26.7	10	US-10-280-340-356	Sequence 356, App
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46	4	26.7	11	US-09-756-594-32	Sequence 32, Appli
47	4	26.7	11	US-10-272-497-27	Sequence 27, Appli
48	4	26.7	11	US-10-272-497-28	Sequence 28, Appli
49	4	26.7	11	US-10-272-497-29	Sequence 29, Appli
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51	4	26.7	11	US-10-272-497-32	Sequence 32, Appli
52	4	26.7	11	US-10-272-497-72	Sequence 72, Appli
53	4	26.7	11	US-10-272-497-74	Sequence 74, Appli
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55	4	26.7	11	US-10-272-497-79	Sequence 79, Appli
56	4	26.7	12	US-08-927-939-38	Sequence 38, Appli
57	4	26.7	12	US-09-798-119-3	Sequence 3, Appli
58	4	26.7	12	US-09-798-121-3	Sequence 3, Appli
59	4	26.7	12	US-09-813-329-37	Sequence 37, Appli
60	4	26.7	12	US-09-813-329-47	Sequence 47, Appli
61	4	26.7	12	US-09-813-329-58	Sequence 58, Appli
62	4	26.7	13	US-09-798-119-2	Sequence 2, Appli
63	4	26.7	13	US-09-798-121-2	Sequence 2, Appli
64	4	26.7	13	US-09-366-955A-31	Sequence 31, Appli
65	4	26.7	13	US-09-966-955A-32	Sequence 32, Appli
66	4	26.7	13	US-10-300-215-10	Sequence 10, Appli
67	4	26.7	13	US-10-300-215-32	Sequence 32, Appli
68	4	26.7	14	US-09-876-904A-194	Sequence 194, App
69	4	26.7	14	US-10-312-691-6	Sequence 6, Appli
70	4	26.7	14	US-10-145-206-29	Sequence 29, Appli
71	4	26.7	16	US-09-880-748-2262	Sequence 2262, Ap
72	4	26.7	16	US-10-234-816-98	Sequence 98, Appli
73	4	26.7	16	US-10-161-791-181	Sequence 181, App
74	4	26.7	16	US-10-225-567A-1075	Sequence 1075, Ap
75	4	26.7	17	US-09-170-919-7	Sequence 7, Appli
76	4	26.7	17	US-09-798-119-1	Sequence 1, Appli
77	4	26.7	17	US-09-798-121-1	Sequence 1, Appli
78	4	26.7	17	US-10-146-999-11	Sequence 11, Appli
79	4	26.7	17	US-10-197-954-46	Sequence 46, Appli
80	4	26.7	18	US-09-864-761-40786	Sequence 40786, A
81	4	26.7	18	US-10-082-014-92	Sequence 92, Appli
82	4	26.7	18	US-10-281-652-22	Sequence 22, Appli
83	4	26.7	18	US-10-281-652-22	Sequence 22, Appli
84	4	26.7	18	US-10-225-567A-1930	Sequence 1930, Ap
85	4	26.7	18	US-10-225-567A-1985	Sequence 1985, Ap
86	4	26.7	19	US-09-864-761-45349	Sequence 45349, A
87	4	26.7	20	US-09-841-132-156	Sequence 156, App
88	4	26.7	20	US-09-757-417-35	Sequence 35, Appli

89                   4   26.7   20   11   US-09-983-802-664   Sequence 664, Appl  
90                   4   26.7   20   12   US-10-181-993A-4   Sequence 4, Appl  
91                   4   26.7   20   12   US-10-280-066-45   Sequence 45, Appl  
92                   4   26.7   20   12   US-09-171-432A-57   Sequence 57, Appl  
93                   4   26.7   20   12   US-10-145-206-4   Sequence 4, Appl  
94                   4   26.7   20   15   US-10-042-945-35   Sequence 35, Appl  
95                   3   20.0   4   11   US-09-300-425B-31   Sequence 31, Appl  
96                   3   20.0   4   12   US-10-237-160-1   Sequence 1, Appl  
97                   3   20.0   4   12   US-10-293-371-72   Sequence 72, Appl  
98                   3   20.0   4   12   US-10-087-942-5   Sequence 5, Appl  
99                   3   20.0   4   12   US-10-313-338A-1   Sequence 1, Appl  
100                  3   20.0   4   12   US-10-313-790A-1   Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-8  
; Sequence 8, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDGOSH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-8

Query Match                   100.0%; Score 15; DB 15; Length 15;  
Best Local Similarity   100.0%; Pred. No. 1.2e-08;  
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY   1 LKPPKLVKVEVFPPF 15  
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Db   1 LKPPKLVKVEVFPPF 15

RESULT 2  
US-10-292-418-15  
; Sequence 15, Application US/10292418  
; Publication No. US20030139365A1  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Li, Yue  
; APPLICANT: Gillies, Stephen D  
; TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as  
; TITLE OF INVENTION: Immunofusins  
; FILE REFERENCE: LEX-006C1  
; CURRENT APPLICATION NUMBER: US/10/292,418  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 09/383,315  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 60/097,883  
; PRIOR FILING DATE: 1998-08-25  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Forward primer  
; OTHER INFORMATION: for human Fc-Angio  
US-10-292-418-15

Query Match                   33.3%; Score 5; DB 12; Length 9;  
Best Local Similarity   100.0%; Pred. No. 6e+05;  
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY   5 PKLKV 9  
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Db   1 PKLKV 5

RESULT 3  
US-10-277-292-451  
; Sequence 451, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 451  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-451

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Best Local Similarity   100.0%; Pred. No. 6e+05;  
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY   5 PKLKV 9  
     |||||  
Db   4 PKLKV 8

RESULT 4  
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; Sequence 452, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA



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/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/277,292
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 452
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-452

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      2 PKLKV 6

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US-10-277-292-551
/ Sequence 551, Application US/10277292
/ Publication No. US20030199470A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/277,292
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 551
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-551

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      2 PKLKV 6

RESULT 6
US-10-277-292-555
/ Sequence 555, Application US/10277292
/ Publication No. US20030199470A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/277,292
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 555
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-555

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      4 PKLKV 8

RESULT 7
US-10-280-340-451
/ Sequence 451, Application US/10280340
/ Publication No. US20030207835A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/280,340
/ CURRENT FILING DATE: 2002-10-25
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 451
/ LENGTH: 9
/ TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-451

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 4 PKLKV 8

RESULT 8
US-10-280-340-452
; Sequence 452, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 452
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-452

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6

RESULT 9
US-10-280-340-551
; Sequence 551, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 452
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-452

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6

RESULT 9
US-10-280-340-551
; Sequence 551, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
```

```
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 551
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-551

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6

RESULT 10
US-10-280-340-555
; Sequence 555, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-555

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 4 PKLKV 8

RESULT 11
US-10-277-292-66
; Sequence 66, Application US/10277292
```

; Publication No. US20030199470A1

; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-66  
Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PKLV 9  
DB 4 PKLV 8  
RESULT 12  
US-10-277-292-607  
; Sequence 607, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-66  
Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PKLV 9  
DB 4 PKLV 8

US-10-277-292-607  
; Sequence 607, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-607  
; Sequence 607, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLV 9  
DB 4 PKLV 8

US-10-277-292-629  
; Sequence 629, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 629  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-629  
Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLV 9  
DB 2 PKLV 6

US-10-280-340-66  
; Sequence 66, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22

US-10-277-292-607  
; Sequence 607, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-66

Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9  
| | | | |  
Db 4 PKLKV 8

RESULT 15  
US-10-280-340-607  
; Sequence 607, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 607  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-607

Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9  
| | | | |  
Db 4 PKLKV 8

RESULT 16  
US-10-280-340-629  
; Sequence 629, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIIS, MARY  
; APPLICANT: HUBERT, RENE

; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 629  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-629

Query Match 33.3%; Score 5; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9  
| | | | |  
Db 2 PKLKV 6

RESULT 17  
US-10-225-567A-1110  
; Sequence 1110, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1110  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1110

Query Match 33.3%; Score 5; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPFPK 6  
| | | | |  
Db 9 KPFPK 13

RESULT 18  
US-10-225-567A-2044  
; Sequence 2044, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:

```
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2044
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2044

Query Match      33.3%; Score 5; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LKVEV 11
      |||||
Db      4 LKVEV 8

RESULT 19
US-09-750-726-4
; Sequence 4, Application US/09750726
; Patent No. US20010010817A1
; GENERAL INFORMATION:
; APPLICANT: Platt, David
; TITLE OF INVENTION: TUMOR DERIVED CARBOHYDRATE BINDING
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gifford, Krass, et al
; STREET: 280 No. US20010010817A1th Woodward Ave., Suite 400
; CITY: Birmingham
; STATE: Michigan
; COUNTRY: US
; ZIP: 48009
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/750,726
; FILING DATE: 28-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Citkowski, Ronald W.
; REGISTRATION NUMBER: 31,005
; REFERENCE/POCKET NUMBER: DPL-00102/16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-647-6000
; TELEFAX: 810-647-5210
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-750-726-4

Query Match      26.7%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VFPF 14
      |||||
Db      1 VFPF 4
```

```
Db      1 VFPF 4
      |||||

RESULT 20
US-09-992-124A-7
; Sequence 7, Application US/09992124A
; Publication No. US20030162289A1
; GENERAL INFORMATION:
; APPLICANT: Heidaran, Mohammad A.
; APPLICANT: Haaland, Perry D.
; APPLICANT: Wilkins, Jamie H.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: Peptides Promoting Cell Adherence, Growth and Secretion
; FILE REFERENCE: 102-410
; CURRENT APPLICATION NUMBER: US/09/992,124A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide selected for biological activity
US-09-992-124A-7

Query Match      26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VFPF 14
      |||||
Db      1 VFPF 4

RESULT 21
US-09-909-062-13
; Sequence 13, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Garguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
```

; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (6).-(6)  
; OTHER INFORMATION: norvaline-C(-O)  
US-09-909-062-13

Query Match 26.7%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVFP 13  
|||  
Db 2 EVFP 5

## RESULT 22

US-10-293-371-15  
; Sequence 15, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELUK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-293-371-15

Query Match 26.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPFP 5  
|||  
Db 2 KPFP 5

## RESULT 23

US-10-293-371-30  
; Sequence 30, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELUK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 30

; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-293-371-30

Query Match 26.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFPP 15  
|||  
Db 2 PFPP 5

## RESULT 24

US-10-293-371-32  
; Sequence 32, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELUK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-293-371-32

Query Match 26.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFPP 15  
|||  
Db 2 PFPP 5

## RESULT 25

US-10-293-371-40  
; Sequence 40, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELUK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0

```
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-40

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPPP 15
Db 2 FPPP 5

RESULT 26
US-10-293-371-41
; Sequence 41, Application US/10293371
; Publication NO. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-41

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPPP 15
Db 2 FPPP 5

RESULT 27
US-10-293-371-42
; Sequence 42, Application US/10293371
; Publication NO. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-42

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPPP 15
Db 2 FPPP 5

RESULT 28
US-09-393-634-91
; Sequence 91, Application US/09393634
; Patent No. US20020051997A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a NO. US20020051997A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Sf01 signature
; OTHER INFORMATION: sequence 4, amino acids encoded by PCR primers
; OTHER INFORMATION: identifying polymorphic variants, interspecies
; OTHER INFORMATION: homologs and alleles of Sf family members
US-09-393-634-91

Query Match          26.7%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 6 PKLK 9

RESULT 29
US-09-824-787B-124
; Sequence 124, Application US/09824787B
; Patent No. US2002015547A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
```

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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-124

Query Match      26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPKL 7
Db 1 PPKL 4

RESULT 30
US-10-383-982-91
; Sequence 91, Application US/10383982
; Publication No. US20030157568A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. US20030157568A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/10/383,982
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/393,634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sf01 signature
; OTHER INFORMATION: sequence 4, amino acids encoded by PCR primers
; OTHER INFORMATION: identifying polymorphic variants, interspecies
; OTHER INFORMATION: homologs and alleles of Sf family members
US-10-383-982-91

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKL 8
Db 6 PPKL 9

RESULT 31
US-10-277-292-333
; Sequence 333, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

```

```

; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-333

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKL 8
Db 6 PPKL 9

RESULT 32
US-10-280-340-333
; Sequence 333, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-333

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKL 8
Db 6 PPKL 9

RESULT 33

```



```
US-09-572-270A-221
; Sequence 221, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 221
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in CYP88A3 OR YUP8H12.23. at 402-411 and
US-09-572-270A-221

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 EVVPF 13
Db      4 EVFP 7

RESULT 34
US-09-572-270A-920
; Sequence 920, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 920
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in AH1. at 339-348 and may interact with
US-09-572-270A-920

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEVF 12
Db      7 VEVF 10

RESULT 35
US-09-573-822C-340
; Sequence 340, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 340
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG370 at 287-296 and may interact with Sequen
```

```
; OTHER INFORMATION: in this patent.
US-09-573-822C-340

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPKL 7
Db      5 FPKL 8

RESULT 36
US-10-277-292-269
; Sequence 269, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-269

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
Db      7 PKLK 10

RESULT 37
US-10-277-292-356
; Sequence 356, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
```

; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 356  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-356

Query Match 26.7%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PKLK 8  
| | | |  
Db 7 PKLK 10

RESULT 38  
US-10-280-340-269  
; Sequence 269, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 269  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-269

Query Match 26.7%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PKLK 8  
| | | |  
Db 7 PKLK 10

RESULT 39  
US-10-280-340-356  
; Sequence 356, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:

; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 356  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-356

Query Match 26.7%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PKLK 8  
| | | |  
Db 7 PKLK 10

RESULT 40  
US-10-033-741-52  
; Sequence 52, Application US/10033741  
; Publication No. US20030049640A1  
; GENERAL INFORMATION:  
; APPLICANT: Herman, et al.  
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of V.  
; TITLE OF INVENTION: Response  
; FILE REFERENCE: 9195-079  
; CURRENT APPLICATION NUMBER: US/10/033,741  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 52  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-741-52

Query Match 26.7%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 VEVF 12  
| | | |  
Db 6 VEVF 9

RESULT 41  
US-10-033-662-47  
; Sequence 47, Application US/10033662  
; Publication No. US20030092197A1  
; GENERAL INFORMATION:  
; APPLICANT: Herman, et al.  
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of C.

```
; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-47

Query Match          26.7%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12
Db 6 VEVF 9

RESULT 42
US-09-756-594-27
; Sequence 27, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-27

Query Match          26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPP 14
Db 4 VFPP 7

RESULT 43
US-09-756-594-28
; Sequence 28, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-28

Query Match          26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPP 14
Db 4 VFPP 7

RESULT 44
US-09-756-594-29
; Sequence 29, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-29

Query Match          26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPP 14
Db 4 VFPP 7

RESULT 45
US-09-756-594-30
; Sequence 30, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-30

Query Match          26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPP 14
Db 4 VFPP 7
```

```
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-30

Query Match          26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
   ||||
Db 4 VFPF 7

RESULT 46
US-09-756-594-32
; Sequence 32, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; TITLE OF INVENTION: VIII-like Proteins
; FILE REFERENCE: dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09756,594
; FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-32

Query Match          26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
   ||||
Db 4 VFPF 7

RESULT 47
US-10-272-497-27
; Sequence 27, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009

; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence
US-10-272-497-28

Query Match          26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
   ||||
Db 4 VFPF 7

RESULT 48
US-10-272-497-28
; Sequence 28, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence
US-10-272-497-28

Query Match          26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
   ||||
Db 4 VFPF 7

RESULT 49
US-10-272-497-29
; Sequence 29, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
```

```

; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-29

```

```

Query Match      26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VFPF 14
        ||||
Db       4 VFPF 7

```

```

RESULT 50
US-10-272-497-30
; Sequence 30, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-30

```

```

Query Match      26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VFPF 14
        ||||
Db       4 VFPF 7

```

```

RESULT 51
US-10-272-497-32
; Sequence 32, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel

```

```

; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-32

```

```

Query Match      26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VFPF 14
        ||||
Db       4 VFPF 7

```

```

RESULT 52
US-10-272-497-72
; Sequence 72, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-72

```

```

Query Match      26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      11 VFPF 14
        ||||
Db       4 VFPF 7

```

```

RESULT 53
US-10-272-497-74
; Sequence 74, Application US/10272497
; Publication No. US20030165822A1

```

US-10-272-497-76

GENERAL INFORMATION:  
; APPLICANT: Yu, Jinan  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Kelley, Brian D.  
; APPLICANT: Deetz, Jeffrey S.  
; APPLICANT: Booth, James E.  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII  
; FILE REFERENCE: 3421.1004-009  
; CURRENT APPLICATION NUMBER: US/10/272,497  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: US 09/756,594  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 74  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Selected Phase Display Sequence

Query Match 26.7%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
Db 4 VFPF 7

RESULT 54

US-10-272-497-76

Sequence 76, Application US/10272497  
; Publication No. US20030165822A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Jinan  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Kelley, Brian D.  
; APPLICANT: Deetz, Jeffrey S.  
; APPLICANT: Booth, James E.  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII  
; FILE REFERENCE: 3421.1004-009  
; CURRENT APPLICATION NUMBER: US/10/272,497  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: US 09/756,594  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Selected Phase Display Sequence

US-10-272-497-76

Query Match 26.7%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
Db 4 VFPF 7

RESULT 55

US-10-272-497-79

Sequence 79, Application US/10272497  
; Publication No. US20030165822A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Jinan  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Kelley, Brian D.  
; APPLICANT: Deetz, Jeffrey S.  
; APPLICANT: Booth, James E.  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII  
; FILE REFERENCE: 3421.1004-009  
; CURRENT APPLICATION NUMBER: US/10/272,497  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: US 09/756,594  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: US 09/224,785  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 79  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Selected Phase Display Sequence

Query Match 26.7%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
Db 4 VFPF 7

RESULT 56

US-08-927-939-38

Sequence 38, Application US/08927939  
; Publication No. US20010006640A1  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatallick, Lauen Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; FILE REFERENCE: 295.022US1  
; CURRENT APPLICATION NUMBER: US/08/927,939  
; CURRENT FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: Selected Phase Display Sequence

Query Match 26.7%; Score 4; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 6 PKLK 9

RESULT 57

US-09-798-119-3

Sequence 3, Application US/09798119  
; Patent No. US20010018420A1  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.

```
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: A METHOD FOR ALLEVIATING PAIN OR PROVIDING AN ANALGESIC EFFECT IN
; TITLE OF INVENTION: PATIENT
; FILE REFERENCE: 500862000610
; CURRENT APPLICATION NUMBER: US/09/798,119
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(2-13)
US-09-798-119-3

Query Match          26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
      ||||
Db      9 PKLK 12

RESULT 58
US-09-798-121-3
; Sequence 3, Application US/09798121
; Patent No. US20010018421A1
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCICEPTIVE AGENT COVALENTLY BONDE
; TITLE OF INVENTION: BLOOD COMPONENT
; FILE REFERENCE: 500862000612
; CURRENT APPLICATION NUMBER: US/09/798,121
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(2-13)
US-09-798-121-3

Query Match          26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
      ||||
Db      9 PKLK 12

RESULT 59
US-09-813-329-37
```

```
; Sequence 37, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class M
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-37

Query Match          26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKPF 4
      ||||
Db      6 LKPF 9

RESULT 60
US-09-813-329-47
; Sequence 47, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class M
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-47

Query Match          26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKPF 4
      ||||
Db      6 LKPF 9

RESULT 61
US-09-813-329-58
; Sequence 58, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Suibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class M
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
```

; SEQ ID NO 58  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-813-329-58

Query Match 26.7%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPF 4  
|||  
Db 6 LKPF 9

RESULT 62  
US-09-798-119-2  
; Sequence 2, Application US/09798119  
; Patent No. US20010018420A1  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; APPLICANT: HOLMES, DARREN L.  
; APPLICANT: MILNER, PETER G.  
; TITLE OF INVENTION: A METHOD FOR ALLEVIATING PAIN OR PROVIDING AN ANALGESIC EFFECT  
; FILE REFERENCE: 500862000610  
; CURRENT APPLICATION NUMBER: US/09/798,119  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/445,986  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US98/23704  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin  
; OTHER INFORMATION: analogue A(1-13)  
US-09-798-119-2

Query Match 26.7%; Score 4; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 10 PKLK 13

RESULT 63  
US-09-798-121-2  
; Sequence 2, Application US/09798121  
; Patent No. US20010018421A1  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; APPLICANT: HOLMES, DARREN L.  
; APPLICANT: MILNER, PETER G.  
; TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCEPTIVE AGENT COVALENTLY BONDED  
; FILE REFERENCE: 500862000612  
; CURRENT APPLICATION NUMBER: US/09/798,121  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/445,986  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US98/23704  
; PRIOR FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin  
; OTHER INFORMATION: analogue A(1-13)  
US-09-798-121-2

Query Match 26.7%; Score 4; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 10 PKLK 13

RESULT 64  
US-09-966-955A-31  
; Sequence 31, Application US/09966955A  
; Patent No. US2002015563A1  
; GENERAL INFORMATION:  
; APPLICANT: Perez-Villar, Juan J.  
; APPLICANT: Chang, Han  
; APPLICANT: Yang, Wen-Pin  
; APPLICANT: Wu, Yuli  
; APPLICANT: Whitney, Gena S.  
; APPLICANT: Kanner, Steven B.  
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human  
; TITLE OF INVENTION: Clnk-related Gene, MIST (Mast Cell Immunoreceptor  
; TITLE OF INVENTION: Signal Transducer)  
; FILE REFERENCE: 3053-4113US1  
; CURRENT APPLICATION NUMBER: US/09/966,955A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: 60/237030  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-966-955A-31

Query Match 26.7%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPK 6  
|||  
Db 10 PFPK 13

RESULT 65  
US-09-966-955A-32  
; Sequence 32, Application US/09966955A  
; Patent No. US2002015563A1  
; GENERAL INFORMATION:  
; APPLICANT: Perez-Villar, Juan J.  
; APPLICANT: Chang, Han  
; APPLICANT: Yang, Wen-Pin  
; APPLICANT: Wu, Yuli  
; APPLICANT: Whitney, Gena S.  
; APPLICANT: Kanner, Steven B.  
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human  
; TITLE OF INVENTION: Clnk-related Gene, MIST (Mast Cell Immunoreceptor  
; TITLE OF INVENTION: Signal Transducer)  
; FILE REFERENCE: 3053-4113US1  
; CURRENT APPLICATION NUMBER: US/09/966,955A  
; CURRENT FILING DATE: 2001-09-28



; PRIOR APPLICATION NUMBER: 60/237030  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-966-955A-32

Query Match 26.7%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPK 6  
Db 1 PPK 4

RESULT 66  
US-10-300-215-10  
; Sequence 10, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments

Query Match 26.7%; Score 4; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEV 11  
Db 8 KVEV 11

RESULT 67  
US-10-300-215-32  
; Sequence 32, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne

; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments

Query Match 26.7%; Score 4; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEV 11  
Db 8 KVEV 11

RESULT 68  
US-09-876-904A-194  
; Sequence 194, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 194  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
; FEATURE:  
; OTHER INFORMATION: Karyophilic peptide

Query Match 26.7%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLKV 9  
Db 6 KLKV 9

```
RESULT 69
US-10-312-691-6
; Sequence 6, Application US/10312691
; Publication No. US20030175975A1
; GENERAL INFORMATION:
; APPLICANT: CARTIER, Regis
; APPLICANT: BOTTIGER, Michael
; APPLICANT: HABERLAND, Annekathrin
; APPLICANT: RESZKA, Regina
; TITLE OF INVENTION: Procedure To Improve The Transfection Efficiency
; FILE REFERENCE: 3658-0108P
; CURRENT APPLICATION NUMBER: US/10/312,691
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: PCT/DE01/02336
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: DE 100.31.900.9
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: DE 100.40.895.8
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic NLS-sequence of the K16-Cyc synthetic peptide
US-10-312-691-6

Query Match          26.7%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLKV 9
Db      2 KLKV 5

RESULT 70
US-10-145-206-29
; Sequence 29, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZHONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred TALL-1 Modulating Domains
US-10-145-206-29

Query Match          26.7%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 PPPP 15
Db      5 PPPP 8

RESULT 71
US-09-880-748-2262
```

```
; Sequence 2262, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2262
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2262

Query Match          26.7%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VPPF 14
Db      10 VPPF 13

RESULT 72
US-10-234-816-98
; Sequence 98, Application US/10234816
; Publication No. US20030157514A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRIN HOMOLOGY DOMAIN AND
; TITLE OF INVENTION: RICH DOMAIN CONTAINING ADAPTER PROTEIN, PKN29
; FILE REFERENCE: D0117 NP
; CURRENT APPLICATION NUMBER: US/10/234,816
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-234-816-98

Query Match          26.7%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLKV 9
Db      8 KLKV 11

RESULT 73
US-10-161-791-181
; Sequence 181, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
```

APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 181:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-181

Query Match 26.7%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPK 6  
Db 5 PPK 8

RESULT 74  
US-10-225-567A-1075  
Sequence 1075, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1075  
LENGTH: 16  
TYPE: PPT  
ORGANISM: Homo sapiens  
US-10-225-567A-1075

Query Match 26.7%; Score 4; DB 15; Length 16;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PKLK 8  
Db 12 PKLK 15

RESULT 75  
US-09-170-919-7  
Sequence 7, Application US/09170919  
Patent No. US20010010919A1  
GENERAL INFORMATION:  
APPLICANT: Grisel, Judith E.  
APPLICANT: Grandy, David K.  
APPLICANT: Mogil, Jeffrey S.  
TITLE OF INVENTION: Opioid Antagonists and Methods  
TITLE OF INVENTION: of Their Use  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klarquist Sparkman Campbell  
ADDRESSEE: Leigh & Whinston LLP  
STREET: 121 S.W. Salmon, Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: USA  
ZIP: 97204  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Version WP6, ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/170,919  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/553,058  
FILING DATE: 11/3/95  
ATTORNEY/AGENT INFORMATION:  
NAME: William D. No. US20010010919Alnan, M.D.  
REGISTRATION NUMBER: 30,878  
REFERENCE/DOCKET NUMBER: 899-40006/WDN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-170-919-7

Query Match 26.7%; Score 4; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
Db 10 PKLK 13

Search completed: November 25, 2003, 20:25:34  
Job time : 30.8404 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 16.3564 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-8  
Perfect score: 15  
Sequence: 1 LKFPKLVKEVFPFP 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-641-803-8
2	5	33.3	12	4	US-08-949-059A-30
3	5	33.3	17	4	US-09-552-802B-40
4	4	26.7	4	1	US-08-540-202-4
5	4	26.7	4	4	US-09-750-726-4
6	4	26.7	5	1	US-08-201-081-6
7	4	26.7	5	2	US-08-288-059-5
8	4	26.7	6	1	US-08-093-741-77
9	4	26.7	6	1	US-08-720-012-77
10	4	26.7	6	3	US-08-981-256A-1
11	4	26.7	8	5	PCT-US93-12679-25
12	4	26.7	9	4	US-09-393-634-91
13	4	26.7	10	3	US-08-649-100-32
14	4	26.7	11	1	US-08-856-053-17
15	4	26.7	11	3	US-09-224-785-27
16	4	26.7	11	3	US-09-224-785-28
17	4	26.7	11	3	US-09-224-785-29
18	4	26.7	11	3	US-09-224-785-30
19	4	26.7	11	3	US-09-224-785-32
20	4	26.7	11	3	US-09-307-265A-14
21	4	26.7	11	4	US-09-756-594-27
22	4	26.7	11	4	US-09-756-594-28
23	4	26.7	11	4	US-09-756-594-29
24	4	26.7	11	4	US-09-756-594-30
25	4	26.7	11	4	US-09-756-594-32
26	4	26.7	12	1	US-08-856-053-7
27	4	26.7	12	1	US-08-856-053-16
28	4	26.7	12	2	US-08-726-306A-136
29	4	26.7	12	4	US-09-445-986B-3
30	4	26.7	12	4	US-09-798-121-3
31	4	26.7	12	4	US-09-552-802B-39
32	4	26.7	13	1	US-08-313-547-2
33	4	26.7	13	1	US-08-482-713-2
34	4	26.7	13	1	US-08-856-053-2
35	4	26.7	13	1	US-08-856-053-6
36	4	26.7	13	1	US-08-856-053-15
37	4	26.7	13	2	US-07-984-469A-19
38	4	26.7	13	3	US-08-855-531D-47
39	4	26.7	13	3	US-08-855-526B-47
40	4	26.7	13	4	US-09-445-986B-2
41	4	26.7	13	4	US-09-798-121-2
42	4	26.7	13	5	PCT-US91-02942-10
43	4	26.7	13	5	PCT-US91-02942-11
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45	4	26.7	14	1	US-08-856-053-5
46	4	26.7	14	1	US-08-856-053-14
47	4	26.7	14	4	US-08-949-059A-1
48	4	26.7	14	4	US-08-949-059A-2
49	4	26.7	14	4	US-08-949-059A-7
50	4	26.7	14	4	US-08-949-059A-8
51	4	26.7	14	4	US-08-949-059A-9
52	4	26.7	14	4	US-08-949-059A-10
53	4	26.7	14	4	US-08-949-059A-11
54	4	26.7	14	4	US-08-949-059A-12
55	4	26.7	14	4	US-08-949-059A-13
56	4	26.7	14	4	US-08-949-059A-14
57	4	26.7	14	4	US-08-949-059A-15
58	4	26.7	15	1	US-08-856-053-4
59	4	26.7	15	1	US-08-856-053-13
60	4	26.7	16	1	US-08-074-210-1
61	4	26.7	16	1	US-08-074-210-2
62	4	26.7	16	1	US-08-201-081-2
63	4	26.7	16	1	US-08-856-053-23
64	4	26.7	16	2	US-07-984-469A-18
65	4	26.7	16	3	US-08-602-999A-181
66	4	26.7	16	4	US-09-500-124-181
67	4	26.7	16	5	PCT-US94-06502A-1
68	4	26.7	16	5	PCT-US94-06502A-2
69	4	26.7	17	1	US-08-482-713-3
70	4	26.7	17	1	US-08-856-053-1
71	4	26.7	17	2	US-07-984-469A-17
72	4	26.7	17	2	US-08-553-058C-7
73	4	26.7	17	2	US-08-514-451A-12
74	4	26.7	17	2	US-08-436-420-1
75	4	26.7	17	2	US-08-927-328A-2
76	4	26.7	17	4	US-09-048-918B-10
77	4	26.7	17	4	US-09-445-986B-1
78	4	26.7	17	4	US-09-798-121-1
79	4	26.7	18	1	US-08-295-085-3
80	4	26.7	18	1	US-08-295-085-5
81	4	26.7	18	1	US-08-295-085-6
82	4	26.7	18	1	US-08-295-085-7
83	4	26.7	18	1	US-08-295-085-8
84	4	26.7	18	3	US-09-056-226-7
85	4	26.7	18	4	US-09-641-803-22
86	4	26.7	18	5	PCT-US95-10741-3
87	4	26.7	18	5	PCT-US95-10741-4
88	4	26.7	18	5	PCT-US95-10741-5
89	4	26.7	18	5	PCT-US95-10741-6
90	4	26.7	18	5	PCT-US95-10741-7
91	4	26.7	18	5	PCT-US95-10741-8
92	4	26.7	19	2	US-08-729-152-17
93	4	26.7	19	4	US-09-552-802B-42
94	4	26.7	20	2	US-08-898-885A-2
95	4	26.7	20	3	US-08-860-656B-11
96	4	26.7	20	4	US-09-227-357-664
97	4	26.7	20	4	US-09-556-877-156
98	4	26.7	20	4	US-09-620-412C-156
99	4	26.7	20	4	US-09-598-419-156
100	4	26.7	20	4	US-09-598-419-156

## ALIGNMENTS

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RESULT 1
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDUGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-8
Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPPKLKVEVFPFP 15
Db 1 LKPPPKLKVEVFPFP 15

RESULT 2
US-08-949-059A-30
; Sequence 30, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Premner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: .McMasters, David D.
```

```
;
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-30
Query Match 33.3%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 8 PKLKV 12

RESULT 3
US-09-552-802B-40
; Sequence 40, Application US/09552802B
; Patent No. 6562943
; GENERAL INFORMATION:
; APPLICANT: Peakman, Mark
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
; TITLE OF INVENTION: CD4+ T LYMPHOCYTES
; FILE REFERENCE: 08191-009002
; CURRENT APPLICATION NUMBER: US/09/552,802B
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,868
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/130,355
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-802B-40
Query Match 33.3%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVKE 10
Db 1 KLVKE 5

RESULT 4
US-08-540-202-4
; Sequence 4, Application US/08540202
; Patent No. 5681923
; GENERAL INFORMATION:
; APPLICANT: Platt, David
; TITLE OF INVENTION: TUMOR DERIVED CARBOHYDRATE BINDING
```

```
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gifford, Krass, et al
; STREET: 280 No. 5681923th Woodward Ave., Suite 400
; CITY: Birmingham
; STATE: Michigan
; COUNTRY: US
; ZIP: 48009
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,202
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Citkowski, Ronald W.
; REGISTRATION NUMBER: 31,005
; REFERENCE/DOCKET NUMBER: DPL-00102/16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-647-6000
; TELEFAX: 810-647-5210
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
;
US-08-540-202-4
Query Match 26.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14
Db 1 VFPF 4

RESULT 5
US-09-750-726-4
; Sequence 4, Application US/09750726
; Patent No. 6423314
; GENERAL INFORMATION:
; APPLICANT: Platt, David
; TITLE OF INVENTION: TUMOR DERIVED CARBOHYDRATE BINDING
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gifford, Krass, et al
; STREET: 280 No. 6423314th Woodward Ave., Suite 400
; CITY: Birmingham
; STATE: Michigan
; COUNTRY: US
; ZIP: 48009
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/750,726
; FILING DATE: 28-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Citkowski, Ronald W.
; REGISTRATION NUMBER: 31,005
; REFERENCE/DOCKET NUMBER: DPL-00102/16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-647-6000
```

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; TELEFAX: 810-647-5210
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
;
US-09-750-726-4
Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14
Db 1 VFPF 4

RESULT 6
US-08-201-081-6
; Sequence 6, Application US/08201081
; Patent No. 5593849
; GENERAL INFORMATION:
; APPLICANT: Roy, Benjamin
; TITLE OF INVENTION: METHOD FOR DETECTING ANTIBODY AGAINST
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS REPLICATION PROTEIN B SEQUENCE
; TITLE OF INVENTION: 275-290 ARG-LYS-LEU-LYS IN HUMAN BODY FLUIDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Levy Zito & Grandinetti
; STREET: 1730 K Street, N.W. Suite 304
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,081
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Grandinetti, Paul
; REGISTRATION NUMBER: 30,754
; REFERENCE/DOCKET NUMBER: MCG0009US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-4560
; TELEFAX: (202)429-4564
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-201-081-6
Query Match 26.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 2 PKLK 5

RESULT 7
US-08-288-059-5
; Sequence 5, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:
```

APPLICANT: FINN, OLIVERA J.  
APPLICANT: FONTENOT, J. D.  
APPLICANT: MONTECARO, RONALD C.  
TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN  
TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,059  
FILING DATE: 08-AUG-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAPIN, MARIANA K.  
REGISTRATION NUMBER: 35,843  
REFERENCE/DOCKET NUMBER: 61137/205204  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3711  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-288-059-5

Query Match 26.7%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 1 PKLK 4

RESULT 8  
US-08-093-741-77  
Sequence 77, Application US/08093741  
Patent No. 5681721  
GENERAL INFORMATION:  
APPLICANT: STEFFENS, GERD J.  
APPLICANT: WENNDT, STEPHAN  
APPLICANT: SCHNEIDER, JOHANNES  
APPLICANT: HEINZEL-WIELAND, REGINA  
APPLICANT: SAUNDERS, DEREK J.  
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH  
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN  
INHIBITING EFFECT  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N. W. Suite 700  
CITY: Washington, D.C.  
COUNTRY: U.S.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,741  
FILING DATE: 20-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P43 23 754.1  
FILING DATE: 15-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, JOSEPH D.  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 148/41345  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)628-8800  
TELEFAX: (202)628-8844  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-093-741-77

Query Match 26.7%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12  
Db 3 VEVF 6

RESULT 9  
US-08-720-012-77  
Sequence 77, Application US/08720012  
Patent No. 5747291  
GENERAL INFORMATION:  
APPLICANT: STEFFENS, GERD J.  
APPLICANT: WENNDT, STEPHAN  
APPLICANT: SCHNEIDER, JOHANNES  
APPLICANT: HEINZEL-WIELAND, REGINA  
APPLICANT: SAUNDERS, DEREK J.  
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH  
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN  
INHIBITING EFFECT  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N. W. Suite 700  
CITY: Washington, D.C.  
COUNTRY: U.S.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/720,012  
FILING DATE: 27-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,741  
FILING DATE: 20-JUL-1993  
APPLICATION NUMBER: DE P43 23 754.1  
FILING DATE: 15-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, JOSEPH D.  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 148/41345  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)628-8800  
TELEFAX: (202)628-8844  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-720-012-77

Query Match      26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12
Db 3 VEVF 6

RESULT 10
US-08-981-256A-1
; Sequence 1, Application US/08981256A
; Patent No. 6046042
; GENERAL INFORMATION:
; APPLICANT: Meinhard HASSLAACHER et al.
; TITLE OF INVENTION: (S)-HYDROXY-NITRILE-LYASE FROM HEVEA BRASILIENSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981.256A
; FILING DATE: December 22, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 1553-OZ1112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-981-256A-1

Query Match      26.7%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVFP 13
Db 3 EVFP 6

RESULT 11
PCT-US93-12679-25
; Sequence 25, Application PC/TUS9312679
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
; PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
```

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; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHELDON & MAK
; STREET: 401 Florence Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12679
; FILING DATE: 30-DEC-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cranfill, Raymond B
; REGISTRATION NUMBER: 32,845
; REFERENCE/DOCKET NUMBER: RATH-10016PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5333
; TELEFAX: 415-322-5499
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-12679-25

Query Match      26.7%; Score 4; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 4 PKLK 7

RESULT 12
US-09-393-634-91
; Sequence 91, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Sf01 signature
; OTHER INFORMATION: sequence 4, amino acids encoded by PCR primers
; OTHER INFORMATION: identifying polymorphic variants, interspecies
; OTHER INFORMATION: homologs and alleles of Sf family members
US-09-393-634-91
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Query Match          26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
DB      6 PKLK 9

RESULT 13
US-08-649-100-32
; Sequence 32, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NATAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-32

Query Match          26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVEV 11
DB      6 KVEV 9

RESULT 14
US-08-856-053-17
; Sequence 17, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-17

Query Match          26.7%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
DB      8 PKLK 11

RESULT 15
US-09-224-785-27
; Sequence 27, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; TITLE OF INVENTION: VIII-like Proteins
; FILE REFERENCE: Dyax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-224-785-27
```

Query Match 26.7%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
|||  
Db 4 VFPF 7

RESULT 16  
US-09-224-785-28  
; Sequence 28, Application US/09224785A  
; Patent No. 6197526  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US sequence listing  
; CURRENT APPLICATION NUMBER: US/09/224,785A  
; CURRENT FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding loop peptide  
US-09-224-785-28

Query Match 26.7%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
|||  
Db 4 VFPF 7

RESULT 17  
US-09-224-785-29  
; Sequence 29, Application US/09224785A  
; Patent No. 6197526  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US sequence listing  
; CURRENT APPLICATION NUMBER: US/09/224,785A  
; CURRENT FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding loop peptide  
US-09-224-785-29

Query Match 26.7%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 VFPF 14  
|||  
Db 4 VFPF 7

RESULT 18  
US-09-224-785-30  
; Sequence 30, Application US/09224785A  
; Patent No. 6197526  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US sequence listing  
; CURRENT APPLICATION NUMBER: US/09/224,785A  
; CURRENT FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding loop peptide  
US-09-224-785-30

Query Match 26.7%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14  
|||  
Db 4 VFPF 7

RESULT 19  
US-09-224-785-32  
; Sequence 32, Application US/09224785A  
; Patent No. 6197526  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US sequence listing  
; CURRENT APPLICATION NUMBER: US/09/224,785A  
; CURRENT FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding loop peptide  
US-09-224-785-32

Query Match 26.7%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14

Db 4 VPPF 7

## RESULT 20

US-09-307-265A-14  
; Sequence 14, Application US/09307265A  
; Patent No. 6225456  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Trent  
; APPLICANT: Orita, Satoshi  
; APPLICANT: Han, Min  
; TITLE OF INVENTION: RAS SUPPRESSOR SUR-5  
; FILE REFERENCE: UTC-03732  
; CURRENT APPLICATION NUMBER: US/09/307,265A  
; CURRENT FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-307-265A-14

Query Match 26.7%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVEV 11

Db 8 KVEV 11

## RESULT 21

US-09-756-594-27  
; Sequence 27, Application US/09756594  
; Patent No. 6492105  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing  
; CURRENT APPLICATION NUMBER: US/09/756,594  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 09/224,785  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-756-594-27

Query Match 26.7%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPF 14

Db 4 VPPF 7

## RESULT 22

US-09-756-594-28  
; Sequence 28, Application US/09756594

; Patent No. 6492105  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing  
; CURRENT APPLICATION NUMBER: US/09/756,594  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 09/224,785  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-756-594-28

Query Match 26.7%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPF 14

Db 4 VPPF 7

## RESULT 23

US-09-756-594-29  
; Sequence 29, Application US/09756594  
; Patent No. 6492105  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing  
; CURRENT APPLICATION NUMBER: US/09/756,594  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 09/224,785  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-756-594-29

Query Match 26.7%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VPPF 14

Db 4 VPPF 7

## RESULT 24

US-09-756-594-30

; Sequence 30, Application US/09756594  
; Patent No. 6492105  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: VIII-like Proteins  
; CURRENT APPLICATION NUMBER: US/09/756,594  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 09/224,785  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding loop peptide

US-09-756-594-30

Query Match 26.7%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14  
Db 4 VFPF 7

RESULT 25

US-09-756-594-32  
; Sequence 32, Application US/09756594  
; Patent No. 6492105  
; GENERAL INFORMATION:  
; APPLICANT: Potter, M. Daniel  
; APPLICANT: Yu, Jinan  
; APPLICANT: Kelley, Brian D  
; APPLICANT: Deetz, Jeffrey S  
; APPLICANT: Booth, James E  
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor  
; FILE REFERENCE: VIII-like Proteins  
; CURRENT APPLICATION NUMBER: US/09/756,594  
; CURRENT FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 09/224,785  
; PRIOR FILING DATE: 1999-01-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding loop peptide

US-09-756-594-32

Query Match 26.7%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14  
Db 4 VFPF 7

RESULT 26

US-08-856-053-7  
; Sequence 7, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,053  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/897,920  
; FILING DATE: 12-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2995.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: porcine  
; US-08-856-053-7

Query Match 26.7%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
Db 9 PKLK 12

RESULT 27

US-08-856-053-16  
; Sequence 16, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.

ZIP: 94111-4121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/856,053  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/897,920  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Siebert, J. Suzanne  
REGISTRATION NUMBER: 28,758  
REFERENCE/DOCKET NUMBER: 2995.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 362-5556  
TELEFAX: (415) 362-5418  
TELEX: 278638 MGPS  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: porcine  
US-08-856-053-16

Query Match 26.7%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 8 PKLK 11

RESULT 28  
US-08-726-306A-136  
Sequence 136, Application US/08726306A  
Patent No. 5958684  
GENERAL INFORMATION:  
APPLICANT: van Leeuwen, Frederik Willem  
APPLICANT: Burbach, Johannes Peter Henri  
APPLICANT: Grosveld, Franklin G.  
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1 Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,306A  
FILING DATE: 02-Oct-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 95/20080.4  
FILING DATE: 02-Oct-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,832  
FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 136:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-726-306A-136

Query Match 26.7%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 6 PKLK 9

RESULT 29  
US-09-445-986B-3  
Sequence 3, Application US/09445986B  
Patent No. 6437092  
GENERAL INFORMATION:  
APPLICANT: CONJUCHEM, INC.  
APPLICANT: EZRIN, ALAN M.  
APPLICANT: BRIDON, DOMINIQUE P.  
APPLICANT: HOLMES, DARREN L.  
APPLICANT: MILNER, PETER G.  
TITLE OF INVENTION: NOVEL CONJUGATES OF OPIOIDS AND ENDOGENOUS CARRIERS  
FILE REFERENCE: RDC-600 USA  
CURRENT APPLICATION NUMBER: US/09/445,986B  
CURRENT FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US98/23704  
PRIOR FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 3  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Dynorphin  
OTHER INFORMATION: analogue A(2-13)  
US-09-445-986B-3

Query Match 26.7%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 9 PKLK 12

RESULT 30  
US-09-798-121-3  
Sequence 3, Application US/09798121  
Patent No. 6500918  
GENERAL INFORMATION:  
APPLICANT: CONJUCHEM, INC.  
APPLICANT: EZRIN, ALAN M.  
APPLICANT: BRIDON, DOMINIQUE P.  
APPLICANT: HOLMES, DARREN L.  
APPLICANT: MILNER, PETER G.  
TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCICEPTIVE AGENT COVALENTLY B  
TITLE OF INVENTION: BLOOD COMPONENT

```

; FILE REFERENCE: 500862000612
; CURRENT APPLICATION NUMBER: US/09/798,121
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Dynorphin
; OTHER INFORMATION: analogue A(2-13)
US-09-798-121-3

```

```

Query Match          26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 PKLK 8
        ||||
Db      9 PKLK 12

```

## RESULT 31

```

US-09-552-802B-39
; Sequence 39, Application US/09552802B
; Patent No. 6562943
; GENERAL INFORMATION:
; APPLICANT: Peakman, Mark
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
; TITLE OF INVENTION: CD4+ T LYMPHOCYTES
; FILE REFERENCE: 08191-009002
; CURRENT APPLICATION NUMBER: US/09/552,802B
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,868
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/130,355
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-802B-39

```

```

Query Match          26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 LKVE 10
        ||||
Db      1 LKVE 4

```

## RESULT 32

```

US-08-313-547-2
; Sequence 2, Application US/08313547
; Patent No. 5428128
; GENERAL INFORMATION:
; APPLICANT: Mensi-Fattochi, Nahla
; APPLICANT: Molineaux, Christopher J.
; APPLICANT: Shorr, Robert G.B.
; TITLE OF INVENTION: Site Specific Synthesis of Conjugated Peptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite No. 5428128 600

```

```

; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,547
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,457
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0977.2170000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-313-547-2

```

```

Query Match          26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 PKLK 8
        ||||
Db      10 PKLK 13

```

## RESULT 33

```

US-08-482-713-2
; Sequence 2, Application US/08482713
; Patent No. 5624932
; GENERAL INFORMATION:
; APPLICANT: Qin, Bo-yi
; APPLICANT: Shen, Ke-fei
; APPLICANT: Gong, Xiong-qi
; APPLICANT: Crain, Stanley M.
; APPLICANT: Huang, Mao
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION OF
; TITLE OF INVENTION: LOW/NON-ADDICTIVE ANALGESICS AND THE USE OF SAID
; TITLE OF INVENTION: ANALGESICS FOR TREATMENT OF OPIOID ADDICTION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: M. Lisa Wilson
; STREET: 25 Davids Drive
; CITY: Huppauge
; STATE: NY
; COUNTRY: USA
; ZIP: 11788
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,713
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, M. Lisa
; REGISTRATION NUMBER: 34,045

```

REFERENCE/DOCKET NUMBER: 2001XC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516)273-2828  
TELEFAX: (516)273-1717  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-713-2

Query Match 26.7%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 10 PKLK 13

RESULT 34  
US-08-856-053-2  
Sequence 2, Application US/08856053  
Patent No. 5807827  
GENERAL INFORMATION:  
APPLICANT: Lee, Nancy M.  
APPLICANT: Loh, Horace H.  
APPLICANT: Takemori, Akira E.  
TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
STREET: Four Embarcadero Center, Suite 1450  
CITY: San Francisco  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94111-4121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/856,053  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/897,920  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Siebert, J. Suzanne  
REGISTRATION NUMBER: 28,758  
REFERENCE/DOCKET NUMBER: 2995.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 362-5556  
TELEFAX: (415) 362-5418  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: porcine  
US-08-856-053-2

Query Match 26.7%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 10 PKLK 13

RESULT 35  
US-08-856-053-6  
Sequence 6, Application US/08856053  
Patent No. 5807827  
GENERAL INFORMATION:  
APPLICANT: Lee, Nancy M.  
APPLICANT: Loh, Horace H.  
APPLICANT: Takemori, Akira E.  
TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
STREET: Four Embarcadero Center, Suite 1450  
CITY: San Francisco  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94111-4121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/856,053  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/897,920  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Siebert, J. Suzanne  
REGISTRATION NUMBER: 28,758  
REFERENCE/DOCKET NUMBER: 2995.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 362-5556  
TELEFAX: (415) 362-5418  
TELEX: 278638 MGPS  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: porcine  
US-08-856-053-6

Query Match 26.7%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 9 PKLK 12

RESULT 36  
US-08-856-053-15  
Sequence 15, Application US/08856053  
Patent No. 5807827  
GENERAL INFORMATION:  
APPLICANT: Lee, Nancy M.  
APPLICANT: Loh, Horace H.  
APPLICANT: Takemori, Akira E.  
TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES

; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,053  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/897,920  
; FILING DATE: 12-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2995.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: porcine  
; US-08-856-053-15

Query Match 26.7%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
Db 8 PKLK 11

RESULT 37  
US-07-984-469A-19  
; Sequence 19, Application US/07984469A  
; Patent No. 5817628  
; GENERAL INFORMATION:  
; APPLICANT: Mary Jeanne Kreek, M.D.  
; TITLE OF INVENTION: Dynorphin A Suppression of Natural  
; TITLE OF INVENTION: Killer Cell Activity  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morgan & Finnegan  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/984,469A  
; FILING DATE: 02 - Dec - 1992

; ATTORNEY/AGENT INFORMATION:  
; NAME: Kenneth H. Sonnenfeld  
; REGISTRATION NUMBER: 33,285  
; REFERENCE/DOCKET NUMBER: 2016-4003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-415-8513  
; TELEX: (212) 751-6849  
; TELEFAX: 421792

; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: Peptide  
; US-07-984-469A-19

Query Match 26.7%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
Db 10 PKLK 13

## RESULT 38

US-08-855-531D-47  
; Sequence 47, Application US/08855531D  
; Patent No. 6110467  
; GENERAL INFORMATION:

; APPLICANT: FRENZ, PAUL S.  
; HALBUR, PATRICK G.  
; MENG, XIANG-JIN  
; LUM, MELISSA A.  
; LYOO, YOUNG S.

TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL

RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND  
REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAIN:  
A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCQUELLAND, MAIER & NEUSTADT,  
P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/855,531D

FILING DATE: 13-May-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/969,071

FILING DATE: 30-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: LAVALLEYE, JEAN-PAUL M.P.

REGISTRATION NUMBER: 31,451

REFERENCE/DOCKET NUMBER: 4625-038-55X DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid



;  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-08-855-531D-47

Query Match 26.7%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 7 PKLK 10

RESULT 39  
US-08-855-526B-47  
; Sequence 47, Application US/08055526B  
; Patent No. 6251404  
; GENERAL INFORMATION:  
; APPLICANT: PREM, PAUL S.  
; APPLICANT: HALBUR, PATRICK G.  
; APPLICANT: MENG, XIANG-JIN  
; APPLICANT: LUM, MELISSA A.  
; APPLICANT: LYCO, YOUNG S.  
; TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL  
; TITLE OF INVENTION: RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND  
; TITLE OF INVENTION: REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST  
; TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OSOLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/855,526B  
; FILING DATE: 13-MAY-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,071  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAVALLEYE, JEAN-PAUL M.P.  
; REGISTRATION NUMBER: 31,451  
; REFERENCE/DOCKET NUMBER: 4625-040-55X DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-855-526B-47

Query Match 26.7%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 7 PKLK 10

RESULT 40  
US-09-445-986B-2  
; Sequence 2, Application US/09445986B  
; Patent No. 6437092  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; APPLICANT: HOLMES, DARREN L.  
; APPLICANT: MILNER, PETER G.  
; TITLE OF INVENTION: NOVEL CONJUGATES OF OPIOIDS AND ENDOGENOUS CARRIERS  
; FILE REFERENCE: REDC-600 USA  
; CURRENT APPLICATION NUMBER: US/09/445,986B  
; CURRENT FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US98/23704  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin  
US-09-445-986B-2

Query Match 26.7%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 10 PKLK 13

RESULT 41  
US-09-798-121-2  
; Sequence 2, Application US/09798121  
; Patent No. 6500918  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; APPLICANT: HOLMES, DARREN L.  
; APPLICANT: MILNER, PETER G.  
; TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCICEPTIVE AGENT COVALENTLY BC  
; FILE REFERENCE: 500862000612  
; CURRENT APPLICATION NUMBER: US/09/798,121  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/445,986  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US98/23704  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin  
US-09-798-121-2

Query Match 26.7%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8

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Db          10 PKLK 13
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RESULT 42
PCT-US91-02942-10
; Sequence 10, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 10:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-10
Query Match          26.7%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 KVEV 11
Db          8 KVEV 11
|||||
RESULT 43
PCT-US91-02942-11
; Sequence 11, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 10:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-10
Query Match          26.7%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 KVEV 11
Db          8 KVEV 11
|||||
RESULT 44
PCT-US91-02942-11
; Sequence 11, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ENZON, INC.
; APPLICANT: 40 Kingsbridge Road
; APPLICANT: Piscataway, New Jersey 08854-3998
; APPLICANT: United States of America
; APPLICANT: Molineaux, Christopher J.
; APPLICANT: Shorr, Robert G.L.
; TITLE OF INVENTION: Site Specific Synthesis of Conjugated Peptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite No. 600
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06953
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,457
; FILING DATE: 21-JUN-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbalà, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0977.2170000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
```

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 11:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-11
Query Match          26.7%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          8 KVEV 11
Db          8 KVEV 11
|||||
RESULT 44
PCT-US94-06953-2
; Sequence 2, Application PC/TUS9406953
; GENERAL INFORMATION:
; APPLICANT: Enzon, Inc.
; APPLICANT: 40 Kingsbridge Road
; APPLICANT: Piscataway, New Jersey 08854-3998
; APPLICANT: United States of America
; APPLICANT: Molineaux, Christopher J.
; APPLICANT: Shorr, Robert G.L.
; TITLE OF INVENTION: Site Specific Synthesis of Conjugated Peptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite No. 600
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06953
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,457
; FILING DATE: 21-JUN-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbalà, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0977.2170000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
```

; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US94-06953-2

Query Match 26.7%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 PKLK 8  
Db 10 PKLK 13

RESULT 45  
US-08-856-053-5  
; Sequence 5, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,053  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/897,920  
; FILING DATE: 12-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2995.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: porcine  
US-08-856-053-5

Query Match 26.7%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 PKLK 8  
Db 9 PKLK 12

RESULT 46  
US-08-856-053-14  
; Sequence 14, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,053  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/897,920  
; FILING DATE: 12-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2995.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: porcine  
US-08-856-053-14

Query Match 26.7%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 PKLK 8  
Db 8 PKLK 11

RESULT 47  
US-08-949-059A-1  
; Sequence 1, Application US/08949059A  
; Patent No. 6358921  
; GENERAL INFORMATION:  
; APPLICANT: Kondejewski, Leslie H.  
; APPLICANT: Hodges, Robert S.  
; APPLICANT: Wishart, David S.  
; APPLICANT: Hancock, Robert E.W.  
; APPLICANT: McElhaney, Ronald N.  
; APPLICANT: Premner, Elmar J.  
; APPLICANT: Lewis, Ruthven N.A.H  
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND

```
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Where Xaa is D-Tyrosine or
; OTHER INFORMATION: D-phenylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Where Xaa is D-Tyrosine or
; OTHER INFORMATION: D-phenylalanine"
; US-08-949-059A-1
;
; Query Match 26.7%; Score 4; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 3.3e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 KLKV 9
; Db 2 KLKV 5
;
; RESULT 48
; US-08-949-059A-2
; Sequence 2, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
```

```
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Valine "
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-2
;
; Query Match 26.7%; Score 4; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 3.3e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 KLKV 9
; Db 2 KLKV 5
;
; RESULT 49
; US-08-949-059A-7
; Sequence 7, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
```

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; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-7

Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLV 9
Db 2 KLV 5

RESULT 50
US-08-949-059A-8
; Sequence 8, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Proline"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-8

Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLV 9
Db 2 KLV 5

RESULT 51
US-08-949-059A-9
; Sequence 9, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Residue is a D-Leucine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-9
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9
DB 2 KLKV 5

RESULT 52
US-08-949-059A-10
; Sequence 10, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 42
; TITLE OF INVENTION: METHOD
; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
```

```
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Residue is a D-Lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-10
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9
DB 2 KLKV 5

RESULT 53
US-08-949-059A-11
; Sequence 11, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 42
; TITLE OF INVENTION: METHOD
; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /note= "Residue is a D-Valine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-11
;
Query Match          26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLVV 9
Db      2 KLVV 5
      ||||
      2 KLVV 5

RESULT 54
US-08-949-059A-12
; Sequence 12, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
```

```
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Residue is a D-Lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-12
;
Query Match          26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLVV 9
Db      2 KLVV 5
      ||||
      2 KLVV 5

RESULT 55
US-08-949-059A-13
; Sequence 13, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

```
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: /note= "Residue is a D-Leucine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-13
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
Db 2 KLVV 5

RESULT 56
US-08-949-059A-14
; Sequence 14, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
```

```
;
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-14
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
Db 2 KLVV 5

RESULT 57
US-08-949-059A-15
; Sequence 15, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /note= "Residue is a D-Proline"
;
US-08-949-059A-15
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Query Match 26.7%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9  
|||  
Db 2 KLKV 5

RESULT 58  
US-08-856-053-4  
; Sequence 4, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,053  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/897,920  
; FILING DATE: 12-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2995.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: porcine  
US-08-856-053-4

Query Match 26.7%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 9 PKLK 12

RESULT 59  
US-08-856-053-13  
; Sequence 13, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/856,053  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/897,920  
; FILING DATE: 12-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2995.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: porcine  
US-08-856-053-4

Query Match 26.7%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 9 PKLK 12

RESULT 60  
US-08-074-210-1  
; Sequence 1, Application US/08074210  
; Patent No. 5482930  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Edward T.  
; APPLICANT: Thomas, Holly A.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD  
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Loh, Horace H.  
APPLICANT: Takemori, Akira E.  
TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
STREET: Four Embarcadero Center, Suite 1450  
CITY: San Francisco  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94111-4121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/856,053  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/897,920  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Siebert, J. Suzanne  
REGISTRATION NUMBER: 28,758  
REFERENCE/DOCKET NUMBER: 2995.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 362-5556  
TELEFAX: (415) 362-5418  
TELEX: 278638 MGPS  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: porcine  
US-08-856-053-13

Query Match 26.7%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
|||  
Db 8 PKLK 11

RESULT 60  
US-08-074-210-1  
; Sequence 1, Application US/08074210  
; Patent No. 5482930  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Edward T.  
; APPLICANT: Thomas, Holly A.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD  
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/074,210  
; FILING DATE: 19930609  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2500.72  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-074-210-1

Query Match 26.7%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 9 PKLK 12

RESULT 61  
US-08-074-210-2  
; Sequence 2, Application US/08074210  
; Patent No. 5482930  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Edward T.  
; APPLICANT: Thomas, Holly A.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD  
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Heue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/074,210  
; FILING DATE: 19930609  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2500.72  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

;  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-074-210-2

Query Match 26.7%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 9 PKLK 12

RESULT 62  
US-08-201-081-2  
; Sequence 2, Application US/08201081  
; Patent No. 5593849  
; GENERAL INFORMATION:  
; APPLICANT: Roy, Benjamin  
; TITLE OF INVENTION: METHOD FOR DETECTING ANTIBODY AGAINST  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS REPLICATION PROTEIN B SEQUENCE  
; TITLE OF INVENTION: 275-290 ARG-LYS-LEU-LYS IN HUMAN BODY FLUIDS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Levy, Zito & Grandinetti  
; STREET: 1730 K Street, N.W. Suite 304  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/201,081  
; FILING DATE: 24-FEB-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Grandinetti, Paul  
; REGISTRATION NUMBER: 30,754  
; REFERENCE/DOCKET NUMBER: MCG00909  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 429-4560  
; TELEFAX: (202) 429-4564  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-201-081-2

Query Match 26.7%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8  
Db 10 PKLK 13

RESULT 63  
US-08-856-053-23  
; Sequence 23, Application US/08856053  
; Patent No. 5807827  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Nancy M.  
; APPLICANT: Loh, Horace H.  
; APPLICANT: Takemori, Akira E.  
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES  
; NUMBER OF SEQUENCES: 23

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
;
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
;
; US-08-856-053-23
;
; Query Match 26.7%; Score 4; DB 1; Length 16;
; Best Local Similarity 100.0%; Pred. No. 3.6e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 PKLK 8
; Db 9 PKLK 12
;
; RESULT 64
; US-07-984-469A-18
; Sequence 18, Application US/07984469A
; Patent No. 5817628
; GENERAL INFORMATION:
; APPLICANT: Mary Jeanne Kreek, M.D.
; TITLE OF INVENTION: Dynorphin A Suppression of Natural
; TITLE OF INVENTION: Killer Cell Activity
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/984,469A
; FILING DATE: 02 - Dec - 1992
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Kenneth H. Sonnenfeld
; REGISTRATION NUMBER: 33,285
; REFERENCE/DOCKET NUMBER: 2016-4003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-415-8513
; TELEFAX: (212) 751-6849
; TELEX: 421792
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; FEATURE:
; OTHER INFORMATION: This peptide is identical to
; OTHER INFORMATION: the mature dynorphin A(1-17) of SEQ ID NO: 17 except
; OTHER INFORMATION: for the removal of the amino terminal Tyr
;
; US-07-984-469A-18
;
; Query Match 26.7%; Score 4; DB 2; Length 16;
; Best Local Similarity 100.0%; Pred. No. 3.6e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 PKLK 8
; Db 9 PKLK 12
;
; RESULT 65
; US-08-602-999A-181
; Sequence 181, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
;
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```
; MOLECULE TYPE: peptide
US-08-602-999A-181
Query Match      26.7%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPK 6
Db      5 PPK 8

RESULT 66
US-09-500-124-181
; Sequence 181, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/500,124
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-181
Query Match      26.7%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPK 6
Db      5 PPK 8

RESULT 67
PCT-US94-06502A-1
; Sequence 1, Application PC/TUS9406502A
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06502A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US94-06502A-1
Query Match      26.7%; Score 4; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
Db      9 PKLK 12

RESULT 68
PCT-US94-06502A-2
; Sequence 2, Application PC/TUS9406502A
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06502A
; FILING DATE:
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Xaa (position 16) is Gln-NH2"
PCT-US94-06502A-2

Query Match 26.7%; Score 4; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 9 PKLK 12

RESULT 69
US-08-482-713-3
; Sequence 3, Application US/08482713
; Patent No. 5624932
; GENERAL INFORMATION:
; APPLICANT: Qin, Bo-yi
; APPLICANT: Shen, Ke-fei
; APPLICANT: Gong, Xiong-qi
; APPLICANT: Crain, Stanley M.
; APPLICANT: Huang, Mao
; APPLICANT: Wang, Chang yi
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION OF
; TITLE OF INVENTION: LOW/NON-ADDICTIVE ANALGESICS AND THE USE OF SAID
; TITLE OF INVENTION: ANALGESICS FOR TREATMENT OF OPIOID ADDICTION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: M. Lisa Wilson
; STREET: 25 Davids Drive
; CITY: Hauppauge
; STATE: NY
; COUNTRY: USA
; ZIP: 11788
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; NAME: Wilson, M. Lisa
; REGISTRATION NUMBER: 34,045
; REFERENCE/DOCKET NUMBER: 2001XC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)273-2828
; TELEFAX: (516)273-1717
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-713-3

Query Match 26.7%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 10 PKLK 13

RESULT 70
US-08-856-053-1
; Sequence 1, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEFAX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-1

Query Match 26.7%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 10 PKLK 13

RESULT 71
```

US-07-984-469A-17  
; Sequence 17, Application US/07984469A  
; Patent No. 5817628  
; GENERAL INFORMATION:  
; APPLICANT: Mary Jeanne Kreek, M.D.  
; TITLE OF INVENTION: Dynorphin A Suppression of Natural  
; TITLE OF INVENTION: Killer Cell Activity  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morgan & Finnegan  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/984,469A  
; FILING DATE: 02 - Dec - 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kenneth H. Sonnenfeld  
; REGISTRATION NUMBER: 33,285  
; REFERENCE/DOCKET NUMBER: 2016-4003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-415-8513  
; TELEFAX: (212) 751-6849  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Unknown  
; MOLECULE TYPE: Peptide  
US-07-984-469A-17  
  
Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PKLK 8  
Db 10 PKLK 13  
  
RESULT 72  
US-08-553-058C-7  
; Sequence 7, Application US/08553058C  
; Patent No. 5821219  
; GENERAL INFORMATION:  
; APPLICANT: Grisel, Judith B.  
; APPLICANT: Grandy, David K.  
; APPLICANT: Mogil, Jeffrey S.  
; TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP  
; STREET: 121 S.W. Salmon, Suite 1600  
; CITY: Portland  
; STATE: Oregon  
; COUNTRY: USA  
; ZIP: 97204  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Version WP6, ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,058C

; FILING DATE: 11/3/95  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William D. No. 5821219nan, M.D.  
; REGISTRATION NUMBER: 30,878  
; REFERENCE/DOCKET NUMBER: 899-40006/WDN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (503) 226-7391  
; TELEFAX: (503) 228-9446  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-08-553-058C-7  
  
Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PKLK 8  
Db 10 PKLK 13  
  
RESULT 73  
US-08-514-451A-12  
; Sequence 12, Application US/08514451A  
; Patent No. 5837809  
; GENERAL INFORMATION:  
; APPLICANT: Bunzow, James R.  
; APPLICANT: Grandy, David K.  
; APPLICANT: Civelli, Olivier  
; APPLICANT: Reinscheid, Rainer K.  
; APPLICANT: Monsma, Frederick J.  
; TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID  
; TITLE OF INVENTION: RECEPTOR LIGAND AND USES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klarquist Sparkman Campbell  
; ADDRESSEE: Leigh & Whinston LLP  
; STREET: 121 S.W. Salmon, Suite 1600  
; CITY: Portland  
; STATE: Oregon  
; COUNTRY: USA  
; ZIP: 97204  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WP5.1 ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/514,451A  
; FILING DATE: 08/11/95  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/553,058  
; FILING DATE: 11/13/95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William D. No. 5837809nan, M.D.  
; REGISTRATION NUMBER: 30,878  
; REFERENCE/DOCKET NUMBER: 899-45995/WDN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (503) 226-7391  
; TELEFAX: (503) 228-9446  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; DESCRIPTION: peptide  
US-08-514-451A-12

Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
| | | |  
Db 10 PKLK 13

## RESULT 74

US-08-436-420-10  
; Sequence 10, Application US/08436420  
; Patent No. 5840524  
; GENERAL INFORMATION:  
; APPLICANT: VAN DAMME, Jo; and  
; APPLICANT: PROOST, Paul  
; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE and DORR LLP  
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: DISTRICT OF COLUMBIA  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,420  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03330  
; FILING DATE: 26-NOV-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/982,539  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BAKER, Hollie L.  
; REGISTRATION NUMBER: 31,321  
; REFERENCE/DOCKET NUMBER: 102379.215  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 942-8400  
; TELEFAX: (202) 942-8484  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-436-420-10

Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEV 11  
| | | |  
Db 12 KVEV 15

## RESULT 75

US-08-927-328A-2  
; Sequence 2, Application US/08927328A  
; Patent No. 5840696  
; GENERAL INFORMATION:  
; APPLICANT: HOWARD LIPPTON  
; TITLE OF INVENTION: DIURETIC AND ANTINATRIURETIC  
; TITLE OF INVENTION: RESPONSES PRODUCED BY ANALOGS OF  
; TITLE OF INVENTION: NOCICEPTIN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger  
; STREET: 1177 West Loop South, 10th Floor  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77027-9095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/927,328A  
; FILING DATE: September 11, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Krieger, Paul E.  
; REGISTRATION NUMBER: 25,886  
; REFERENCE/DOCKET NUMBER: 42740/1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713-850-0909  
; TELEFAX: 713-850-0165  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acids  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-08-927-328A-2

Query Match 26.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8  
| | | |  
Db 10 PKLK 13

Search completed: November 25, 2003, 20:16:04  
Job time : 17.3564 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 4.60106 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-9  
Perfect score: 5  
Sequence: 1 VMEV 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 283308 seqs, 96168682 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 3883  
Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3	60.0	13	2	PL0157	Ig kappa chain V-I
2	3	60.0	16	2	S29137	aminopyrine N-deme
3	3	60.0	18	2	PL0025	T-cell surface gly
4	3	60.0	18	2	S48862	murine cyclin H -
5	2	40.0	4	2	A61300	22K superhelical D
6	2	40.0	4	2	I57745	D-mannosate hydrol
7	2	40.0	4	2	E4823	synaptosomal-assoc
8	2	40.0	6	2	S02617	alcohol dehydrogen
9	2	40.0	6	2	B44510	hypothetical prote
10	2	40.0	6	2	A49792	acylaminoacyl-pept
11	2	40.0	6	2	A20186	fatty-acid synthas
12	2	40.0	7	2	B34818	vicilin 57K chain
13	2	40.0	7	2	PQ0727	H2 class I protein
14	2	40.0	7	2	PT0246	Ig heavy chain CRD
15	2	40.0	7	2	I48086	DNA topoisomerase
16	2	40.0	7	4	S15597	orf 4 rara 5'-regi
17	2	40.0	8	2	S16324	hypothetical prote
18	2	40.0	8	2	A21440	variant surface gl
19	2	40.0	8	2	G33098	205K exoantigen -
20	2	40.0	8	2	A05169	neuropeptide M-I -
21	2	40.0	8	2	PT0298	Ig heavy chain CRD
22	2	40.0	8	2	A54823	olfactory receptor
23	2	40.0	8	2	A35768	T-cell receptor al
24	2	40.0	8	2	B54823	olfactory receptor
25	2	40.0	8	2	I49404	prealbumin - weste
26	2	40.0	8	2	I57532	gene Tnislw prote
27	2	40.0	8	2	B47594	aspartate kinase (
28	2	40.0	9	2	D24180	fibrinogen beta ch
29	2	40.0	9	2	PA0033	protein QA300033 -

30	2	40.0	9	2	D48186	ATPase R1 subunit
31	2	40.0	9	2	S70345	amine oxidase (cop
32	2	40.0	9	2	A56029	N-methylpurine DNA
33	2	40.0	10	2	S39392	calpain (EC 3.4.22
34	2	40.0	10	2	JC1367	thyloliberin poten
35	2	40.0	10	2	A47593	mercury resistance
36	2	40.0	10	2	TQ0943	hypothetical 1.3K
37	2	40.0	10	2	B39517	probable methionin
38	2	40.0	10	2	C35389	urease (EC 3.5.1.5
39	2	40.0	10	2	JN0440	peptide-N4-(N-acet
40	2	40.0	10	2	PS0209	24K protein 4407 -
41	2	40.0	10	2	S19296	16K protein - poul
42	2	40.0	10	2	A43977	PMRFamide-like pro
43	2	40.0	10	2	C39111	Ig heavy chain C r
44	2	40.0	10	2	B56899	serum heterodimer,
45	2	40.0	10	2	S77980	cytochrome-c oxida
46	2	40.0	10	2	B45482	platelet activatin
47	2	40.0	10	2	B49033	T-cell receptor ga
48	2	40.0	10	2	S71948	matrix metalloprot
49	2	40.0	10	2	S36849	Ig heavy chain V r
50	2	40.0	10	2	B61288	hypothetical prote
51	2	40.0	11	2	S68392	H4-transporing tw
52	2	40.0	11	2	A40693	transgelin - sheep
53	2	40.0	11	2	A57458	gene Gax protein -
54	2	40.0	11	2	A55149	tetracenomycin A2
55	2	40.0	11	2	S33519	probable secreted
56	2	40.0	11	2	H54346	pyruvate synthase
57	2	40.0	11	2	PQ0731	unidentified 5.7/3
58	2	40.0	11	2	PC2173	triacylglycerol li
59	2	40.0	11	2	S45698	gamma-MSH-like pro
60	2	40.0	11	2	I52980	glucocerebrosidase
61	2	40.0	11	2	S23364	T-cell receptor al
62	2	40.0	11	2	S09024	carboxylesterase (
63	2	40.0	11	2	PH0891	T-cell receptor be
64	2	40.0	11	2	PH0924	T-cell receptor be
65	2	40.0	11	2	PH0922	T-cell receptor be
66	2	40.0	11	4	I52708	ELAV-like neuronal
67	2	40.0	12	2	S09082	proteasome chain 1
68	2	40.0	12	2	S26558	T-cell receptor be
69	2	40.0	12	2	S26559	T-cell receptor be
70	2	40.0	12	2	A39233	myosin heavy chain
71	2	40.0	12	2	S65629	protoporphyrinogen
72	2	40.0	12	2	S69123	proton-translocati
73	2	40.0	12	2	S36899	ribosomal protein
74	2	40.0	12	2	S52561	5-enolpyruvylshiki
75	2	40.0	12	2	PA0019	acidic ribosomal p
76	2	40.0	12	2	PA0037	plastocyanin 2 - A
77	2	40.0	12	2	PQ0730	unidentified 5.4/3
78	2	40.0	12	2	S70344	amine oxidase (cop
79	2	40.0	12	2	A33099	163K exoantigen -
80	2	40.0	12	2	S16204	6-phosphofructokin
81	2	40.0	12	2	I39390	acetylcholine rece
82	2	40.0	12	2	PT0257	Ig heavy chain CRD
83	2	40.0	12	2	S21205	Ig heavy chain V r
84	2	40.0	12	2	A60528	insulin-like growt
85	2	40.0	12	2	A33520	inhibitory diffusi
86	2	40.0	12	2	PH1466	T-cell receptor be
87	2	40.0	12	2	S39762	T-cell receptor be
88	2	40.0	12	2	PH0930	pollen major aller
89	2	40.0	12	2	A53252	aminotransferase c
90	2	40.0	12	4	JX0315	melanotropin alpha
91	2	40.0	13	1	MTGMAD	melanotropin alpha
92	2	40.0	13	1	A32734	enkephalin precurs
93	2	40.0	13	2	S39413	tubulin beta chain
94	2	40.0	13	2	A61288	spore proteinase g
95	2	40.0	13	2	S20578	ribosomal protein
96	2	40.0	13	2	PC1149	equinatoxin 1A - s
97	2	40.0	13	2	I57532	Ig kappa chain V-I
98	2	40.0	13	2	D61458	Ig kappa chain V-I
99	2	40.0	13	2	E61458	Ig kappa chain V-I
100	2	40.0	13	2	S65612	tubulin alpha-chai



## ALIGNMENTS

RESULT 1  
 PLO157  
 Ig kappa chain V-II region (anti-myeelin-associated glycoprotein, PEC) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Feb-1997  
 C:Accession: PLO157; C61458  
 R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
 J. Exp. Med. 170, 1551-1558, 1989  
 A:Title: Expression of a public idiotypic by human monoclonal IGM directed to myelin-associated glycoprotein  
 A:Reference number: A61458; MUID:90039128; PMID:2478651  
 A:Accession: PLO157  
 A:Molecule type: protein  
 A:Residues: 1-13 <BRO>  
 A:Accession: C61458  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-13 <BR2>  
 C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein  
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3  
 |||  
 Db 2 VWM 4

RESULT 2  
 S29137  
 aminopyrine N-demethylase (EC 1.14.14.-) cytochrome P450 betaNF-B - chicken (fragment)  
 N:Alternate names: aniline monooxygenase  
 C:Species: Gallus gallus (chicken)  
 C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 05-Mar-1999  
 C:Accession: S29137  
 R:Dupka, R.P.; Lapadula, D.M.; Abou-Donia, M.B.  
 Arch. Biochem. Biophys. 282, 170-182, 1990  
 A:Title: Purification and characterization of cytochrome P450 isozymes from beta-naphthol  
 A:Reference number: S13263; MUID:91024193; PMID:2171427  
 A:Accession: S29137  
 A:Molecule type: protein  
 A:Residues: 1-16 <GUP>  
 C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology  
 C:Keywords: heme; membrane protein; microsome; monooxygenase; oxidoreductase

Query Match 60.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
 |||  
 Db 1 MEV 3

RESULT 3  
 PLO025  
 T-cell surface glycoprotein rta - rabbit (fragment)  
 N:Alternate names: thymocyte specific class I-like antigen, heavy chain  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 07-Feb-1997  
 C:Accession: PLO025  
 R:Wang, C.R.; Chen, G.H.; Newkirk, M.; Capra, J.D.; Mandy, W.J.  
 Mol. Immunol. 25, 945-952, 1988  
 A:Title: Biochemical properties of a novel rabbit thymocyte specific class I-like antigen  
 A:Reference number: PLO025; MUID:89096985; PMID:3264985  
 A:Accession: PLO025  
 A:Molecule type: protein  
 A:Residues: 1-18 <WAN>  
 A:Experimental source: thymus

C:Keywords: glycoprotein; surface antigen

Query Match 60.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
 |||  
 Db 12 VME 14

RESULT 4  
 S48862  
 murine cyclin H - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S48862  
 R:Hall, F.L.; Wu, L.  
 Submitted to the EMBL Data Library, October 1994  
 A:Reference number: S48862  
 A:Accession: S48862  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-18 <HAL>  
 A:Cross-references: EMBL:X82441; NID:G563899; PIDN:CAA57822.1; PID:G563900

Query Match 60.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
 |||  
 Db 5 VME 7

RESULT 5  
 A61300  
 22k superhelical DNA-binding protein - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C:Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
 C:Accession: A61300  
 R:Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.  
 J. Biochem. 92, 1059-1068, 1982  
 A:Title: Purification and characterization of a protein from Escherichia coli which fo  
 A:Reference number: A61300; MUID:83082696; PMID:6294066  
 A:Accession: A61300  
 A:Molecule type: protein  
 A:Residues: 1-4 <KIS>  
 C:Comment: This protein resembles some of the histone-like protein of bacteria in amin  
 C:Keywords: DNA binding; monomer

Query Match 40.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 |||  
 Db 1 ME 2

RESULT 6  
 I57745  
 D-mannonate hydrolase (uxuA) - Escherichia coli  
 C:Species: Escherichia coli  
 C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999  
 C:Accession: I57745  
 R:Blanco, C.; Ritzenthaler, P.; Kolb, A.  
 Mol. Gen. Genet. 202, 112-119, 1986  
 A:Title: The regulatory region of the uxuAB operon in Escherichia coli K12.  
 A:Reference number: I57745; MUID:86174344; PMID:3083215  
 A:Accession: I57745  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A;Residues: 1-4 <RES>  
A;Cross-references: EMBL:X03411; NID:G43300; PIDN:CAA27147.1; PID:G581254

Query Match 40.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4  
Db 1 ME 2

RESULT 7  
E44823  
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)  
N:Alternate names: superprotein peptide 1  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C;Accession: E44823  
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A;Reference number: A44823; MUID:92044785; PMID:1941090  
A;Accession: E44823  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-4 <LOE>  
A;Experimental source: visual tissue  
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)  
C;Keywords: membrane trafficking

Query Match 40.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4  
Db 2 ME 3

RESULT 8  
S02617  
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)  
C;Species: Equus caballus (domestic horse)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 31-Jan-1997  
C;Accession: S02617  
P;Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall  
FEBS Lett. 222, 99-103, 1987  
A;Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differenc  
A;Reference number: S02617; MUID:88005160; PMID:3653405  
A;Accession: S02617  
A;Molecule type: protein  
A;Residues: 1-6 <FAI>  
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5  
Db 3 EV 4

RESULT 9  
B44510  
hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)  
C;Species: Lactococcus lactis  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 30-Sep-1993  
C;Accession: B44510  
R;Renault, P.; Gallardin, C.; Heslot, H.  
J. Bacteriol. 171, 3108-3114, 1989

A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation i;  
A;Reference number: A44510; MUID:89255069; PMID:2498286  
A;Accession: B44510  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-6 <REN>  
A;Cross-references: EMBL:M90762

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4  
Db 1 ME 2

RESULT 10  
A49792  
acylaminoacyl-peptidase (EC 3.4.19.1) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C;Accession: A49792  
R;Krishna, R.G.; Chin, C.C.O.; Wold, F.  
Anal. Biochem. 199, 45-50, 1991  
A;Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking  
A;Reference number: A49792; MUID:92222120; PMID:1807161  
A;Accession: A49792  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <KRI>  
C;Keywords: acetylated amino end; hydrolase; omega peptidase  
F;I/Modified site: acetylated amino end (Met) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4  
Db 1 ME 2

RESULT 11  
A20186  
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 05-May-2000  
C;Accession: A20186  
P;McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.  
FEBS Lett. 160, 296-300, 1983  
A;Title: Amino acid sequence around the active serine in the acyl transferase domain o;  
A;Reference number: A20186; MUID:83287768; PMID:6554204  
A;Accession: A20186  
A;Molecule type: protein  
A;Residues: 1-6 <MCC>  
C;Keywords: acyltransferase; coenzyme A

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5  
Db 4 EV 5

RESULT 12  
B34818  
vicilin 57K chain - pigeon pea (fragment)  
C;Species: Cajanus cajan (pigeon pea)  
C;Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
C;Accession: B34818

R.Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.  
 Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
 A>Title: Unusual denaturation properties of vicilin from Cajanus cajan.  
 A:Reference number: A34818; MUID:90165956; PMID:2306256  
 A:Accession: B34818  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <MAW>

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 Db 4 ME 5

## RESULT 13

PQ0727  
 H2 class I protein [imported] - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: PQ0727  
 R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A>Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
 A:Reference number: PQ0696  
 A:Accession: PQ0727  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <KOM>

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
 ||  
 Db 5 VV 6

## RESULT 14

PT0246  
 Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0246  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and f  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0246  
 A:Molecule type: DNA  
 A:Residues: 1-7 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 Db 2 EV 3

## RESULT 15

I48086  
 DNA topoisomerase II alpha - Chinese hamster (fragment)  
 C:Species: Cricetus griseus (Chinese hamster)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I48086

R.Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.  
 J. Biol. Chem. 270, 25850-25858, 1995  
 A>Title: Molecular cloning and characterization of the promoter for the Chinese hamste  
 A:Reference number: I48086; MUID:96029684; PMID:7592770  
 A:Accession: I48086  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7 <RES>  
 A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 Db 1 ME 2

## RESULT 16

S15597  
 orf 4 rara 5'-region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999  
 C:Accession: S15597  
 R:Brand, N.J.; Petkovich, M.; Chambon, P.  
 Nucleic Acids Res. 18, 6799-6806, 1990  
 A>Title: Characterization of a functional promoter for the human retinoic acid recepto  
 A:Reference number: S15594; MUID:91088249; PMID:2175878  
 A:Accession: S15597  
 A:Molecule type: DNA  
 A:Residues: 1-7 <BRA>

A:Cross-references: EMBL:X56058; NID:g35876  
 A>Note: this ORF from Fig. 2 is not annotated in GenBank entry HSEARA2, release 111.0  
 C:Comment: This sequence is not thought to be translated.  
 C:Genetics:  
 A:Gene: GDB:RARA  
 A:Cross-references: GDB:I20337; OMIM:180240  
 A:Map position: 17q12-17q12

Query Match 40.0%; Score 2; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
 ||  
 Db 6 VV 7

## RESULT 17

S16324  
 hypothetical protein 2 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
 C:Accession: S16324  
 R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
 EMBO J. 10, 1787-1791, 1991  
 A>Title: A novel class of plant proteins containing a homeodomain with a closely linke  
 A:Reference number: S16323; MUID:91266907; PMID:1675603  
 A:Accession: S16324  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RUB>  
 A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 Db 1 ME 2

## RESULT 18

A21440  
variant surface glycoprotein pSLc1 - Trypanosoma brucei (fragment)  
C;Species: Trypanosoma brucei  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Mar-1998  
C;Accession: A21440  
R;Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.  
Cell 38, 309-316, 1984  
A;Title: Trypanosome mRNAs share a common 5' spliced leader sequence.  
A;Reference number: A90853; MUID:84282716; PMID:6088073  
A;Accession: A21440  
A;Molecule type: mRNA  
A;Residues: 1-8 <PAR>  
A;Cross-references: GB:K02195; NID:g162150; PID:g162151  
C;Keywords: glycoprotein

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
Db 5 EV 6

## RESULT 19

G33098  
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C;Accession: G33098  
R;Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A;Reference number: A33098  
A;Accession: G33098  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <NIC>

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 7 VV 8

## RESULT 20

A05169  
neuropeptide M-I - American cockroach  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Dec-1993  
C;Accession: A05169  
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.I.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry  
A;Reference number: A90118; MUID:85046530; PMID:6548628  
A;Accession: A05169  
A;Molecule type: protein  
A;Residues: 1-8 <WIT>  
C;Keywords: neuropeptide

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
Db 1 EV 2

## RESULT 21

PT0298  
Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0298  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0298  
A;Molecule type: DNA  
A;Residues: 1-8 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 4 VV 5

## RESULT 22

A54823  
olfactory receptor 17 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
C;Accession: A54823  
R;Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
Cell 78, 823-834, 1994  
A;Title: Allelic inactivation regulates olfactory receptor gene expression.  
A;Reference number: A54823; MUID:94373818; PMID:8087849  
A;Accession: A54823  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-8 <CHE>

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
||  
Db 1 ME 2

## RESULT 23

A35768  
T-cell receptor alpha chain V-J region (34S-281) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 30-May-1997  
C;Accession: A35768  
R;Koseki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriuchi, K.; Taniguchi, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5248-5252, 1990  
A;Title: Homogeneous junctional sequence of the V14+ T-cell antigen receptor alpha chain  
A;Reference number: A35768; MUID:90319089; PMID:2371269  
A;Accession: A35768  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-8 <KOS>  
A;Note: the sequence shown follows the authors' translation at position 1 of TGT  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 2 VV 3

```
RESULT 24
B54823
C:Species: Mus spretus (western wild mouse)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54823
R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A:Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; MUID:94373818; PMID:8087849
A:Accession: B54823
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <CHE>

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ME 4
Db      1 ME 2

RESULT 25
I49404
prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49404
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49404
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05689; NID:G497008; PID:ARB60461.1; PID:G642825

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VV 2
Db      2 VV 3

RESULT 26
I57532
gene TnIslow protein - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C:Accession: I57532
R:Banerjee-Basu, S.; Buonanno, A.
Mol. Cell. Biol. 13, 7019-7028, 1993
A:Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and develop
A:Reference number: I57532; MUID:94019373; PMID:8413291
A:Accession: I57532
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: GB:S66172; NID:G432603
C:Genetics:
A:Gene: TnIslow

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VV 2
Db      2 VV 3

RESULT 27
B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C:Species: Corynebacterium flavum
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B47594
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinsky, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A:Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd opero
A:Reference number: A47594; MUID:93308089; PMID:8100567
A:Accession: B47594
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <FOL>
C:Keywords: phosphotransferase

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ME 4
Db      1 ME 2

RESULT 28
D24180
fibrinogen beta chain - red guenon (fragment)
N:Contains: fibrinopeptide B
C:Species: Brythrocebus patas (red guenon, hussar)
C:Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: D24180
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A:Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey
uenons, and baboons.
A:Reference number: A91990; MUID:85289140; PMID:3928610
A:Accession: D24180
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disul

Query Match      40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EV 5
Db      3 EV 4

RESULT 29
PA0033
protein QA300033 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0033
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JPIID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensio
A:Reference number: PA0001
A:Accession: PA0033
A:Molecule type: protein
A:Residues: 1-9 <KAM>
A:Experimental source: leaf

Query Match      40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
```

```
QY      4 EV 5
Db      3 EV 4

RESULT 27
B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C:Species: Corynebacterium flavum
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B47594
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinsky, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A:Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd opero
A:Reference number: A47594; MUID:93308089; PMID:8100567
A:Accession: B47594
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <FOL>
C:Keywords: phosphotransferase

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ME 4
Db      1 ME 2

RESULT 28
D24180
fibrinogen beta chain - red guenon (fragment)
N:Contains: fibrinopeptide B
C:Species: Brythrocebus patas (red guenon, hussar)
C:Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: D24180
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A:Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey
uenons, and baboons.
A:Reference number: A91990; MUID:85289140; PMID:3928610
A:Accession: D24180
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disul

Query Match      40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EV 5
Db      3 EV 4

RESULT 29
PA0033
protein QA300033 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0033
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JPIID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensio
A:Reference number: PA0001
A:Accession: PA0033
A:Molecule type: protein
A:Residues: 1-9 <KAM>
A:Experimental source: leaf

Query Match      40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
8 VV 9

Db

RESULT 30

D48186

ATPase R1 subunit - wood tobacco (fragment)

C;Species: Nicotiana sylvestris (wood tobacco)

C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Feb-1997

C;Accession: D48186

R;De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.

Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993

A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase

A;Reference number: A48186; MUID:93317598; PMID:8327463

A;Accession: D48186

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <DEI>

A;Experimental source: pollen

A;Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
2 VV 3

Db

RESULT 31

S70345

amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)

C;Species: Aspergillus niger

C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C;Accession: S70345

R;Rebort, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.

Biochim. Biophys. Acta 1295, 59-72, 1996

A;Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the

A;Reference number: S70344; MUID:96283794; PMID:8679675

A;Accession: S70345

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5;6-9 <FRE>

C;Keywords: oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
1 VV 2

Db

RESULT 32

A56029

N-methylpurine DNA glycosylase - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 19-Jan-1996

C;Accession: A56029

R;Roy, R.; Brooks, C.; Mitra, S.

Biochemistry 33, 15131-15140, 1994

A;Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA

A;Reference number: A56029; MUID:95092772; PMID:7999773

A;Accession: A56029

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <ROY>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
1 VV 2

Db

RESULT 33

S39392

calpain (EC 3.4.22.17) II light chain - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 18-Feb-1994 #sequence\_revision 24-Jul-1998 #text\_change 29-Sep-1999

C;Accession: S39392

R;Crawford, C.; Brown, N.R.; Willis, A.C.

Biochem. J. 296, 135-142, 1993

A;Title: Studies of the active site of m-calpain and the interaction with calpastatin.

A;Reference number: S39391; MUID:94071815; PMID:8250833

A;Accession: S39392

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CEA>

C;Superfamily: calpain small chain; calmodulin repeat homology

C;Keywords: cysteine proteinase; EF hand; hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
6 EV 7

Db

RESULT 34

JC1367

thyroliberin potentiating neuropeptide - bovine

N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiating

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1997

C;Accession: JC1367

R;Rulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.

Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992

A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovine

A;Reference number: JC1367; MUID:93111999; PMID:1472021

A;Accession: JC1367

A;Molecule type: protein

A;Residues: 1-10 <BUL>

A;Experimental source: hypothalamus

C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precursor

C;Function:

A;Description: potentiates thyroliberin-induced thyrotropin secretion

C;Superfamily: thyroliberin precursor

C;Keywords: hypothalamus; neuropeptide

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
||  
5 ME 6

Db

RESULT 35

A47593

mercury resistance regulatory protein merR - Pseudomonas aeruginosa transposon Tn501 (f

C;Species: Pseudomonas aeruginosa

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Aug-1998

C;Accession: A47593

R;O'Halloran, T.; Walsh, C.

Science 235, 211-214, 1987

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
4 EV 5

Db

RESULT 33

S39392

calpain (EC 3.4.22.17) II light chain - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 18-Feb-1994 #sequence\_revision 24-Jul-1998 #text\_change 29-Sep-1999

C;Accession: S39392

R;Crawford, C.; Brown, N.R.; Willis, A.C.

Biochem. J. 296, 135-142, 1993

A;Title: Studies of the active site of m-calpain and the interaction with calpastatin.

A;Reference number: S39391; MUID:94071815; PMID:8250833

A;Accession: S39392

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CEA>

C;Superfamily: calpain small chain; calmodulin repeat homology

C;Keywords: cysteine proteinase; EF hand; hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
6 EV 7

Db

RESULT 34

JC1367

thyroliberin potentiating neuropeptide - bovine

N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiating

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1997

C;Accession: JC1367

R;Rulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.

Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992

A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovine

A;Reference number: JC1367; MUID:93111999; PMID:1472021

A;Accession: JC1367

A;Molecule type: protein

A;Residues: 1-10 <BUL>

A;Experimental source: hypothalamus

C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precursor

C;Function:

A;Description: potentiates thyroliberin-induced thyrotropin secretion

C;Superfamily: thyroliberin precursor

C;Keywords: hypothalamus; neuropeptide

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
||  
5 ME 6

Db

RESULT 35

A47593

mercury resistance regulatory protein merR - Pseudomonas aeruginosa transposon Tn501 (f

C;Species: Pseudomonas aeruginosa

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Aug-1998

C;Accession: A47593

R;O'Halloran, T.; Walsh, C.

Science 235, 211-214, 1987

A:Title: Metalloregulatory DNA-binding protein encoded by the merR gene: isolation and d  
 A:Reference number: A47593; PMID:87094195; PMID:3798107  
 A:Accession: A47593  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <OAH>  
 C:Superfamily: transcription repressor glnr

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 1 ME 2

## RESULT 36

JQ0943

hypothetical 1.3K protein - infectious bursal disease virus (strain 52/70)  
 C:Species: Infectious bursal disease virus  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 08-Oct-1999  
 C:Accession: JQ0943  
 R:Bayliss, C.D.; Spies, U.; Shaw, K.; Peters, R.W.; Papageorgiou, A.; Mueller, H.; Bours  
 J. Gen. Virol. 71, 1303-1312, 1990  
 A:Title: A comparison of the sequences of segment A of four infectious bursal disease vi  
 A:Reference number: JQ0941; PMID:90278420; PMID:2161902  
 A:Accession: JQ0943  
 A>Status: translation not shown  
 A:Molecule type: genomic RNA  
 A:Residues: 1-10 <BAY>  
 A:Cross-references: GB:D00869; NID:g221038; PIDN:BAA00743.1; PID:d1001203; PID:g221039

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 1 ME 2

## RESULT 37

B39517

probable methionine-tRNA ligase attenuator peptide - Thermus aquaticus  
 C:Species: Thermus aquaticus  
 C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 18-Jun-1993  
 C:Accession: B39517  
 R:Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T  
 J. Biol. Chem. 266, 3268-3277, 1991  
 A:Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilu  
 esis.  
 A:Reference number: A39517; PMID:91131636; PMID:1993699  
 A:Accession: B39517  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-10 <NUR>  
 A:Cross-references: GB:J05744

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 1 ME 2

## RESULT 38

C35389

urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)  
 C:Species: Morganella morganii  
 C:Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 23-Jun-1993

C:Accession: C35389  
 R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
 J. Bacteriol. 172, 3073-3080, 1990  
 A:Title: Morganella morganii urease: purification, characterization, and isolation of  
 A:Reference number: A35389; PMID:90264298; PMID:2345135  
 A:Accession: C35389  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <HUA>  
 C:Keywords: hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 7 EV 8

## RESULT 39

JN0440

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) - sweet almond  
 N:Alternate names: glycopeptidase  
 C:Species: Prunus dulcis var. sativa (sweet almond)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 19-May-2000  
 C:Accession: JN0440  
 R:Kaliberda, E.I.; Shemyakin, V.V.; Antonov, V.K.  
 Bioorg. Khim. 16, 751-757, 1990  
 A:Title: Purification of sweet almond glycopeptidase and sequencing of N-terminal prot  
 A:Reference number: JN0440  
 A:Accession: JN0440  
 A:Molecule type: protein  
 A:Residues: 1-10 <KAL>  
 C:Keywords: hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
 ||  
 5 VV 6

## RESULT 40

PS0209

24K protein 4407 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C:Accession: PS0209  
 R:Tsuigita, A.; Kamo, M.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0209  
 A:Accession: PS0209  
 A:Molecule type: protein  
 A:Residues: 1-10 <TSU>  
 A:Experimental source: callus  
 C:Comment: molecular weight 24K, pI 4.6.

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 4 EV 5

## RESULT 41

S19296

16K protein - poulard wheat  
 C:Species: Triticum turgidum (poulard wheat)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C;Accession: S19296  
 R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.  
 Biochem. J. 281, 401-405, 1992  
 A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subunit  
 A;Reference number: S19296; MUID:92143804; PMID:1736890  
 A;Accession: S19296  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <SAN>

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 Db 9 ME 10

RESULT 42  
 A43977  
 PMRFamide-like protein - tobacco hornworm  
 C;Species: Manduca sexta (tobacco hornworm)  
 C;Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 17-Mar-1999  
 C;Accession: A43977  
 R;Kingsan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;  
 Peptides 11, 849-856, 1990  
 A;Title: A new peptide in the PMRFamide family isolated from the CNS of the hawkmoth, Ma  
 A;Reference number: A43977; MUID:91045350; PMID:2235684  
 A;Accession: A43977  
 A;Molecule type: protein  
 A;Residues: 1-10 <KIN>  
 A;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 3 VW 4

RESULT 43  
 C39111  
 Ig heavy chain C region - Pacific hagfish (fragment)  
 C;Species: Eptatretus stoutii (Pacific hagfish)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
 C;Accession: C39111  
 R;Varner, J.; Neame, P.; Litman, G.W.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991  
 A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil  
 A;Reference number: A39111; MUID:91156684; PMID:2000382  
 A;Accession: C39111  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <VAR>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 9 VW 10

RESULT 44  
 B56899

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C;Accession: S19296  
 R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.  
 Biochem. J. 281, 401-405, 1992  
 A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subunit  
 A;Reference number: S19296; MUID:92143804; PMID:1736890  
 A;Accession: S19296  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <SAN>

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 Db 9 ME 10

RESULT 42  
 A43977  
 PMRFamide-like protein - tobacco hornworm  
 C;Species: Manduca sexta (tobacco hornworm)  
 C;Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 17-Mar-1999  
 C;Accession: A43977  
 R;Kingsan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;  
 Peptides 11, 849-856, 1990  
 A;Title: A new peptide in the PMRFamide family isolated from the CNS of the hawkmoth, Ma  
 A;Reference number: A43977; MUID:91045350; PMID:2235684  
 A;Accession: A43977  
 A;Molecule type: protein  
 A;Residues: 1-10 <KIN>  
 A;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 3 VW 4

RESULT 43  
 C39111  
 Ig heavy chain C region - Pacific hagfish (fragment)  
 C;Species: Eptatretus stoutii (Pacific hagfish)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
 C;Accession: C39111  
 R;Varner, J.; Neame, P.; Litman, G.W.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991  
 A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil  
 A;Reference number: A39111; MUID:91156684; PMID:2000382  
 A;Accession: C39111  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <VAR>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 9 VW 10

RESULT 44  
 B56899

serum heterodimer, 24K chain - sandbar shark (fragment)  
 C;Species: Carcharhinus plumbeus (sandbar shark)  
 C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Jun-2000  
 C;Accession: B56899  
 R;Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.  
 Comp. Biochem. Physiol. B 103, 563-569, 1992  
 A;Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum  
 A;Reference number: A56899; MUID:93092592; PMID:1458832  
 A;Accession: B56899  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <VAZ>  
 C;Keywords: glycoprotein; plasma

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 1 VW 2

RESULT 45  
 S77980  
 Cytochrome-c oxidase (EC 1.9.3.1) chain IV - bigeye tuna (fragment)  
 C;Species: Thunnus obesus (bigeye tuna)  
 C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998  
 C;Accession: S77980  
 R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
 submitted to the Protein Sequence Database, June 1997  
 A;Reference number: S77980  
 A;Accession: S77980  
 A;Molecule type: protein  
 A;Residues: 1-10 <ARN>  
 A;Experimental source: heart; liver  
 C;Genetics:  
 A;Genome: nuclear  
 C;Function:  
 A;Pathway: oxidative phosphorylation; respiratory chain  
 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 Db 6 EV 7

RESULT 46  
 B45482  
 platelet activating factor acetylhydrolase - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 05-May-1995 #sequence\_revision 05-May-1995 #text\_change 05-May-1995  
 C;Accession: B45482  
 R;Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.  
 J. Biol. Chem. 268, 3857-3865, 1993  
 A;Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purifi  
 A;Reference number: A45482; MUID:93179380; PMID:8440881  
 A;Accession: B45482  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <STA>

Query Match 40.0%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 4 VW 5



## RESULT 47

E49033  
T-cell receptor gamma chain V-D-J region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-Dec-1993 #sequence\_revision 25-Aug-1995 #text\_change 21-Jul-2000  
C:Accession: E49033; D49033  
R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
Eur. J. Immunol. 21, 2999-3007, 1991  
A>Title: Functionally distinct subsets of human gamma/delta T cells.  
A:Reference number: A49033; MUID:92083926; PMID:1684157  
A:Accession: E49033  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <MOR>  
A:CROSS-references: GB:S7587; NID:9240696; PIDN:AAB20630.1; PID:9240697  
A>Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)  
A:Accession: D49033  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <MOR2>  
A:CROSS-references: GB:S7587; NID:9240696; PIDN:AAB20630.1; PID:9240697  
A>Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)  
C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5  
||  
Db 5 EV 6

## RESULT 48

S71948  
matrix metalloproteinase 3 precursor - bovine (fragments)  
N:Alternate names: MMP-3 protein; stromelysin precursor MMP-3  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C:Accession: S71948  
R:Arner, E.C.; Pratta, M.A.; Freimark, B.; Lischwe, M.; Trzaskos, J.M.; Magolda, R.L.; W  
Biochem. J. 318, 417-424, 1996  
A>Title: Isothiazolones interfere with normal matrix metalloproteinase activation and in  
A:Reference number: S71948; MUID:96404887; PMID:8809028  
A:Accession: S71948  
A:Molecule type: protein  
A:Residues: 1-5; 6-10 <ARN>  
C:Function:  
A:Description: degrades a wide range of extracellular matrix components, including carti  
A>Note: may be involved in arthritis formation

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VM 3  
||  
Db 1 VM 2

## RESULT 49

S36849  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1994 #sequence\_revision 01-Dec-1995 #text\_change 05-Nov-1999  
C:Accession: S36849  
R:Jacob, J.; Kelsoe, G.  
submitted to the EMBL Data Library, July 1992  
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny  
A:Reference number: S25024  
A:Accession: S36849

A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-10 <UAC>  
A:CROSS-references: EMBL:X67382; NID:950070; PIDN:CAA47794.1; PID:es1590; PID:g1333861  
C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2  
||  
Db 6 VW 7

## RESULT 50

E86128  
hypothetical protein Z5903 [imported] - Escherichia coli (strain O157:H7, substrain EDI  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: E86128  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: E86128  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <STO>  
A:CROSS-references: GB:AE005174; NID:gl2519314; PIDN:AAG59489.1; GSPDB:GN00145; UWGP:Z:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5903

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2  
||  
Db 7 VW 8

## RESULT 51

S68392  
H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas reinhardtii ch  
N:Alternate names: ATP synthase chain I  
C:Species: chloroplast Chlamydomonas reinhardtii  
C>Date: 04-Dec-1987 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002  
C:Accession: S68392  
R:Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.  
FEBS Lett. 377, 163-166, 1995  
A>Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termina  
A:Reference number: S68388; MUID:96128220; PMID:8543042  
A:Accession: S68392  
A:Molecule type: protein  
A:Residues: 1-11 <FIE>  
A:Experimental source: strain CW15  
C:Genetics:  
A:Genome: chloroplast  
C:Superfamily: H+-transporting ATP synthase protein 6  
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thy

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5  
||  
Db 1 EV 2

## RESULT 52

A40693  
transgelin - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997  
C:Accession: A40693  
R:Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.  
J. Cell Biol. 121, 1065-1073, 1993  
A:Title: Purification and properties of transgelin: a transformation and shape change se  
A:Reference number: A40693; MUID:93273790; PMID:8501116  
A:Accession: A40693  
A:Molecule type: protein  
A:Residues: 1-11 <SHA>  
A:Experimental source: aorta  
C:Comment: This protein gets actin and is down regulated by transformation or loss of ce  
C:Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle prote  
C:Keywords: actin binding; cytoskeleton

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
Db 10 EV 11

## RESULT 53

A57458  
gene Gax protein - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999  
C:Accession: A57458  
R:Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.  
Mol. Cell. Biol. 15, 4272-4281, 1995  
A:Title: Regulation of Gax homeobox gene transcription by a combination of positive fact  
A:Reference number: A57458; MUID:95349593; PMID:7623821  
A:Accession: A57458  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-11 <RES>  
A:Cross-references: GB:S79168; NID:g1050991  
C:Genetics: Gax  
A:Gene: Gax  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
||  
Db 1 ME 2

## RESULT 54

A55149  
tetragenomycin A2 oxygenase (EC 1.-.-.-) - Streptomyces glaucescens (fragment)  
N:Alternate names: tcmA2 oxygenase; tcmG  
C:Species: Streptomyces glaucescens  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Mar-1996  
C:Accession: A55149  
R:Shen, B.; Hutchinson, C.R.  
J. Biol. Chem. 269, 30726-30733, 1994  
A:Title: Triple hydroxylation of tetragenomycin A2 to tetragenomycin C in Streptomyces 9  
A2 oxygenase.  
A:Reference number: A55149; MUID:95074090; PMID:7982994  
A:Accession: A55149  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <SHA>  
C:Genetics:

A:Start codon: TTG  
C:Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
Db 5 EV 6

## RESULT 55

S33519  
probable secreted protein - Acholeplasma laidlawii (fragment)  
C:Species: Acholeplasma laidlawii  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Oct-1999  
C:Accession: S33519  
R:Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.  
submitted to the EMBL data library, June 1993  
A:Description: Sequence regions from Acholeplasma laidlawii which restore export of bet  
A:Reference number: S33518  
A:Accession: S33519  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-11 <BOY>  
A:Cross-references: EMBL:222875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3  
||  
Db 6 VM 7

## RESULT 56

H54346  
pyruvate synthase (EC 1.2.7.1) alpha chain - Pyrococcus furiosus (fragment)  
C:Species: Pyrococcus furiosus  
C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-May-2000  
C:Accession: H54346  
R:Blamey, J.M.; Adams, M.W.  
Biochemistry 33, 1000-1007, 1994  
A:Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase fr  
A:Reference number: A54346; MUID:94137707; PMID:8305426  
A:Accession: H54346  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <BLA>  
C:Keywords: coenzyme A; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3  
||  
Db 2 VM 3

## RESULT 57

PQ0731  
unidentified 5.7/35K protein [imported] - rice (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: PQ0731  
R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimensic  
A:Reference number: PQ0696  
A:Accession: PQ0731

A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <KOH>

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
DB 3 VV 4

## RESULT 58

PC2173

triacylglycerol lipase (EC 3.1.1.3) II - Rhizopus niveus (strain IFO 4759) (fragments)

C:Species: Rhizopus niveus  
C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C:Accession: PC2173

R;Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.

Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994.

A&gt;Title: Purification, characterization, and crystallization of two types of lipase from

A:Reference number: PC2171; MUID:94319059; PMID:7765029

A:Accession: PC2173

A:Molecule type: protein

A:Residues: 1-10;11 &lt;KOH&gt;

C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds of triacylglycerols a

C:Comment: This enzyme is produced from lipase I by limited proteolysis due to the actio

C:Keywords: carboxylic ester hydrolase

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
DB 6 VV 7

## RESULT 59

S45698

gamma-MSH-like protein - duck leech

C:Species: Theromyzon tessulatatum (duck leech)

C&gt;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997

C:Accession: S45698

R;Salzet, M.; Watter, C.; Bulet, P.; Malecha, J.

FEBS Lett. 348, 102-106, 1994

A&gt;Title: Isolation and structural characterization of a novel peptide related to gamma-m

A:Reference number: S45698; MUID:94298944; PMID:8026574

A:Accession: S45698

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 &lt;SAL&gt;

Query Match 40.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3  
DB 2 VM 3

## RESULT 60

I52980

glucocerebrosidase - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I52980; I55971

R;Reiner, O.; Wigderson, M.; Horowitz, M.

DNA 7, 107-116, 1988

A&gt;Title: Structural analysis of the human glucocerebrosidase genes.

A:Reference number: I52980; MUID:88195776; PMID:3359914

A:Accession: I52980

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 &lt;RES&gt;

A:Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024

A:Accession: I55971

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 &lt;RE2&gt;

A:Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

## Query Match

40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4

DB 1 ME 2

## RESULT 61

S23364

T-cell receptor alpha chain J region - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C:Accession: S23364

R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichm

Eur. J. Immunol. 21, 2749-2754, 1991

A&gt;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rh

A:Reference number: S23364; MUID:92037820; PMID:1657615

A:Accession: S23364

A&gt;Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-11 &lt;PLU&gt;

A:Cross-references: EMBL:X58164

C:Keywords: T-cell receptor

## Query Match

40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2

DB 1 VV 2

## RESULT 62

S09024

carboxylesterase (EC 3.1.1.1), microsomal - golden hamster (fragment)

C:Species: Mesocricetus auratus (golden hamster)

C&gt;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 28-Apr-1993

C:Accession: S09024

R;Hosokawa, M.; Maki, T.; Satoh, T.

Arch. Biochem. Biophys. 277, 219-227, 1990

A&gt;Title: Characterization of molecular species of liver microsomal carboxylesterases o

A:Reference number: S09021; MUID:90179180; PMID:2310190

A:Accession: S09024

A:Molecule type: protein

A:Residues: 1-11 &lt;HOS&gt;

C:Keywords: carboxylic ester hydrolase

## Query Match

40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2

DB 7 VV 8

## RESULT 63

PH0891

T-cell receptor beta chain V-D-J region (clone 6-1) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0891  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0891  
 A;Molecule type: mRNA  
 A;Residues: 1-11 <GOL>  
 A;Experimental source: myelin basic protein-immunized T-cell  
 C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 10 EV 11

Db

RESULT 64  
 PH0924  
 T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0924  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0924  
 A;Molecule type: mRNA  
 A;Residues: 1-11 <GOL>  
 A;Experimental source: concanavalin A-activated lymphoblast  
 C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
 ||  
 9 ME 10

Db

RESULT 65  
 PH0922  
 T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0922  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0922  
 A;Molecule type: mRNA  
 A;Residues: 1-11 <GOL>  
 A;Experimental source: concanavalin A-activated lymphoblast  
 C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3  
 ||  
 6 VM 7

Db

RESULT 66

I52708  
 ELAV-like neuronal protein 1, truncated splice form - human  
 N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen  
 C;Species: Homo sapiens (man)  
 C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C;Accession: I52708  
 R;Skidjo, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.  
 Cancer Res. 54, 4988-4992, 1994  
 A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis  
 A;Reference number: I52708; MUID:94349312; PMID:8069866  
 A;Accession: I52708  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-11 <SEK>  
 A;Cross-references: GB:S73887; NID:G688242; PIDN:AA14142.1; PID:94261842  
 C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726  
 C;Genetics:  
 A;Gene: GDB:ELAVL4; HUD; PNEM  
 A;Cross-references: GDB:I41875; OMIM:168360  
 A;Map position: lp36-lp36  
 C;Keywords: alternative splicing

Query Match 40.0%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3  
 ||  
 2 VM 3

Db

RESULT 67  
 S09082  
 proteasome chain 1 - rat (fragment)  
 N;Alternate names: multicatalytic proteinase chain 1  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
 C;Accession: S09082  
 R;Lilley, K.S.; Davison, M.D.; Rivett, A.J.  
 FEBS Lett. 262, 327-329, 1990  
 A;Title: N-terminal sequence similarities between components of the multicatalytic prot  
 A;Reference number: S09082; MUID:90242957; PMID:2335214  
 A;Accession: S09082  
 A;Molecule type: protein  
 A;Residues: 1-12 <LIL>  
 C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
 ||  
 6 VV 7

Db

RESULT 68  
 S26558  
 T-cell receptor beta chain (clone Cw3/5B8) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
 C;Accession: S26558  
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi  
 J. Exp. Med. 176, 439-447, 1992  
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recept  
 A;Reference number: S26512; MUID:92364546; PMID:1380061  
 A;Accession: S26558  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>  
 A;Cross-references: EMBL:X68008  
 A;Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3  
 ||  
 Db 7 VM 8

RESULT 69  
 S26559  
 T-cell receptor beta chain (clone Cw3/Cas15) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
 C:Accession: S26559  
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A:Reference number: S26512; MUID:92364546; PMID:1380061  
 A:Accession: S26559  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <CAS>  
 A:Cross-references: EXBL:X68009  
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas15  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 Db 8 EV 9

RESULT 70  
 A39233  
 myosin heavy chain 1, smooth muscle - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Sep-1991 #sequence\_revision 20-Sep-1991 #text\_change 13-Feb-1998  
 C:Accession: A39233  
 R:Kelley, C.A.; Adelstein, R.S.  
 J. Biol. Chem. 265, 17876-17882, 1990  
 A:Title: The 204-kDa smooth muscle myosin heavy chain is phosphorylated in intact cells  
 A:Reference number: A39233; MUID:91009254; PMID:2170399  
 A:Accession: A39233  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <KEL>  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: smooth muscle

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
 ||  
 Db 11 EV 12

RESULT 71  
 S65629  
 protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-May-2000  
 C:Accession: S65629  
 R:Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Ino  
 Eur. J. Biochem. 230, 760-765, 1995  
 A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m  
 A:Reference number: S65629; MUID:95333135; PMID:7607249

A:Accession: S65629  
 A:Molecule type: protein  
 A:Residues: 1-12 <TAK>  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Pathway: heme biosynthesis; porphyrin biosynthesis  
 C:Superfamily: phytylene dehydrogenase  
 C:Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 4 VW 5

RESULT 72  
 S69123  
 proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)  
 C:Species: Rhodospirillum rubrum  
 C:Date: 10-Mar-1998 #sequence\_revision 24-Apr-1998 #text\_change 24-Apr-1998  
 C:Accession: S69123  
 R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.  
 Eur. J. Biochem. 228, 719-726, 1995  
 A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrog  
 A:Reference number: S69123; MUID:9525277; PMID:7737169  
 A:Accession: S69123  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <DIG>

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 4 VW 5

RESULT 73  
 S36899  
 ribosomal protein S6 - Mycobacterium bovis (fragment)  
 C:Species: Mycobacterium bovis  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
 C:Accession: S36899  
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycob.  
 A:Reference number: S36887; MUID:94009653; PMID:8405418  
 A:Accession: S36899  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <OHA>  
 C:Keywords: protein biosynthesis; ribosome

Query Match 40.0%; Score 2; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
 ||  
 Db 8 VW 9

RESULT 74  
 S52561  
 5-enolpyruvylshikimate-3-phosphate - Euglena gracilis  
 C:Species: Euglena gracilis  
 C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 01-Sep-1995

C;Accession: S52561  
R;Reinbothe, C.; Ortel, B.; Parthier, B.; Reinbothe, S.  
Mol. Gen. Genet. 245, 618-622, 1994  
A;Title: Cytosolic and plastid forms of 5-enolpyruvylshikimate-3-phosphate synthase in R  
A;Reference number: S52561; MUID:95107260; PMID:7808412  
A;Accession: S52561  
A;Status: preliminary  
A;Molecule type: Protein  
A;Residues: 1-12 <RE1>

Query Match 40.0%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred.No. 9.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2  
||  
Db 10 VV 11

RESULT 75  
PA0019  
acidic ribosomal P2-like protein - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 11-Apr-1995  
C;Accession: PA0019  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
Submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
A;Reference number: PA0001  
A;Accession: PA0019  
A;Molecule type: protein  
A;Residues: 1-12 <KAM>  
A;Experimental source: callus

Query Match 40.0%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred.No. 9.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2  
||  
Db 3 VV 4

Search completed: November 25, 2003, 18:28:20  
Job time : 5.60106 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 2.42021 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-9  
Perfect score: 5  
Sequence: 1 VMEV 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3	60.0	15	1	MCPA_METTE
2	3	60.0	19	1	PSBM_SYNVU
3	3	60.0	20	1	DNAX_CLOPA
4	3	60.0	20	1	DNAX_THIFE
5	2	40.0	5	1	UC22_MAIZE
6	2	40.0	6	1	ACPH_RABIT
7	2	40.0	8	1	CPD1_ENTEA
8	2	40.0	8	1	NS3_MYCTU
9	2	40.0	8	1	WPI_PBRAT
10	2	40.0	9	1	FIBB_ERYPA
11	2	40.0	9	1	UF02_MOUSE
12	2	40.0	10	1	FARP_MANSE
13	2	40.0	10	1	RT02_BOVIN
14	2	40.0	10	1	URE3_MORMO
15	2	40.0	11	1	MLG_THETS
16	2	40.0	11	1	PKV1_PERAM
17	2	40.0	12	1	HCVB_MEGCR
18	2	40.0	12	1	HS9A_RAT
19	2	40.0	12	1	NO40_SOYBN
20	2	40.0	12	1	PORD_METTM
21	2	40.0	12	1	UN39_CLOPA
22	2	40.0	12	1	UP01_CAEEL
23	2	40.0	12	1	V23K_WSSV
24	2	40.0	12	1	V25K_WSSV
25	2	40.0	13	1	FIBB_RABIT
26	2	40.0	13	1	IDRA_CANFA
27	2	40.0	13	1	IDHP_RAT
28	2	40.0	13	1	MLA_ANOCA
29	2	40.0	13	1	MLA_CAMDR
30	2	40.0	13	1	PED1_HYDAT
31	2	40.0	13	1	UN41_CLOPA
32	2	40.0	13	1	UP71_LITWE
33	2	40.0	14	1	ADFA_TENNO

34	2	40.0	14	1	GR75_CANFA
35	2	40.0	14	1	IF2G_RAT
36	2	40.0	14	1	KLPS_SCARA
37	2	40.0	14	1	KPPI_SELMI
38	2	40.0	14	1	PH1_PRUSE
39	2	40.0	14	1	PPK6_PREAM
40	2	40.0	14	1	UC15_MAIZE
41	2	40.0	14	1	UN04_CLOPA
42	2	40.0	15	1	CDN2_LITCI
43	2	40.0	15	1	CDN4_LITCE
44	2	40.0	15	1	COXI_THUOB
45	2	40.0	15	1	EF1A_MICCR
46	2	40.0	15	1	ESTB_SCHGA
47	2	40.0	15	1	ESTU_MANSE
48	2	40.0	15	1	FKB7_PINPS
49	2	40.0	15	1	GR78_HORSE
50	2	40.0	15	1	KPP2_SELMI
51	2	40.0	15	1	MALT_BACTQ
52	2	40.0	15	1	MAOX_CHICK
53	2	40.0	15	1	NXSO_PSETE
54	2	40.0	15	1	PGTS_PELAC
55	2	40.0	15	1	PH3_PRUSE
56	2	40.0	15	1	R13A_SPTOL
57	2	40.0	15	1	RKGG_CARCR
58	2	40.0	15	1	RML2_YEAST
59	2	40.0	15	1	THL_CLOPA
60	2	40.0	15	1	UBL1_MONDO
61	2	40.0	15	1	UC08_MAIZE
62	2	40.0	15	1	UC16_MAIZE
63	2	40.0	15	1	UP01_METAN
64	2	40.0	15	1	VORA_METTM
65	2	40.0	16	1	AU21_LITRA
66	2	40.0	16	1	AU22_LITAU
67	2	40.0	16	1	AU23_LITAU
68	2	40.0	16	1	AU24_LITAU
69	2	40.0	16	1	AU25_LITRA
70	2	40.0	16	1	CT12_LITCI
71	2	40.0	16	1	DHE2_THUTH
72	2	40.0	16	1	HTPG_ACICA
73	2	40.0	16	1	LE05_BIOGL
74	2	40.0	16	1	PGTL_PELAC
75	2	40.0	16	1	PH2_PRUSE
76	2	40.0	17	1	B29K_PORGI
77	2	40.0	17	1	EFG_THEAQ
78	2	40.0	17	1	FIBA_PIG
79	2	40.0	17	1	GAST_MACMU
80	2	40.0	17	1	ITHB_HIRME
81	2	40.0	17	1	LCK_RAT
82	2	40.0	17	1	LPW_AZOBR
83	2	40.0	17	1	NEP_HV1J3
84	2	40.0	17	1	PSBL_SYNVU
85	2	40.0	17	1	SP51_BACLI
86	2	40.0	17	1	UN15_CLOPA
87	2	40.0	17	1	UP31_UPEIN
88	2	40.0	17	1	UP32_UPEIN
89	2	40.0	17	1	UP33_UPEIN
90	2	40.0	17	1	UP36_UPEMJ
91	2	40.0	17	1	UP37_UPEMJ
92	2	40.0	17	1	UP41_UPEIN
93	2	40.0	17	1	YALA_TRYBB
94	2	40.0	18	1	AROF_STRBM
95	2	40.0	18	1	CT1C_LITCI
96	2	40.0	18	1	CT1D_LITCI
97	2	40.0	18	1	DRPH_PANBO
98	2	40.0	18	1	DRPH_UCAPU
99	2	40.0	18	1	FIXA_RHILE
100	2	40.0	18	1	HEX_ADECU

## ALIGNMENTS

RESULT 1

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MCRA, METTE
ID MCRA_METTE STANDARD; PRT; 15 AA.
AC P22948;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase alpha subunit (EC 2.8.4.1) (Coenzyme-B
DE sulfothioltransferase alpha) (Fragment).
OS Methanosarcina thermophila.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2210;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 1825 / TM-1;
RX MEDLINE=91193204; PubMed=2013570;
RA Jablonski P.E., Perry J.G.;
RT "Purification and properties of methyl coenzyme M methylreductase
RT from acetate-grown Methanosarcina thermophila.";
RL J. Bacteriol. 173:2481-2487(1991).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
CC to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: 2-(methylthio)ethanesulfonate (methyl-CoM) +
CC N-(7-mercaptoheptanoyl)threonine 3-O-phosphate (coenzyme B) = CoM-
CC S-S-CoB + methane.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
CC Coenzyme F430 is a yellow nickel porphyrinoid (By similarity).
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: TRIMER OF AN ALPHA, A BETA, AND A GAMMA SUBUNIT.
CC -!- MISCELLANEOUS: THE OPTIMAL TEMPERATURE FOR ENZYME ACTIVITY IS 60
CC DEGREES CELSIUS.
CC -!- MISCELLANEOUS: REDUCED FERREDOXIN COULD REDUCTIVELY REACTIVATE THE
CC ENZYME.
KW Methanogenesis; Transferase; Nickel.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1686 MW; D5D59892FCA5F63C CRC64;

Query Match 60.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 12 MEV 14

RESULT 2
PSEB_SYNVU STANDARD; PRT; 19 AA.
AC P12312;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem II reaction center M protein (PSII-M) (Fragment).
GN PSBM.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338735; PubMed=2503398;
RA Ikeuchi M., Koike H., Inoue Y.;
RT "N-terminal sequencing of low-molecular-mass components in
RT cyanobacterial photosystem II core complex. Two components correspond
RT to unidentified open reading frames of plant chloroplast DNA.";
RL FEBS Lett. 253:178-182(1989).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: Belongs to the psbm family.
DR HAMAP; MF 00438; -; 1.
DR Pfam; PF05151; Psbm; 1.
KW Photosystem II; Transmembrane.
FT MOD_RES 1 1
MOD_RES 1 1 BLOCKED.
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FT TRANSMEM 5 >19 POTENTIAL.
SQ NON_TER 19 19
SQ SEQUENCE 19 AA; 2049 MW; 339319BD8B0CFF24 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 3
DNAK_CLOPA STANDARD; PRT; 20 AA.
AC P81341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70) (CP 2) (Fragment).
GN DNAK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HAMAP; MF 00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW Chaperone; ATP-binding; Heat shock.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2001 MW; 2E2E68F21E7AD48F CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 17 VME 19

RESULT 4
DNAK_THIFE STANDARD; PRT; 20 AA.
AC P29133;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70) (Fragment).
GN DNAK.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE.
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RC STRAIN=ATCC 19859;
RX MEDLINE=93093401; PubMed=1360930;
RA Varela P., Jerez C.A.;
RT "Identification and characterization of GroEL and DnaK homologues in
  Thiobacillus ferrooxidans.";
RL FEMS Microbiol. Lett. 77:149-153 (1992).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=96242312; PubMed=9026439;
RA Seeger M., Osorio G., Jerez C.A.;
RT "Phosphorylation of GroEL, DnaK and other proteins from Thiobacillus
  ferrooxidans grown under different conditions.";
RL FEMS Microbiol. Lett. 138:129-134 (1996).
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HAMAP; MF 00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PROSITE; PS00297; HSP70.1; 1.
DR PROSITE; PS00329; HSP70.2; PARTIAL.
DR PROSITE; PS01036; HSP70.3; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 1985 MW; 2E2E86EC1F9AD48F CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 VME 4
DB 17 VME 19

RESULT 5
UC22_MAIZE
ID UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
  genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005 (1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
  PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR Maize-2DPAGE; P80628; COLEOPTILE.
DR MaizeDB; 123954; -.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 4 EV 5

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RESULT 6
ACPH_RABBIT
ID ACPH_RABBIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=9222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
  unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50 (1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
  TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
  AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
  + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR InterPro; IPR002471; Prol endopep ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 7
CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, CPD1.";
RL Science 226:849-850 (1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
  BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

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Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
   ||
Db 3 VM 4

RESULT 8
NS3_MYCTU STANDARD; PRT; 8 AA.
AC P81152;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 3 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19C0C2D2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
   ||
Db 1 VW 2

RESULT 9
WP1_PERAT STANDARD; PRT; 8 AA.
AC P83195;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Wall protein-1 (PWP-1) (Fragment).
OS Perkinsus atlanticus.
OC Eukaryota; Alveolata; Perkinsea; Perkinsea; Perkinsea; Perkinsus.
OX NCBI_TaxID=106964;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX MEDLINE=22044350; PubMed=12049410;
RA Montes J.F., Durfort M., Llado A., Garcia-Valero J.;
RT "Characterization and immunolocalization of a main proteinaceous
RT component of the cell wall of the protozoan parasite Perkinsus
RT atlanticus."
RL Parasitology 124:477-484(2002).
CC -!- FUNCTION: Is a major protein component of the cell wall. May play
CC a key role in the organization of the cell wall and in promoting
CC the survival of this parasite.
CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell
CC wall components.
CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
CC stages.
KW Cell wall.
FT NON_TER 8
SQ SEQUENCE 8 AA; 765 MW; F1787DD87B1AAB16 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
   ||
Db 3 EV 4

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
   ||
Db 3 EV 4

RESULT 11
UF02_MOUSE STANDARD; PRT; 9 AA.
ID UF02_MOUSE
AC P38640;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=75231108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
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RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis IS:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1102 MW; 7E73BAB6D05B1AAB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
Db 1 ME 2

RESULT 12
FARP MANSE STANDARD; PRT; 10 AA.
AC P18523;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FWRamide-like neuropeptide.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045350; PubMed=2235684;
RA Kegan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
RA Hildebrand J.G., Homborg U., Kammer A.E., Jardine I., Griffin P.R.,
RA Hunt D.F.;
RT "A new peptide in the FWRamide family isolated from the CNS of the
RT hawkmoth, Manduca sexta."
RL Peptides 11:849-856(1990).
CC -1- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
CC FLIGHT BEHAVIOR PATTERNS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FWRamide RELATED PEPTIDE)
CC FAMILY.
CC PIR; A43977;
DR Amidation; Neuropeptide; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 3 VV 4

RESULT 13
RT02_BOVIN STANDARD; PRT; 10 AA.
AC P82923;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
GN MRP52.
OS Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome;
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00318; Ribosomal_S2; PARTIAL.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1246 MW; 6A3A6679C04B476B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
Db 2 ME 3

RESULT 14
URE3_MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREA.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=30264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 7 EV 8

RESULT 15
MLG_THETS STANDARD; PRT; 11 AA.
ID MLG_THETS
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech)
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Watzet C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum.";
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR FIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACB6409C1E8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
Db ||
2 VM 3

RESULT 16
ID_PVK1 PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT perisymphathetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
Db ||
8 VM 9

RESULT 17
ID_HCYB MEGCR STANDARD; PRT; 12 AA.
AC Q10584;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin B chain (KLH-B) (Fragment).
OS Megathura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Fissurelloidea; Fissurellidae; Megathura.
OX NCBI_TaxID=55429;
RN [1]
RP SEQUENCE.
RX MEDLINE=96208935; PubMed=8829804;
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional
RT characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
CC ARTHROPODS.
CC -!- SUBUNIT: DODECAMERS AND EXTENDED MULTIMERS.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Hemolymph.
CC -!- BIOTECHNOLOGY: Potent immunogen used classically as a carrier
CC protein for haptens and more recently in human vaccines and for
CC immunotherapy of bladder cancer.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR InterPro; IPR000896; Hemocyanin.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Oxygen transport; Transport; Copper; Glycoprotein;
KW Hemolymph.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1345 MW; CBFEEAA44A432412 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
Db ||
4 VW 5

RESULT 18
ID_HS9A RAT STANDARD; PRT; 12 AA.
AC P82995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Protoplasm 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 4 4
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 6 6
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FT NON TER 12 12 SIMILARITY).
SQ SEQUENCE 12 AA; 1432 MW; DB47C322CAB6C1B6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 11 ME 12

RESULT 19
N040_SOYBN
ID N040_SOYBN STANDARD; PRT; 12 AA.
AC P55960;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams;
RX MEDLINE=94035161; PubMed=8220464;
RA Yang W.C., Katinakis P., Hendriks P., Smolders A., de Vries F.,
RA Spee J., van Kammen A., Bisseling T., Franssen H.;
RT "Characterization of GmENOD40, a gene showing novel patterns of cell-
RT specific expression during soybean nodule development.";
RL Plant J. 3:573-585(1993).
CC -!- GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
CC SIMILARITY).
CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
CC DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
CC DEVELOPMENT.
CC -----
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CC -----
DR EMBL; X69154; -; NOT_ANNOTATED_CDS.
KW Nodulation.
SQ SEQUENCE 12 AA; 1391 MW; 3C6958AE78B1A733 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 20
PORD_METTM
ID_PORD_METTM STANDARD; PRT; 12 AA.
AC P80903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit pORD (EC 1.2.7.1) (Pyruvate oxidoreductase
DE delta chain) (PORD) (Pyruvic-ferredoxin oxidoreductase delta subunit)
DE (Fragment).

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GN PORD.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
CC Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
KW NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1241 MW; 2D54065D1BD1ADD8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 21
UN39_CLOPA
ID_UN39_CLOPA STANDARD; PRT; 12 AA.
AC P81359;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 39 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengserud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 29.5 kDa.
FT NON TER 12
SQ SEQUENCE 12 AA; 1432 MW; 940561E66BD2CB01 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 6 EV 7

RESULT 22
UP01_CAEEL
ID_UP01_CAEEL STANDARD; PRT; 12 AA.
AC P55954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unknown protein from 2D-page (Spot 1) (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE.
RC STRAIN=Bristol N2;
RX MEDLINE=97295299; PubMed=9150941;
RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwillling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
RT homogenates and identification of protein spots by microsequencing.";
RL Electrophoresis 18:1557-562(1997).
DR Siena-2DPAGE; P55954; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 7 ME 8

RESULT 23
V23K WSSV
ID V23K WSSV STANDARD; PRT; 12 AA.
AC P82005;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 23 kDa structural polyprotein (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=32652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
RT virus.";
RL Arch. Virol. 145:263-274(2000).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 24
V25K WSSV
ID V25K WSSV STANDARD; PRT; 12 AA.
AC P82004;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 25 kDa structural polyprotein (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;

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RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
RT virus.";
RL Arch. Virol. 145:263-274(2000).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

RESULT 25
FIBB RABIT
ID FIBB RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 7 EV 8

RESULT 26
IDHA CANFA
ID IDHA CANFA STANDARD; PRT; 13 AA.
AC P54836;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial
DE (EC 1.1.1.41) (isocitric dehydrogenase) (NAD+-specific ICDH)
DE (Fragment).
RN IDH3A.

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OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=9816340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC CC -!- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) +  
 CC NADH.  
 CC -!- SUBUNIT: HETEROOLIGOMER OF SUBUNITS ALPHA, BETA, AND GAMMA IN THE  
 CC APPARENT RATIO OF 2:1:1 (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE  
 CC DEHYDROGENASES FAMILY.  
 DR HSC-2DPAGE; P54836; DOG.  
 DR InterPro; IPR001804; Isohdh.  
 DR PROSITE; PS00470; IDH\_IMDH; PARTIAL.  
 KW Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.  
 FT NON TER 13  
 FT SEQUENCE 13 AA; 1356 MW; 9ABPBC2B2A34B2D1 CRC64;  
 SQ SEQUENCE 13 AA; 1356 MW; 9ABPBC2B2A34B2D1 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 EV 5  
 DB |||  
 DB 3 EV 4  
 RESULT 27  
 IDHP\_RAT IDHP\_RAT STANDARD; PRT; 13 AA.  
 AC P54574;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)  
 DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP) (ICD-  
 DE M) (Fragment).  
 GN IDH2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY  
 CC PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE  
 CC DEHYDROGENASE COMPLEX (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)  
 CC + NADPH.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN  
 CC (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE  
 CC DEHYDROGENASES FAMILY.  
 DR InterPro; IPR001804; Isohdh.  
 DR PROSITE; PS00470; IDH\_IMDH; PARTIAL.  
 KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;  
 KW Mitochondrion.  
 FT NON TER 13  
 FT SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;  
 SQ SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 WV 2  
 DB |||  
 DB 11 WV 12  
 RESULT 28  
 MLA\_ANOCA  
 ID MLA\_ANOCA STANDARD; PRT; 13 AA.  
 AC P41589;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melanotropin alpha (Alpha-MSH).  
 OS Anolis carolinensis (Green anole) (American chameleon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
 OX NCBI\_TaxID=28377;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pituitary;  
 RX MEDLINE=92270473; PubMed=1667689;  
 RA Dore R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;  
 RT "Detection of a novel sequence change in the major form of alpha-MSH  
 RT isolated from the intermediate pituitary of the reptile, Anolis  
 RT carolinensis.";  
 RL Peptides 12:1261-1266(1991).  
 CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.  
 DR InterPro; IPR001941; Mcortin\_ACTH.  
 DR Pfam; PF00976; ACTH\_domain; I.  
 KW Hormone; Amidation.  
 FT MOD RES 13  
 FT SEQUENCE 13 AA; 1608 MW; FF990A7358BB09C1 CRC64;  
 SQ SEQUENCE 13 AA; 1608 MW; FF990A7358BB09C1 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 ME 4  
 DB |||  
 DB 4 ME 5  
 RESULT 29  
 MLA\_CAMDR  
 ID MLA\_CAMDR STANDARD; PRT; 13 AA.  
 AC P01198;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melanotropin alpha (Alpha-MSH).  
 OS Camelus dromedarius (Dromedary) (Arabian camel), and  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
 OX NCBI\_TaxID=9838, 9796;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=C.dromedarius;  
 RX MEDLINE=75146434; PubMed=1125179;  
 RA Li C.H., Danho W.O., Chung D., Rao A.J.;  
 RT "Isolation, characterization, and amino acid sequence of  
 RT melanotropins from camel pituitary glands.";  
 RL Biochemistry 14:947-952(1975).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=Horse; TISSUE=Pituitary;  
 RA Dixon J.S., Li C.H.;  
 RT "The isolation and structure of alpha-melanocyte-stimulating hormone

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RT from horse pituitaries.";
RL J. Am. Chem. Soc. 82:4568-4572 (1960).
CC -I- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR; A01464; MTCMAD.
DR PIR; A91785; MTHOAD.
DR InterPro; IPR001941; Mcootin_ACTH.
DR Pfam; PF00976; ACTH domain; 1.
KW Hormone; Acetylation; Amidation.
FT MOD_RES 1 1 ACETYLTATION (IN ABOUT 50% OF CAMEL
FT MOD_RES 13 13 MOLECULES).
FT MOD_RES 13 13 AMIDATION.
FT SEQUENCE 13 AA; 1624 MW; FF991CA958B809C1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 4 ME 5

RESULT 30
PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydrozoa; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -I- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 6 EV 7

RESULT 31
UN41_CLOPA STANDARD; PRT; 13 AA.
AC P81360;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 41 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal

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RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.6, ITS MW IS: 23.5 kDa.
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1402 MW; 738AECF1E66CA2CB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 6 EV 7

RESULT 32
UP71_LITEW STANDARD; PRT; 13 AA.
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 7.1 [Contains: Uperin 7.1.1].
OS Litoria ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104896;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=skin secretion;
RA Steinbörner S.F., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combination of peptides from the skin glands of Ewing's
RT tree frog, Litoria ewingi. Sequence determination and antimicrobial
RT activity.";
RL Aust. J. Chem. 50:889-894(1997).
CC -I- FUNCTION: UPERIN 7.1 SHOWS ANTIBACTERIAL ACTIVITY AGAINST L.LACTIS
CC AND S.UBERS. UPERIN 7.1.1 IS INACTIVE.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -I- MASS SPECTROMETRY: MW=1427; METHOD=FAB; RANGE=1-13.
CC -I- MASS SPECTROMETRY: MW=1184; METHOD=FAB; RANGE=3-13.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT PEPTIDE 1 13 UPERIN 7.1.
FT PEPTIDE 3 13 AMIDATION.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1429 MW; DE17C7204CCAB322 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 5 VV 6

RESULT 33
ADFA_TENMO STANDARD; PRT; 14 AA.
AC P82955;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor A (ADFA) (ADF) (Antidiuretic hormone A) (ADHA).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.

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RC TISSUE=Head;
RX MEDLINE=21642653; PubMed=11756661;
RA Eigenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
RT "Identification of a potent antidiuretic factor acting on beetle
RL Malpighian tubules.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
CC -!- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian
CC tubules. Uses cGMP as a second messenger and inhibits fluid
CC production by decreasing cAMP concentration.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
CC PROTEIN LPCP29.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0005184; F:neuropeptide hormone activity; NAS.
DR GO: GO:0007218; P:neuropeptide signaling pathway; NAS.
KW Neuropeptide; Hormone.
SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 1 VV 2

RESULT 34
GR75 CANFA STANDARD; PRT; 14 AA.
AC P99502;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Mitochondrial stress-70 protein (75 kDa glucose regulated protein)
DE (GRP 75) (Fragment).
GN HSPA9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATION AND
CC CELLULAR AGING. MAY ALSO ACT AS A CHAPERONE.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HSC-2DPAGE; P99502; DOG.
DR InterPro: IPR001023; Hsp70.
DR PROSITE; PS00297; HSP70.1; PARTIAL.
DR PROSITE; PS00329; HSP70.2; PARTIAL.
DR PROSITE; PS01036; HSP70.3; PARTIAL.
KW ATP-binding; Mitochondrion.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1438 MW; 2AAEDD1AACBAC8D8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 9 VV 10

RESULT 35

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IP2G_RAT
ID _IP2G_RAT STANDARD; PRT; 14 AA.
AC P81795;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic
DE translation initiation factor 2 gamma subunit) (eif-2-gamma) (pp42)
DE (Fragment).
DN EIP2S3 OR EIP2G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96374441; PubMed=8780732;
RA Gil C., Plana M., Riera M., Itarte E.;
RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eif-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA. THIS
CC COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING
CC TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL
CC SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY
CC HYDROLYSIS OF THE GTP BOUND TO EIF-2 TO RELEASE OF AN EIF-2-GDP
CC BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER
CC ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP
CC BY WAY OF A REACTION CATALYZED BY EIF-2B.
CC -!- SUBUNIT: Heterotrimer composed of an alpha, a beta, and a gamma
CC chain.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EIF2G SUBFAMILY.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1511 MW; D86EDA955ABEFA12 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 6 EV 7

RESULT 36
KLPS SCARA STANDARD; PRT; 14 AA.
AC P58356;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Kinin-like peptide-S (Fragment).
OS Scaptocosa raptoria (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Lycosidae; Scaptocosa.
OX NCBI_TaxID=180440;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98257639; PubMed=9604280;
RA Ferreira L.A.F., Lucas S.M., Alves E.W., Hermann V.V., Reichl A.P.,
RA Habermehl G., Zingali R.B.;
RT "Isolation, characterization and biological properties of two
RT kinin-like peptides (peptide-S and peptide-R) from Scaptocosa
RT raptoria venom.";
RL Toxicon 36:31-39(1998).
CC -!- FUNCTION: Has kinin-like biological properties. Causes contraction

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CC on the of mammalian ileum; relaxes the duodenum and increases the  
 CC capillary permeability.  
 KW Vasodilator. 14 14  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1510 MW; E811E25D52E27CA CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EV 5  
 Db ||  
 5 EV 6  
 RESULT 37  
 KPPI\_SELMI  
 ID\_KPPI\_SELMI STANDARD; PRT; 14 AA.  
 AC P25933;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoribulokinase, 40 kDa subunit (EC 2.7.1.19) (phosphopentokinase)  
 DE (Fragment)  
 OS Selenastrum minutum.  
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae;  
 CC Selenastrum.  
 CC Selenastrum.  
 OX NCBI\_TaxID=39955;  
 RN [1]  
 RP SEQUENCE.  
 RA Lin M., Turpin D.H.;  
 RT "Purification and molecular and immunological characterization of a  
 RT unique phosphoribulokinase from the green alga Selenastrum minutum.";  
 RL Plant Physiol. 98:82-88(1992).  
 CC -!- CATALYTIC ACTIVITY: ATP + D-ribose 5-phosphate = ADP + D-  
 CC ribulose 1,5-bisphosphate.  
 CC -!- PATHWAY: Calvin cycle.  
 CC -!- SUBUNIT: HETERODIMER OF A 40 kDa AND A 41 kDa SUBUNIT.  
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.  
 DR InterPro; IPR006082; PRX.  
 DR PROSITE; PS00567; PHOSPHORIBULOKINASE; PARTIAL.  
 KW Transferase; Kinase; Calvin cycle; ATP-binding.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1379 MW; C4B1D8CD2F891062 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 Db ||  
 6 VV 7  
 RESULT 38  
 PH1\_PRUSE  
 ID\_PH1\_PRUSE STANDARD; PRT; 14 AA.  
 AC P29263;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase  
 DE isozyme I) (PH I) (Fragment).  
 OS Prunus serotina (Black cherry).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";

RL Plant Physiol. 100:282-290(1992).  
 CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
 CC glucose.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -!- PTM: GLYCOSYLATED.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1575 MW; FB3D7F4FB90CA9CA CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 Db ||  
 5 VV 6  
 RESULT 39  
 PPK6\_PERAM  
 ID\_PPK6\_PERAM STANDARD; PRT; 14 AA.  
 AC P82693;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-6 (Pea-PK-6) (FXPRU-amide).  
 OS Periplaneta americana (American cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
 RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRlamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.  
 CC -!- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN  
 CC ABDOMINAL PERISYPHATHETIC ORGANS.  
 CC -!- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Amidation; Pyrokinin.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EV 5  
 Db ||  
 4 EV 5  
 RESULT 40  
 UC15\_MAIZE  
 ID\_UC15\_MAIZE STANDARD; PRT; 14 AA.  
 AC P80621;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)  
 DE (Fragment).  
 OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Fernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.  
 DR Maize-2DPAGE; P80621; COLEOPTILE.  
 DR Maize2DB; 123947; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 Db 7 VV 8  
 RESULT 41  
 UN04\_CLOPA STANDARD; PRT; 14 AA.  
 ID UN04\_CLOPA  
 AC P81349;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Unknown protein CP 4 from 2D-page (Fragment).  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flensburg R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.7, ITS MW IS: 45.7 kDa.  
 FT NON\_TER 14 14  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1608 MW; D424A7069460EBD2 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EV 5  
 Db 3 EV 4  
 RESULT 42  
 CDN2\_LITGI STANDARD; PRT; 15 AA.  
 ID CDN2\_LITGI  
 AC P56247;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Caeridin 2.  
 OS Litoria gilleni (Centralian tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=39405;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RA "Peptides from Australian frogs. The structures of the caeridins and  
 RT caeridins from Litoria gilleni.";  
 RL J. Chem. Res. 139:937-961(1993).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC ANTIBIOTIC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
 CC glands.  
 CC -1- MASS SPECTROMETRY: MW=1408; METHOD=FAB.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 15 15  
 FT MOD\_RES 15 15  
 SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF272550CBF CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 Db 5 VV 6  
 RESULT 43  
 CDN4\_LITCE STANDARD; PRT; 15 AA.  
 ID CDN4\_LITCE  
 AC P82076;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Caeridin 4.  
 OS Litoria caerulea (Green tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=30344;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. Structures of the caeridins from  
 RT Litoria caerulea.";  
 RL J. Chem. Soc. Perkin Trans. 1:573-576(1993).  
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC ANTIBIOTIC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
 CC glands.  
 CC -1- MASS SPECTROMETRY: MW=1504; METHOD=FAB.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 15 15  
 FT MOD\_RES 15 15  
 SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFBBC5195F CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 Db 5 VV 6  
 RESULT 44  
 COXI\_THUOB STANDARD; PRT; 15 AA.  
 ID COXI\_THUOB  
 AC P80978;  
 DT 01-NOV-1997 (Rel. 35, Created)



CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.  
 CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-  
 CC trimethyltrideca-2,6-dienoate + H<sub>2</sub>O = (2E,6E)-(10R,11S)-10,11-  
 CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR PIR; A36527; A36527.  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; PARTIAL.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; PARTIAL.  
 KW Hydrolase; Serine esterase.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1659 MW; D321EA432E58B848 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EV 5  
 DB ||  
 ||  
 7 EV 8  
 RESULT 48  
 FKBP PINPS STANDARD; PRT; 15 AA.  
 AC P81104; 1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans  
 DE isomerase) (Cyclophilin) (PPIase) (S1205-06) (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RA Plomion C., Costa P., Bahrman N., Frigerio J.-M.;  
 RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping  
 RT dominant and codominant protein markers assayed on diploid tissue, in  
 RT a haploid-based genetic map."; *Plant Cell Rep.* 1997; 16:161-165.  
 RL Silvae Genet. 46:161-165(1997).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins."; *Electrophoresis* 20:1098-1108(1999).  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING  
 CC PROTEIN SYNTHESIS. THIS PPIASE BINDS CALMODULIN (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
 CC (omega=0).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 5.3, ITS MW IS: 72 kDa.  
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.  
 CC InterPro: IPR001179; FKBP\_PPIASE.  
 DR PROSITE; PS00453; FKBP\_PPIASE\_1; PARTIAL.  
 DR PROSITE; PS00454; FKBP\_PPIASE\_2; PARTIAL.  
 DR PROSITE; PS00059; FKBP\_PPIASE\_3; PARTIAL.  
 KW Isomerase; Rotamase; Repeat; Calmodulin-binding.  
 FT NON TER 1  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1675 MW; 2B53999722277F3F CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EV 5

Db ||  
 ||  
 13 EV 14  
 RESULT 49  
 GR78 HORSE STANDARD; PRT; 15 AA.  
 ID GR78\_HORSE  
 AC P16392;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE 78 kDa glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain  
 DE binding protein) (BiP) (Fragment).  
 GN HSP45 OR GRP78.  
 OS Equus caballus (Horse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90147817; PubMed=1689156;  
 RA Oblas B., Boyd N.D., Luber-Narod J., Reyes V.E., Lesman S.E.;  
 RT "Isolation and identification of a polypeptide in the Hsp 70 family  
 RT that binds substance P."; *Biochem. Biophys. Res. Commun.* 166:978-983(1990).  
 RL Biochem. Biophys. Res. Commun. 166:978-983(1990).  
 CC -1- FUNCTION: Probably plays a role in facilitating the assembly of  
 CC multimeric protein complexes inside the ER.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 DR InterPro: IPR001023; Hsp70.  
 DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
 DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
 DR PROSITE; PS01036; HSP70\_3; PARTIAL.  
 KW ATP-binding; Endoplasmic reticulum.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1647 MW; 81119D21D0EC26DB CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 DB ||  
 ||  
 12 VV 13  
 RESULT 50  
 KPP2 SELMI STANDARD; PRT; 15 AA.  
 ID KPP2\_SELMI  
 AC P25934;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoribulokinase, 41 kDa subunit (EC 2.7.1.19) (Phosphopentokinase)  
 DE (Fragment).  
 OS Selenastrum minutum.  
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae;  
 CC Selenastrum.  
 OX NCBI\_TaxID=39955;  
 RN [1]  
 RP SEQUENCE.  
 RA Lin M., Turpin D.H.;  
 RT "Purification and molecular and immunological characterization of a  
 RT unique phosphoribulokinase from the green alga Selenastrum minutum."; *Plant Physiol.* 98:82-88(1992).  
 RL Plant Physiol. 98:82-88(1992).  
 CC -1- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-  
 CC ribulose 1,5-bisphosphate.  
 CC -1- PATHWAY: Calvin cycle.  
 CC -1- SUBUNIT: HETERODIMER OF A 40 kDa AND A 41 kDa SUBUNIT.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.  
 DR InterPro: IPR006082; PRK.  
 DR PROSITE; PS00567; PHOSPHORIBULOKINASE; PARTIAL.  
 KW Transferase; Kinase; Calvin cycle; ATP-binding.

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FT  NON TER      15
SQ  SEQUENCE    15 AA; 1455 MW; 07A97BCD2F922C75 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 VV 2
Db  6 VV 7

RESULT 51
MALT BACTQ STANDARD; PRT; 15 AA.
AC P80072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).
OS Bacillus thermoamyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1425;
RN [1]
RP SEQUENCE.
RC STRAIN=KPI071 / FERM P8477;
RX MEDLINE=92209510; PubMed=1555585;
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
RT "Assignment of Bacillus thermoamyloliquefaciens KPI071
RT alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
RT similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
RT and in structural parameters calculated from the amino acid
RT composition.";
RL Eur. J. Biochem. 205:249-256(1992).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
CC linked D-glucose residues with release of D-glucose.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC -!- KNOWN AS THE ALPHA-AMYLASE FAMILY.
DR PIR; S21240; S21240.
KW Hydrolase; Glycosidase.
FT  NON TER      15
SQ  SEQUENCE    15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 VV 2
Db  10 VV 11

RESULT 52
MAOX CHICK STANDARD; PRT; 15 AA.
AC Q92060;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Fragment).
GN ME1
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97056061; PubMed=8900406;
RA Hodnett D.W., Fantozzi D.A., Thurmond D.C., Klautsky S.A.,
RA Macphree K.G., Estrem S.T., Xu G., Goodridge A.G.;
RT "The chicken malic enzyme gene: structural organization and
RT identification of triiodothyronine response elements in the

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RT  5'-flanking DNA.";
RL Arch. Biochem. Biophys. 334:309-324(1996).
CC -!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2) +
CC NADPH.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U49693; AAA92721.1; -.
DR InterPro; IPR001891; Malic_oxred.
DR PROSITE; PS00331; MALIC_ENZYMES; PARTIAL.
KW Oxidoreductase; NADP.
FT  NON TER      15
SQ  SEQUENCE    15 AA; 1842 MW; CFEF180B2BA84C2B CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4 EV 5
Db  6 EV 7

RESULT 53
NKSO PSETE STANDARD; PRT; 15 AA.
AC P59073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short neurotoxin N2 (Alpha neurotoxin) (Fragment).
OS Pseudonaja textilis (Eastern brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=8673;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99449602; PubMed=10518793;
RA Gong N.L., Armugam A., Jeyaseelan K.;
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
RT cloning, expression and protein characterization.";
RL Eur. J. Biochem. 265:982-989(1999).
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
CC acetylcholine receptors (nAChR).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=6345; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 0.80 mg/kg by intravenous injection.
CC -!- SIMILARITY: Belongs to the snake toxin family.
DR InterPro; IPR003571; Snake toxin.
DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT  UNSURE      3
FT  UNSURE     13
FT  NON TER     15
SQ  SEQUENCE    15 AA; 1727 MW; E149FD4BFD1EF0DD CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VV 2
      ||
Db      11 VV 12

RESULT 54
PGTS PELAC
ID _PGTS PELAC STANDARD; PRT; 15 AA.
AC P80564;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pyrogallol hydroxyltransferase small subunit (EC 1.9.7.1.2)
DE (Transhydroxylase) (Fragment).
OS Pelobacter acidigallici.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OX NCBI_TaxID=35816;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 2377 / Braunschweig;
RX MEDLINE=96215436; PubMed=8647079;
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;
RT "One molecule of molybdopterin guanine dinucleotide is associated
RT with each subunit of the heterodimeric Mo-Fe-S protein
RT transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE
RT and mass spectrometry.";
RL Eur. J. Biochem. 237:406-413(1996).
CC -|- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-
CC trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
CC tetrahydroxybenzene.
CC -|- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
DR PIR; S65429; S65429.
KW Oxidoreductase; Molybdenum; Iron-sulfur.
FT NON TER 15
SQ SEQUENCE 15 AA; 1843 MW; 0567BDD004C28499 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ME 4
      ||
Db      1 ME 2

RESULT 55
PH3 PRUSE
ID _PH3 PRUSE STANDARD; PRT; 15 AA.
AC P29265;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme IIB) (PH IIB) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992)
CC -|- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC glucose.
CC -|- SUBUNIT: Monomer.
CC -|- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR

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CC      EMBRYONAL TISSUES.
KW Glycosylase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 15
SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VV 2
      ||
Db      6 VV 7

RESULT 56
R13A SPIOL
ID _R13A SPIOL STANDARD; PRT; 15 AA.
AC P82454;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L13a (Fragment).
GN RPL13A.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Alvaro; TISSUE=Leaf;
RA Yamaguchi K., Subramanian A.R.;
RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein
RT L13a.";
RL Submitted (APR-2000) to the SWISS-PROT data bank.
CC -|- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR005822; Rib_prot_L13.
DR PROSITE; PS00783; RIBOSOMAL_L13; PARTIAL.
KW Ribosomal protein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1489 MW; C7B9C80F5A099EB3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VV 2
      ||
Db      11 VV 12

RESULT 57
RKGG CARCR
ID _RKGG CARCR STANDARD; PRT; 15 AA.
AC P21586;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Rathke's gland glycoprotein (Fragment).
OS Carretta caretta (Loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Chelonioidae; Cheloniidae; Carretta.
OX NCBI_TaxID=8467;
RN [1]
RP SEQUENCE.
RC TISSUE=Rathke's gland;
RA MEDLINE=90075703; PubMed=2591198;
RA Radhakrishna G., Chin C.C.Q., Wold F., Weldon P.J.;
RT "Glycoproteins in Rathke's gland secretions of loggerhead (Carretta
RT caretta) and Kemp's ridley (Leptodochelys kempi) sea turtles.";
RL Comp. Biochem. Physiol. 94B:375-378(1989).
CC -|- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES,

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CC AS PREDATOR REPELLANTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE
CC TURTLE SHELL.
CC -|- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY
CC SEA TURTLE.
CC PIR; PL0154; PL0154.
CC GLYCOPROTEIN.
CC NON TER 15 15
CC SEQUENCE 15 AA; 1477 MW; CC893BAAAAB1B5ED CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 7 VV 8

RESULT 58
RM12_YEAST STANDARD; PRT; 15 AA.
AC P36522;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein l12 (Yml12) (Fragment).
GN MRPL12.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1] Kitakawa M.;
RP SEQUENCE. PubMed=2060626;
RX MEDLINE=91285106; Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Grohmann L., Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR SGD; L0002687; MRPL12.
KW Ribosomal protein; Mitochondrion.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1851 MW; 74BCD9FEDDB3900 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 8 EV 9

RESULT 59
THL_CLOPA STANDARD; PRT; 15 AA.
AC P81347;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)
DE (CP 13) (Fragment).
GN THL.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal

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RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- CATALYTIC ACTIVITY: 2 acetyl-CoA = CoA + acetoacetyl-CoA.
CC -|- PATHWAY: JUNCTION IN THE PATHWAY LEADING TO THE PRODUCTION OF
CC EITHER ACIDS (ACETATE OR BUTYRATE) OR SOLVENTS (ACETONE, BUTANOL
CC OR ETHANOL).
CC -|- SUBUNIT: Homotrimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
DR InterPro; IPR002155; Thiolase.
DR PROSITE; PS00098; THIOLASE 1; PARTIAL.
DR PROSITE; PS00737; THIOLASE 2; PARTIAL.
DR PROSITE; PS00099; THIOLASE 3; PARTIAL.
KW Transferase; Acyltransferase.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1496 MW; 9735820D61BB35FC CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 3 EV 4

RESULT 60
UBL1_MONDO STANDARD; PRT; 15 AA.
ID UBL1_MONDO
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowen A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -|- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -|- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U32208; AAA89059.1; -.
DR InterPro; IPR001578; UCH_1.
DR PROSITE; PS00140; UCH_1; PARTIAL.
KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
FT NON TER 15 15

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SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
||  
6 ME 7

Db

RESULT 61

UC08\_MAIZE STANDARD; PRT; 15 AA.

AC P80614;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159) (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.

RC Tissue=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.

CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family.

DR Maize-2DPAGE; P80614; COLEOPTILE.  
DR MaizeDB; 123934; -.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
||  
10 VW 11

Db

RESULT 62

UC16\_MAIZE STANDARD; PRT; 15 AA.

AC P80622;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 308) (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.

RC Tissue=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.9, ITS MW IS: 18.6 kDa.  
CC Maize-2DPAGE; P80622; COLEOPTILE.  
DR MaizeDB; 123948; -.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1796 MW; D331A518F7440BE7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
||  
7 EV 8

Db

RESULT 63

UP01\_METAN STANDARD; PRT; 15 AA.

AC P83440;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Unknown protein (Fragment).  
OS Metarhizium anisopliae.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;  
OC mitosporic Clavicipitaceae; Metarhizium.  
OX NCBI\_TaxID=5530;  
RN [1]  
RP SEQUENCE.

RC STRAIN=54A-1b;  
RX MEDLINE=22343006; PubMed=12455610;  
RA Kamp A.M., Bidochka M.J.;  
RT "Protein analysis in a pleomorphically deteriorated strain of the insect-pathogenic fungus Metarhizium anisopliae.";  
RL Can. J. Microbiol. 48:787-792(2002).  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1651 MW; FED76D69E1F0F4F CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2  
||  
5 VW 6

Db

RESULT 64

VORA\_METTM STANDARD; PRT; 15 AA.

AC P80907;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ketoisovalerate oxidoreductase subunit vora (EC 1.-.-.-) (VOR) (2-oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-ferredoxin oxidoreductase alpha subunit) (Fragment).  
GN VORA.  
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=79929;  
RN [1]  
RP SEQUENCE.

RC MEDLINE=97261844; PubMed=9108258;  
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;  
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum.";  
RL Eur. J. Biochem. 244:862-868(1997).

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CC -!- SUBUNIT: HETROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC -!- MISCELLANEOUS: As a pH optimum of 9.7 and an optimal temperature
CC of 75 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531CA528F CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 13 EV 14

RESULT 65
AU21_LITRA
ID AU21_LITRA STANDARD; PRT; 16 AA.
AC P82388;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aurein 2.1 [Contains: Aurein 2.1.1].
OS Litoria raniformis (Southern bell frog), and
OS Litoria aurea (Green and golden bell frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
ON NCBI_TaxID=116057, 8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC SPECIES=L.raniformis, and L.aurea;
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS,
CC L.LACTIS, L.INNOCUA, M.LUTEUS, S.EPIDERMIDIS AND S.UBERISAND.
CC PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS
CC AMPHIPATHIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT PEPTIDE 1 16 AUREIN 2.1.
FT PEPTIDE 3 16 AUREIN 2.1.1.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DAD4D240F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

RESULT 66
AU22_LITAU
ID AU22_LITAU STANDARD; PRT; 16 AA.
AC P82389;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aurein 2.2 [Contains: Aurein 2.2.1].
OS Litoria aurea (Green and golden bell frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

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OC Pelodyadinae; Litoria.
OX NCBI_TaxID=8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC L.INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMIDIS AND S.UBERISAND.
CC PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS
CC AMPHIPATHIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT PEPTIDE 1 15 AUREIN 2.2.
FT PEPTIDE 3 16 AUREIN 2.2.1.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA354DAE2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

RESULT 67
AU23_LITAU
ID AU23_LITAU STANDARD; PRT; 16 AA.
AC P82390;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aurein 2.3.
OS Litoria aurea (Green and golden bell frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
ON NCBI_TaxID=8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC L.INNOCUA, M.LUTEUS, S.AUREUS AND S.EPIDERMIDIS. PROBABLY ACTS BY
CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA424DAE2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

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## RESULT 68

AU24\_LITAU STANDARD; PRT; 16 AA.  
 ID AU24\_LITAU STANDARD; PRT; 16 AA.  
 AC P82391;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Aurein 2.4 [Contains: Aurein 1.2.1].  
 OS Litoria aurea (Green and golden bell frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20408845; PubMed=10951191;  
 RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,  
 Wallace J.C., Tyler M.J.;  
 RT "The antibiotic and anticancer active aurein peptides from the  
 RT Australian bell frogs Litoria aurea and Litoria raniformis the  
 RT solution structure of aurein 1.2.";  
 RL Eur. J. Biochem. 267:5330-5341(2000).  
 CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,  
 CC L-INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMIDIS AND S.UBERIS.  
 CC PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS  
 CC AMPHIPATHIC STRUCTURE. SHOWS ANTICANCER ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC Amphibian defense peptide; Amidation; Antibiotic.  
 FT PEPTIDE 1 16 AUREIN 2.4.  
 FT PEPTIDE 3 16 AUREIN 2.4.1.  
 FT MOD RES 16 AMIDATION.  
 SQ SEQUENCE 16 AA; 1630 MW; 1D87980438AAE2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VV 2  
 ||  
 Db 9 VV 10

## RESULT 69

AU25\_LITRA STANDARD; PRT; 16 AA.  
 ID AU25\_LITRA STANDARD; PRT; 16 AA.  
 AC P82392;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Aurein 2.5.  
 OS Litoria raniformis (Southern bell frog), and  
 OS Litoria aurea (Green and golden bell frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=116057, 8371;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC SPECIES=L.raniformis, and L.aurea;  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20408845; PubMed=10951191;  
 RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,  
 Wallace J.C., Tyler M.J.;  
 RT "The antibiotic and anticancer active aurein peptides from the  
 RT Australian bell frogs Litoria aurea and Litoria raniformis the  
 RT solution structure of aurein 1.2.";  
 RL Eur. J. Biochem. 267:5330-5341(2000).  
 CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,  
 CC L-INNOCUA, M.LUTEUS, S.AUREUS, AND S.EPIDERMIDIS. PROBABLY ACTS BY  
 CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.

CC SHOWS ANTICANCER ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide; Amidation; Antibiotic.  
 FT MOD RES 16 AMIDATION.  
 SQ SEQUENCE 16 AA; 1650 MW; 1D9A5DADB4DAB2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VV 2  
 ||  
 Db 9 VV 10

## RESULT 70

CT12\_LITCI STANDARD; PRT; 16 AA.  
 ID CT12\_LITCI STANDARD; PRT; 16 AA.  
 AC P81840; P81841; P81842; P81843;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Citropin 1.2 [Contains: Citropin 1.2.1; Citropin  
 DE 1.2.3].  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=99435977; PubMed=10504394;  
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
 Wallace J.C., Tyler M.J.;  
 RT "Host defence peptides from the skin glands of the Australian blue  
 RT mountains tree-frog Litoria citropa. Solution structure of the  
 RT antibacterial peptide citropin 1.1.";  
 RL Eur. J. Biochem. 265:627-637(1999).  
 CC -!- FUNCTION: BACTERIOSTATIC ACTION FOR GRAM-POSITIVE BACTERIA.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT PEPTIDE 1 16 CITROPIN 1.2.  
 FT PEPTIDE 3 14 CITROPIN 1.2.1.  
 FT PEPTIDE 4 14 CITROPIN 1.2.2.  
 FT PEPTIDE 1 11 CITROPIN 1.2.3.  
 FT MOD RES 16 16 AMIDATION  
 SQ SEQUENCE 16 AA; 1616 MW; 1D878515ABD73DE9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VV 2  
 ||  
 Db 12 VV 13

## RESULT 71

DHE2\_THUTH STANDARD; PRT; 16 AA.  
 ID DHE2\_THUTH STANDARD; PRT; 16 AA.  
 AC P20016;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE NAD-specific glutamate dehydrogenase (EC 1.4.1.2) (NAD-GDH  
 DE (Fragment)).  
 OS Thunnus thynnus (Bluefin tuna).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

OC Scornbridae; Thunus.  
 OX NCBI\_TaxID=8237;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=76253947; PubMed=182270;  
 RA Veronese F.M., Bevilacqua R., Boccu E., Brown D.M.;  
 RT "Purification, characteristics and sequence of a peptide containing  
 an essential lysine residue."  
 RL Biochim. Biophys. Acta 445:1-13 (1976).  
 CC -|- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(+) = 2-oxoglutarate  
 + NH(3) + NADH.  
 CC -|- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.  
 DR PIR; A12729; A12729.  
 DR InterPro; IPR006095; GLFV dehydrog.  
 DR InterPro; IPR006097; GLFV dehydrog\_N.  
 DR Pfam; PF02812; GLFV dehydrog\_N; 1.  
 DR PROSITE; PS00074; GLFV DEHYDROGENASE; PARTIAL.  
 KW Oxidoreductase; NAD.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 12 12  
 FT NON\_TER 16 16  
 FT SEQUENCE 16 AA; 1518 MW; FF299AA7C5F1062F CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 ||  
 DB 3 VV 4  
 RESULT 72  
 HTPG ACICA STANDARD; PRT; 16 AA.  
 ID HTPG ACICA  
 AC P81876;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chaperone protein htpG (Heat shock protein htpG) (High temperature  
 protein G) (Fragment).  
 GN HTPG.  
 OS Acinetobacter calcoaceticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=471;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=69-V;  
 RX MEDLINE=99274045; PubMed=10344248;  
 RA Benndorf D., Loffhagen N., Babel W.;  
 RT "Induction of heat shock proteins in response to primary alcohols in  
 Acinetobacter calcoaceticus."  
 RL Electrophoresis 20:781-789 (1999).  
 CC -|- FUNCTION: Molecular chaperone. Has ATPase activity (By  
 similarity).  
 CC -|- SUBUNIT: Homodimer (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- INDUCTION: BY HEAT SHOCK AND PRIMARY ALCOHOLS.  
 CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.  
 DR HAMAP; MF 00505; 1.  
 DR InterPro; IPR001404; Hsp90.  
 DR PROSITE; PS00298; HSP90; PARTIAL.  
 KW Chaperone; ATP-binding; Heat shock.  
 FT NON\_TER 16 16  
 FT SEQUENCE 16 AA; 1769 MW; 316C70D8928CB482 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EV 5

DB 13 EV 14  
 ||  
 RESULT 73  
 LE05 BIOGL STANDARD; PRT; 16 AA.  
 ID LE05 BIOGL  
 AC P80744;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hemolymph 65 kDa lectin BG05 (Fragment).  
 GN BG05.  
 OS Biomphalaria glabrata (Bloodfluke planorb).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Planorbidae; Biomphalaria.  
 OX NCBI\_TaxID=6526;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=M-LINE; TISSUE=Hemolymph;  
 RX MEDLINE=97385165; PubMed=9238039;  
 RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;  
 RT "A family of fibrinogen-related proteins that precipitates parasite-  
 derived molecules is produced by an invertebrate after infection."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696 (1997).  
 CC -|- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE  
 ECHINOSTOMA PARAENSEI.  
 CC -|- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.  
 CC -|- INDUCTION: By infection.  
 KW Lectin.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 FT SEQUENCE 16 AA; 1790 MW; 57489A8F2EEDAA94 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VV 2  
 ||  
 DB 10 VV 11  
 RESULT 74  
 PGTL PELAC STANDARD; PRT; 16 AA.  
 ID PGTL PELAC  
 AC P80563;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Pyrogallol hydroxyltransferase large subunit (EC 1.97.1.2)  
 DE (Transhydroxylase) (Fragment).  
 OS Pelobacter acidigallici.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
 OC Pelobacteraceae; Pelobacter.  
 OX NCBI\_TaxID=35816;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 2377 / Braunschweig;  
 RX MEDLINE=96215436; PubMed=8647079;  
 RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;  
 RT "One molecule of molybdopterin guanine dinucleotide is associated  
 with each subunit of the heterodimeric Mo-Fe-S protein  
 transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE  
 and mass spectrometry."  
 RL Eur. J. Biochem. 237:406-413 (1996).  
 CC -|- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-  
 trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-  
 tetrahydroxybenzene.  
 CC -|- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).  
 CC -|- SUBUNIT: Heterodimer of a large and a small subunit.  
 DR PIR; S65430; S65430.  
 KW Oxidoreductase; Molybdenum; Iron-sulfur.

FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1620 MW; 56348D53A0AD6EE3 CRC64;  
Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred.No. 7.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
Db 2 EV 3

## RESULT 75

ID PH2\_PRUSE STANDARD; PRT; 16 AA.  
AC P29264;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Prunasin beta-glucosidase IIA (EC 3.2.1.118) (Prunasin hydrolase  
isozyme IIA) (PH IIA) (Fragment).  
OS Prunus serotina (Black cherry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
OX NCBI\_TaxID=23207;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Seed;  
RA Li C.P., Swain E., Poulton J.E.;  
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
RL Plant Physiol. 100:282-290(1992).  
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
glucose.  
CC -!- SUBUNIT: Homodimer.  
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH CORYLEDON  
DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
EMBRYONAL TISSUES.  
CC -!- PTM: GLYCOSYLATED.  
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1703 MW; FC4D7F4FB90CFE01 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred.No. 7.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
Db 7 VV 8

Search completed: November 25, 2003, 18:17:29  
Job time : 3.42021 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 12.0479 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-9  
Perfect score: 5  
Sequence: 1 VMEV 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 810525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rcdent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	3	60.0	9	10 Q9FXL0	Q9FXL0 lilium long
2	3	60.0	10	13 Q42355	Q42355 brachydanio
3	3	60.0	11	2 Q47606	Q47606 escherichia
4	3	60.0	14	11 Q70544	Q70544 mesocricetu
5	3	60.0	15	4 Q9Y429	Q9Y429 homo sapien
6	3	60.0	15	4 Q9UCH0	Q9UCH0 homo sapien
7	3	60.0	15	6 Q9TRP9	Q9TRP9 bos taurus
8	3	60.0	16	2 Q9RP22	Q9RP22 citrobacter
9	3	60.0	16	5 Q95Y34	Q95Y34 caenorhabdi
10	3	60.0	16	10 Q9S8L1	Q9S8L1 sorghum bic
11	3	60.0	17	12 Q85719	Q85719 reovirus (t
12	3	60.0	18	8 Q9ZY80	Q9ZY80 scellio fulg
13	3	60.0	19	10 Q94L06	Q94L06 brassica na
14	3	60.0	19	11 Q922T5	Q922T5 mus musculu
15	3	60.0	20	2 Q47614	Q47614 escherichia
16	3	60.0	20	12 Q38539	Q38539 human torov

17	3	60.0	20	12	Q72059	O72059 bovine toro
18	2	40.0	7	2	Q47029	Q47029 enterobacte
19	2	40.0	7	13	Q8JJ20	Q8JJ20 gallus gall
20	2	40.0	8	2	P72279	P72279 rhodococcus
21	2	40.0	8	2	O68485	O68485 klebsiella
22	2	40.0	8	2	Q56759	Q56759 xanthobacte
23	2	40.0	8	3	Q05403	Q05403 saccharomyc
24	2	40.0	8	4	Q16428	Q16428 homo sapien
25	2	40.0	8	4	Q9P285	Q9P285 homo sapien
26	2	40.0	8	4	Q81V87	Q81V87 homo sapien
27	2	40.0	8	5	Q9UB13	Q9UB13 albinaria h
28	2	40.0	8	5	Q94623	Q94623 manduca sex
29	2	40.0	8	5	Q94695	Q94695 physarum po
30	2	40.0	8	6	Q9MYL5	Q9MYL5 pongo pygma
31	2	40.0	8	10	Q9SB24	Q9SB24 nicotiana t
32	2	40.0	8	10	Q42507	Q42507 triticum ae
33	2	40.0	8	10	P82324	P82324 pisum sativ
34	2	40.0	8	11	Q9ET21	Q9ET21 mus musculu
35	2	40.0	8	11	Q62527	Q62527 mus spretus
36	2	40.0	8	12	Q9E8Q5	Q9E8Q5 beet soil-b
37	2	40.0	8	12	Q9E8Q2	Q9E8Q2 beet soil-b
38	2	40.0	8	12	Q9E8P9	Q9E8P9 beet soil-b
39	2	40.0	8	12	Q9E8Q3	Q9E8Q3 beet soil-b
40	2	40.0	8	12	Q9E8Q1	Q9E8Q1 beet soil-b
41	2	40.0	8	12	Q9DSN2	Q9DSN2 beet soil-b
42	2	40.0	8	12	Q9E8Q4	Q9E8Q4 beet soil-b
43	2	40.0	8	12	Q9DSN5	Q9DSN5 beet soil-b
44	2	40.0	8	12	Q9E8P7	Q9E8P7 beet soil-b
45	2	40.0	8	12	Q9DSN1	Q9DSN1 beet soil-b
46	2	40.0	8	12	Q9DSN3	Q9DSN3 beet soil-b
47	2	40.0	8	12	Q9DSN4	Q9DSN4 beet soil-b
48	2	40.0	8	12	Q9E8Q0	Q9E8Q0 beet soil-b
49	2	40.0	8	12	Q9E8Q7	Q9E8Q7 beet soil-b
50	2	40.0	8	12	Q9DSN6	Q9DSN6 beet soil-b
51	2	40.0	8	12	Q9DSN0	Q9DSN0 beet soil-b
52	2	40.0	8	12	Q9E8Q6	Q9E8Q6 beet soil-b
53	2	40.0	8	12	Q9E8P8	Q9E8P8 beet soil-b
54	2	40.0	8	13	Q98TU5	Q98TU5 xenopus lae
55	2	40.0	9	2	Q9R735	Q9R735 streptomyce
56	2	40.0	9	2	P82568	P82568 streptococc
57	2	40.0	9	3	Q9P8E5	Q9P8E5 kluyveromyc
58	2	40.0	9	4	Q9H4B1	Q9H4B1 homo sapien
59	2	40.0	9	4	Q9UGB4	Q9UGB4 homo sapien
60	2	40.0	9	4	Q8NHL3	Q8NHL3 homo sapien
61	2	40.0	9	5	Q27396	Q27396 babesia bov
62	2	40.0	9	6	Q9XSL0	Q9XSL0 capra hircu
63	2	40.0	9	9	Q38340	Q38340 lactococcus
64	2	40.0	9	10	Q8LPT5	Q8LPT5 zea mays (m
65	2	40.0	9	11	Q92012	Q92012 mus musculu
66	2	40.0	9	12	Q91IX6	Q91IX6 macaca neme
67	2	40.0	10	2	Q47091	Q47091 escherichia
68	2	40.0	10	2	P82588	P82588 streptococc
69	2	40.0	10	4	O00493	O00493 homo sapien
70	2	40.0	10	4	Q13318	Q13318 homo sapien
71	2	40.0	10	4	Q9UCQ8	Q9UCQ8 homo sapien
72	2	40.0	10	4	Q96QT9	Q96QT9 homo sapien
73	2	40.0	10	4	Q8WTI4	Q8WTI4 homo sapien
74	2	40.0	10	4	Q81ZA2	Q81ZA2 homo sapien
75	2	40.0	10	5	P82384	P82384 drosophila
76	2	40.0	10	5	P82222	P82222 bombyx mori
77	2	40.0	10	6	Q8WP04	Q8WP04 ateles belz
78	2	40.0	10	6	Q9GKI5	Q9GKI5 pan troglod
79	2	40.0	10	6	Q9GKI4	Q9GKI4 macaca arct
80	2	40.0	10	6	Q8HZ71	Q8HZ71 didelphis m
81	2	40.0	10	8	Q8WGD2	Q8WGD2 heparatus eph
82	2	40.0	10	8	Q8SL54	Q8SL54 aconium haw
83	2	40.0	10	10	Q8LPT7	Q8LPT7 zea mays (m
84	2	40.0	10	10	P83091	P83091 spinacia ol
85	2	40.0	10	12	Q39957	Q39957 hepatitis g
86	2	40.0	10	12	Q9W8B6	Q9W8B6 hepatitis g
87	2	40.0	10	12	Q39948	Q39948 hepatitis g
88	2	40.0	10	12	Q39952	Q39952 hepatitis g
89	2	40.0	10	12	Q9W910	Q9W910 hepatitis g

90 Q82625 infectious  
 91 Q9wie4 hepatitis g  
 92 Q90344 hepatitis g  
 93 Q39949 hepatitis g  
 94 Q84266 human papil  
 95 Q73589 gallus gall  
 96 Q54980 avian myelo  
 97 Q75595 human immun  
 98 Q8x4e5 escherichia  
 99 Q9r4b1 streptococc  
 100 Q93mi7 escherichia

## ALIGNMENTS

RESULT 1  
 Q9FXLO PRELIMINARY; PRT; 9 AA.  
 AC Q9FXLO;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE LIM8 protein (Fragment).  
 GN LIM8  
 OS Lilium longiflorum (Trumpet lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.  
 OX NCBI\_TaxID=4690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Hinomoto;  
 RA Uefuji H., Takase H., Hiratsuka K.;  
 RT "Lilium longiflorum LIM8 gene, promoter region and partial sequence."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB050987; BAB17856.1; -.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 60.0%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
 DB 1 MEV 3  
 RESULT 2  
 Q42355 PRELIMINARY; PRT; 10 AA.  
 ID Q42355  
 AC Q42355;  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE GATA-2 (Fragment).  
 GN GATA2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97322361; PubMed=9177206;  
 RA Meng A., Tang H., Ong B.A., Farrell M.J., Lin S.;  
 RT "Promoter analysis in living embryos identifies a cis-acting motif  
 required for neuronal expression of GATA-2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6267-6272(1997).  
 DR EMBL; AF001220; AAB61711.1; -.  
 DR ZFIN; ZDB-GENE-980526-260; gata2.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1192 MW; C82A2CA6DAADDCC2 CRC64;

Query Match 60.0%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 DB 1 MEV 3  
 RESULT 3  
 Q47606 PRELIMINARY; PRT; 11 AA.  
 ID Q47606  
 AC Q47606;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE REase protein (Fragment).  
 GN REase  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139577; PubMed=1995588;  
 RA Tao T., Bourne J.C., Blumenthal R.M.;  
 RT "A family of regulatory genes associated with type II restriction-  
 modification systems.";  
 RL J. Bacteriol. 173:1367-1375(1991).  
 DR EMBL; M63622; AAA24562.1; -.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 60.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 DB 1 MEV 3

RESULT 4  
 O70544 PRELIMINARY; PRT; 14 AA.  
 ID O70544  
 AC O70544;  
 DT 01-AUG-1998 (TReMBLrel. 07, Created)  
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Uteroglobulin/clara cell 10kDa protein (Fragment).  
 GN UG/CC10.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98141958; PubMed=9473294;  
 RA Gutierrez-Sagal R., Nieto A.;  
 RT "Molecular cloning of the cDNA and the promoter of the hamster  
 uteroglobulin/clara cell 10 kDa gene (ug/cc10): tissue-specific and  
 Arch. Biochem. Biophys. 350:214-222(1998).  
 RL Arch. Biochem. Biophys. 350:214-222(1998).  
 DR EMBL; Y13765; CAA74098.1; -.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1507 MW; AB8BCA79F72AF4D6 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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OX NCBI_TaxID=6239;
RP SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Courtney L.;
RT "The sequence of C. elegans cosmid Y108G3AL.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024744; AAL13326.1; -.
DR WormPep; Y108G3AL.6; CE29605.
KW Hypothetical protein
SQ SEQUENCE 16 AA; 1504 MW; 4932099B5AA361E5 CRC64;

Query Match 60.0%; Score 3; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db |||
1 MEV 3

RESULT 10
Q9S8L1 PRELIMINARY; PRT; 16 AA.
ID Q9S8L1;
AC Q9S8L1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Cytochrome P-450 (fragment).
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE.
RX MEDLINE=95024036; PubMed=7937883;
RA Sibbesen O., Koch B., Halkier B.A., Moller B.L.;
RT "Isolation of the heme-thiolate enzyme cytochrome P-450TYR, which
RT catalyzes the committed step in the biosynthesis of the cyanogenic
RT glucoside dhurrin in Sorghum bicolor (L.) Moench.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9740-9744(1994).
SQ SEQUENCE 16 AA; 1516 MW; D5488D84E9FD489 CRC64;

Query Match 60.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db |||
3 MEV 5

RESULT 11
Q85719 PRELIMINARY; PRT; 17 AA.
ID Q85719;
AC Q85719;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Reovirus serotype 3 S4 (Fragment).
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10886;
RN [1]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=82032340; PubMed=6270271;
RA McCrae M.A.;
RT "Terminal structure of reovirus RNAs.";
RL J. Gen. Virol. 55:393-403(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017876; PubMed=6927854;
RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
RT "Sequences at both termini of the 10 genes of reovirus serotype 3
RT (strain Dearing).";
RL Virology 121:307-319(1982).
DR EMBL; J02332; AAA47284.1; -.
DR InterPro; IPR000153; Reovirus_cap.
DR Pfam; PF00979; Reovirus_cap; 1.
FT NON TER 17
SQ SEQUENCE 17 AA; 1852 MW; A7EAB7E4649C1F0D CRC64;

Query Match 60.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db |||
1 MEV 3

RESULT 12
Q9ZY80 PRELIMINARY; PRT; 18 AA.
ID Q9ZY80;
AC Q9ZY80;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Scelio fulgidus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastridae;
OC Scelionidae; Scelio.
OX NCBI_TaxID=32419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF082921; AAD17781.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 18 AA; 2224 MW; 981713ABC608BB17 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db |||
2 VME 4

RESULT 13
Q94L06 PRELIMINARY; PRT; 19 AA.
ID Q94L06;
AC Q94L06;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Isopropyl malate synthase (Fragment).
GN MYJ24-1-BN-7.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Yudal.
RA Fournann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
RT of Arabidopsis-known-function genes in Brassica.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258256; AAK49052.1; -.
FT NON_TER 1
FT TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 1989 MW; A41FC1E46CFC0E6D CRC64;

Query Match 60.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 9 VVM 11

RESULT 14
Q922T5 ID Q922T5 PRELIMINARY; PRT; 19 AA.
AC Q922T5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown (Protein for IMAGE:3586282) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006792; AAK06792.1; -.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 19 AA; 2143 MW; 62431F68A3580579 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 4 VME 6

RESULT 15
Q47614 ID Q47614 PRELIMINARY; PRT; 20 AA.
AC Q47614;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE URF protein.
GN URF.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91232952; PubMed=1709493;
RA Albrechtsen B., Ross B.M., Squires C., Squires C.L.;
RT "Transcriptional termination sequence at the end of the Escherichia
RT coli ribosomal RNA G operon: complex terminators and
RT antitermination.";
RL Nucleic Acids Res. 19:1845-1852(1991).
DR EMBL; X56780; CAA40098.1; -.
SQ SEQUENCE 20 AA; 2162 MW; D952ACD71417E163 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 16
O38539 ID O38539 PRELIMINARY; PRT; 20 AA.
AC O38539;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nucleocapsid protein (Fragment).
OS Human torovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Torovirus.
OX NCBI_TaxID=67605;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=38087835; PubMed=9426455;
RA Duckmanton L., Luan B., Devenish J., Tellier R., Petric M.;
RT "Characterization of torovirus from human fecal specimens.";
RL Virology 239:158-168(1997).
DR EMBL; AF024539; AAC40323.1; -.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 20 AA; 2224 MW; CBD4007B9199F122 CRC64;

Query Match 60.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 17 VVM 19

RESULT 17
O72059 ID O72059 PRELIMINARY; PRT; 20 AA.
AC O72059;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nucleocapsid protein (Fragment).
OS Bovine torovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Torovirus.
OX NCBI_TaxID=74501;
RN [1]
RP SEQUENCE FROM N.A.
RA Duckmanton L., Carman S., Nagy E., Petric M.;
RT "Detection of Bovine Torovirus in Fecal Specimens of Calves with
RT Diarrhea from Ontario farms.";
RL J. Clin. Microbiol. 36:0-0(1998).
DR EMBL; AF053061; AAC15709.1; -.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 20 AA; 2225 MW; CBD4007B8D6BF122 CRC64;

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Query Match      60.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
DB 17 VVM 19

RESULT 18
Q47029 PRELIMINARY; PRT; 7 AA.
AC Q47029;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Aad A1 protein (Fragment).
GN Aad A1.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94079349; PubMed=8257126;
RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
RT "Analysis of the aac(3)-VIA gene encoding a novel 3'-N-
RT acetyltransferase.";
RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
DR EMBL; M88012; AAAL6193.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match      40.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 4 VV 5

RESULT 19
Q8JU20 PRELIMINARY; PRT; 7 AA.
AC Q8JU20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Extracellular fatty acid binding protein (Fragment).
GN EXFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of 3' UTR of EXFABP gene in chicken.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF487519; AAL96665.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 780 MW; 72C81AB2D5BEBB70 CRC64;

Query Match      40.0%; Score 2; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 6 EV 7

RESULT 20
P72279 PRELIMINARY; PRT; 8 AA.
AC P72279;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Biphenyl dioxygenase (Fragment).
GN BPHS.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz E., Timmis K.N.;
RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
RT positive bacterium Rhodococcus globerulus P6 to multicomponent
RT dioxygenases of gram-negative bacteria.";
RL Gene 156:111-18(1995).
DR EMBL; X80041; CAA56350.1; -.
KW Dioxygenase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 7 VV 8

RESULT 21
O68485 PRELIMINARY; PRT; 8 AA.
AC O68485;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
GN ADAD1.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98287600; PubMed=9624504;
RA Centron D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
RT aac(6')-Iq from the integron of a natural multiresistance plasmid.";
RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
DR EMBL; AF047556; AAC25501.1; -.
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 4 EV 5

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## RESULT 22.

Q56759 PRELIMINARY; PRT; 8 AA.  
 AC Q56759;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Haloacid dehalogenase (Fragment).  
 GN DHLB.  
 OS Xanthobacter autotrophicus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Hyphomicrobiaceae; Xanthobacter.  
 OX NCBI\_TaxID=280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GJ10, and CV. M50;  
 RX MEDLINE=95173113; PubMed=7868610;  
 RA Van der Ploeg J., Willemsen M., van Hall G., Janssen D.B.;  
 RT "Adaptation of xanthobacter autotrophicus GJ10 to bromoacetate due to  
 RT activation and mobilization of the haloacetate dehalogenase gene by  
 RT insertion element IS1247.";  
 RL J. Bacteriol. 177:1348-1356(1995).  
 DR EMBL: X84038; CAA58857.1; -.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2  
 Db 5 VV 6

## RESULT 23

Q05403 PRELIMINARY; PRT; 8 AA.  
 AC Q05403;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE DNA for ORF'S from chromosome XV (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FY1679;  
 RX MEDLINE=96021609; PubMed=8533473;  
 RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;  
 RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains  
 RT more than twice as many unknown as known open reading frames.";  
 RL Yeast 11:975-986(1995).  
 DR EMBL: X83121; CAA58183.1; -.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 40.0%; Score 2; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2  
 Db 5 VV 6

## RESULT 24

Q16428 PRELIMINARY; PRT; 8 AA.  
 ID Q16428  
 AC Q16428;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 GN DYSTROPHIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96163501; PubMed=8566960;  
 RA Holder E., Maeda M., Bies R.D.;  
 RT "Expression and regulation of the dystrophin Purkinje promoter in  
 RT human skeletal muscle, heart, and brain.";  
 RL Hum. Genet. 97:232-239(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kitano T., Kobayakawa H., Saitou N.;  
 RT "Silver Project.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: S81419; AAD14363.1; -.  
 DR EMBL: AB037493; BAA90413.1; -.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CE05B6 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5  
 Db 3 EV 4

## RESULT 25

Q9P285 PRELIMINARY; PRT; 8 AA.  
 AC Q9P285;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Clotting factor VIII (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shibata M., Shima M., Morichika S., Yoshiola A.;  
 RT "Human clotting factor VIII gene, junction regions of the deletion of  
 RT exon 4 through 7.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB040872; BAA94312.1; -.  
 FT NON TER 1  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4  
 Db 7 ME 8

## RESULT 26

Q8IV87 PRELIMINARY; PRT; 8 AA.  
 ID Q8IV87  
 AC Q8IV87;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit
GN SPTLC2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050320; CAD54807.1; -.
KW Transferase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
Db ||
5 VM 6

RESULT 27
Q9UB13 PRELIMINARY; PRT; 8 AA.
ID Q9UB13;
AC Q9UB13;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Calmodulin (Fragment).
OS Albinaria hippolyti.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Clausilloidea; Clausiliidae; Alopinae; Albinaria.
OX NCBI_TaxID=69418;
RN [1]
RP SEQUENCE FROM N.A.
RA Schilthuisen M., Hoekstra R.F., Gittenberger E.;
RL "Selective maintenance of a rare haplotype in a land snail hybrid
zone."
RL Proc. R. Soc. Lond., B, Biol. Sci. 266:2181-2185(1999).
DR EMBL; AF132316; AAD34386.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 906 MW; F3ADDAB2CB144056 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
4 EV 5

RESULT 28
Q94623 PRELIMINARY; PRT; 8 AA.
ID Q94623;
AC Q94623;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE MSUSP-2 protein (Fragment).
GN USP.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Epidermis;
RX MEDLINE=97165493; PubMed=9013254;
RA Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
RT "Identification and mRNA developmental profiles of two ultraspiracle
RT isoforms in the epidermis and wings of Manduca sexta.";
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U5921; AAB64235.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 892 MW; F165BB0415A76B16 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
1 ME 2

RESULT 29
Q94695 PRELIMINARY; PRT; 8 AA.
ID Q94695;
AC Q94695;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Actin (Fragment).
GN ARDC.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96182101; PubMed=8622700;
RA Benard M., Lagnel C., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RT polycephalum.";
RL Mol. Cell. Biol. 16:968-976(1996).
DR EMBL; M73459; AAB03706.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 878 MW; F4C6C2CAAB187B16 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
1 ME 2

RESULT 30
Q9MYL5 PRELIMINARY; PRT; 8 AA.
ID Q9MYL5;
AC Q9MYL5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Dystrophin.
OS Pongo pygmaeus (Orangutan).
OS Pan troglodytes (Chimpanzee), and
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600; 9598, 9593;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.pygmaeus, P.troglodytes, and G.gorilla;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB037496; BAA90419.1; -.
DR EMBL; AB037494; BAA90415.1; -.
DR EMBL; AB037495; BAA90417.1; -.
SQ SEQUENCE 8 AA; 825 MW; F21865ASA2CB05B6 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 6; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
3 EV 4

RESULT 31
Q9SB24 PRELIMINARY; PRT; 8 AA.
AC Q9SB24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ParAt protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Niwa Y., Muranaka T., Baba A., Machida Y.;
RT "Organ-specific and auxin-inducible expression of two tobacco para-
RT related genes in transgenic plants.";
RL DNA Res. 0:0-0(1994).
DR EMBL; D42119; BAA07700.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 905 MW; FE32D2C44455BB16 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 10; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
6 VV 7

RESULT 32
Q42507 PRELIMINARY; PRT; 8 AA.
AC Q42507;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein (Fragment).
GN HSP70C OR HSP70A OR HSP70B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV MUSTANG;
RX MEDLINE=96189275; PubMed=8605312;
RA Joshi C.P., Kumar S., Nguyen H.T.;
RT "Application of modified differential display technique for cloning
RT and sequencing of the 3' region from three putative members of wheat
RT HSP70 gene family.";
RL Plant Mol. Biol. 30:641-646(1996).
DR EMBL; L41507; AAB02333.1; -.
DR EMBL; L41505; AAB02331.1; -.
DR EMBL; L41506; AAB02332.1; -.
KW Heat shock.

FT NON_TER 1
SQ SEQUENCE 8 AA; 886 MW; 71B2CB1B10532768 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 10; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
6 EV 7

RESULT 33
P82324 PRELIMINARY; PRT; 8 AA.
AC P82324;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT105) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson P.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON ITS 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.7, ITS MW IS: 16.8 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 839 MW; DDC68B5DDDC2D2D5 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 10; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
2 VV 3

RESULT 34
Q9ET21 PRELIMINARY; PRT; 8 AA.
AC Q9ET21;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Placenta growth factor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21182783; PubMed=11289150;
RA Green C.J., Lichtlen P., Huynh N.T., Yanovsky M., Laderoute K.R.,
RA Schaffner W., Murphy B.J.;
RT "Placenta growth factor gene expression is induced by hypoxia in
RT fibroblasts: a central role for metal transcription factor-1.";
RL Cancer Res. 61:2696-2703(2001).

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DR EMBL; AF285629; AAG00527.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 982 MW; E8A9C7233682C726 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 11; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VM 3
   ||
Db 3 VM 4

RESULT 35
Q62527
ID Q62527 PRELIMINARY; PRT; 8 AA.
AC Q62527;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Transthyretin (Prealbumin) (Fragment).
GN TTR.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
EX MEDLINE=94319082; PubMed=8043949;
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maeraki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
CC -!- FUNCTION: THYROID HORMONE-BINDING PROTEIN. PROBABLY TRANSPORTS
CC THYROXINE FROM THE BLOODSTREAM TO THE BRAIN.
CC -!- SUBUNIT: HOMOTETRAMER.
DR EMBL; U05689; AAB60461.1; -.
DR MGD; MGI:98865; Ttr.
KW Albumin; Transport; Retinol-binding; Vitamin A; Thyroid hormone.
FT NON_TER 1
SQ SEQUENCE 8 AA; 828 MW; 9156C76455A2D2CD CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 11; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 2 VV 3

RESULT 36
Q9E8Q5
ID Q9E8Q5 PRELIMINARY; PRT; 8 AA.
AC Q9E8Q5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162921; AAG21077.1; -.
FT NON_TER 1

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SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 12; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 3 VV 4

RESULT 37
Q9E8Q2
ID Q9E8Q2 PRELIMINARY; PRT; 8 AA.
AC Q9E8Q2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=31a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162928; AAG21080.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 12; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 3 VV 4

RESULT 38
Q9E8P9
ID Q9E8P9 PRELIMINARY; PRT; 8 AA.
AC Q9E8P9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=37b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162933; AAG21083.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 12; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 3 VV 4

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RESULT 39
Q9EBQ3 ID Q9EBQ3 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and Variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162924; AAG21079.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
Db ||
3 VW 4

RESULT 40
Q9EBQ1 ID Q9EBQ1 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=31b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162929; AAG21081.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
Db ||
3 VW 4

RESULT 41
Q9DSN2 ID Q9DSN2 PRELIMINARY; PRT; 8 AA.
AC Q9DSN2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21b;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
RT Pomovirus - a Virus with Uncertain Pathogenic Effects.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162927; AAG43392.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
Db ||
3 VW 4

RESULT 42
Q9EBQ4 ID Q9EBQ4 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162922; AAG21078.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 935 MW; ECA40EB322D2C056 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
Db ||
3 VW 4

RESULT 43
Q9DSN5 ID Q9DSN5 PRELIMINARY; PRT; 8 AA.
AC Q9DSN5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6b;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
RT Pomovirus - a Virus with Uncertain Pathogenic Effects.";
```



RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF162923; AAG43389.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 935 MW; ECA40EB322D2C056 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 3 VV 4

## RESULT 44

Q9EBP7 PRELIMINARY; PRT; 8 AA.  
AC Q9EBP7;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE 22K protein (Fragment).  
OS Beet soil-borne virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.  
OX NCBI\_TaxID=46436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=41b;  
RX MEDLINE=20403266; PubMed=10948990;  
RA Koenig R., Pleij C.W., Buettner G.;  
RT "Structure and variability of the 3', end of RNA 3 of Beet soil-borne  
pomovirus--a virus with uncertain pathogenic effects.";  
RL Arch. Virol. 145:1173-1181(2000).  
DR EMBL; AF162935; AAG21085.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 3 VV 4

## RESULT 45

Q9DSN1 PRELIMINARY; PRT; 8 AA.  
AC Q9DSN1;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE 22K protein (Fragment).  
OS Beet soil-borne virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.  
OX NCBI\_TaxID=46436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=33a;  
RA Koenig R., Pleij C., Huth W.;  
RT "Structure and variability of the 3'End of RNA 3 of Beet Soil-Borne  
Pomovirus - a Virus with Uncertain Pathogenic Effects.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF162930; AAG43393.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 3 VV 4

## RESULT 46

Q9DSN3 PRELIMINARY; PRT; 8 AA.  
AC Q9DSN3;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE 22K protein (Fragment).  
OS Beet soil-borne virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.  
OX NCBI\_TaxID=46436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=21a;  
RA Koenig R., Pleij C., Huth W.;  
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne  
Pomovirus - a Virus with Uncertain Pathogenic Effects.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF162926; AAG43391.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 3 VV 4

## RESULT 47

Q9DSN4 PRELIMINARY; PRT; 8 AA.  
AC Q9DSN4;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE 22K protein (Fragment).  
OS Beet soil-borne virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.  
OX NCBI\_TaxID=46436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=10b;  
RA Koenig R., Pleij C., Huth W.;  
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne  
Pomovirus - a Virus with Uncertain Pathogenic Effects.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF162925; AAG43390.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 3 VV 4

## RESULT 48

Q9E8Q0 PRELIMINARY; PRT; 8 AA.  
AC Q9E8Q0;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

Query Match 40.0%; Score 2; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
||  
Db 3 VV 4

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DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=37a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162932; AAG21082.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 49
Q9E8Q7 PRELIMINARY; PRT; 8 AA.
AC Q9E8Q7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162916; AAG21075.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 50
Q9DSN6 PRELIMINARY; PRT; 8 AA.
AC Q9DSN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5a;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne

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RT Pomovirus - a Virus with Uncertain Pathogenic Effects.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF162920; AAG43388.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 51
Q9DSNO PRELIMINARY; PRT; 8 AA.
AC Q9DSNO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=33b;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF162931; AAG43394.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 52
Q9E8Q6 PRELIMINARY; PRT; 8 AA.
AC Q9E8Q6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162919; AAG21076.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

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Qy 1 VV 2
Db 3 VV 4

RESULT 53
Q98P8 PRELIMINARY; PRT; 8 AA.
AC Q98P8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22k protein (fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=41a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162934; AAG21084.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 3 VV 4

RESULT 54
Q98TU5 PRELIMINARY; PRT; 8 AA.
AC Q98TU5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1d transcript 2 (fragment).
GN ELRD.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21226152; PubMed=11327714;
RA Nassar F., Wegnez M.;
RT "Characterization of two promoters of the Xenopus laevis elrD gene.";
RL Biochem. Biophys. Res. Commun. 283:392-398(2001).
DR EMBL; AF329448; AAK01428.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 1008 MW; FF93372874537B16 CRC64;

Query Match 40.0%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
Db 1 ME 2

RESULT 55
Q9R735 PRELIMINARY; PRT; 9 AA.
ID Q9R735
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AC Q9R735;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fkba protein (fragment).
GN FKBA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT of two FKBP-12 binding domains with its gene transcriptionally coupled
RT to the FKBP-12 gene.";
RL EMBO J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84282.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 7 EV 8

RESULT 56
P82568 PRELIMINARY; PRT; 9 AA.
ID P82568;
AC P82568;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whittom M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -!- MASS SPECTROMETRY; MW=22592.04; METHOD=ELECTROSPRAY.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 5 EV 6

RESULT 57
Q9P8E5 PRELIMINARY; PRT; 9 AA.
ID Q9P8E5;
AC Q9P8E5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HIS4 protein (fragment).
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GN HIS4.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99448382; PubMed=10518937;
RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
RT and differences to Saccharomycetes cerevisiae HIS4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR EMBL; AJ238494; CAB87125.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 40.0%; Score 2; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db |||
4 VV 5

RESULT 58
ID Q9H4B1 PRELIMINARY; PRT; 9 AA.
AC Q9H4B1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IGS12 protein (Fragment).
GN P27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Martensen P.M., Soegaard T.M., Gjermansen I.M., Buttenschoen H.N.,
RA Rossing A.B., Bonnevie-Nielsen V., Rosada C., Simonsen J.L.,
RA Justesen J.;
RT "The interferon alpha induced protein ISG12 is localized to the
RT nuclear membrane.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ294851; CAC10503.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 896 MW; 6B9CA1A72DC5BDD8 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db |||
1 ME 2

RESULT 59
ID Q9UGE4 PRELIMINARY; PRT; 9 AA.
AC Q9UGE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE D34105.1 (Remainder of gene in sequence AL023513) (Fragment).
GN SZ6L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078460; CAB51751.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1125 MW; 8154A2CB0B5B0411 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db |||
6 EV 7

RESULT 60
ID Q8NHL3 PRELIMINARY; PRT; 9 AA.
AC Q8NHL3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Killer-cell immunoglobulin-like receptor KIR2DL5.3 (Fragment).
GN KIR2DL5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540100; PubMed=11086080;
RA Vilches C., Gardiner C.M., Farham P.;
RT "Gene structure and promoter variation of expressed and nonexpressed
RT variants of the KIR2DL5 gene.";
RL J. Immunol. 165:6416-6421(2000).
DR EMBL; AF260137; AAG38010.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 968 MW; 9DEF85A3D2C69735 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db |||
5 VV 6

RESULT 61
ID Q27396 PRELIMINARY; PRT; 9 AA.
AC Q27396;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rhopty associated protein 1.
GN RAP-1.
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=No7;
RA Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
RT "The Babesia bovis rhopty associated protein-1 intergenic region
RT encodes a functional eukaryotic promoter.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; L77326; AAA96415.1; -.
DR EMBL; L77245; AAD15061.1; -.
SQ SEQUENCE 9 AA; 931 MW; 6D5BD2C865B05044 CRC64;

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Query Match 40.0%; Score 2; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
DB 7 VV 8

RESULT 62  
Q9XSLO PRELIMINARY; PRT; 9 AA.  
AC Q9XSLO; (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DE Alpha s2-casein (Fragment).  
GN CSN1S2.  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Capra.  
OX NCBI\_TaxID=9925;  
RN [1]\_TaxID=9925;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=21313038; PubMed=11419340;  
RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,  
Cosenza G., Mariani P., Pastore N., Masina P.;  
RT "An allele associated with a non detectable amount of as2 casein in  
goat milk.";  
RL Anim. Genet. 32:19-26(2001).  
DR EMBL; AJ238475; CAB44298.1; --.  
FT NON\_TER 1 1  
FT VARIANT 5 5 I -> V.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
DB 2 ME 3

RESULT 63  
Q38340 PRELIMINARY; PRT; 9 AA.  
AC Q38340;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Orf protein (Fragment).  
GN ORF.  
OS Lactococcus phage 936.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC psiM1-like viruses.  
OX NCBI\_TaxID=39838;  
RN [1]\_TaxID=39838;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96084945; PubMed=7489923;  
RA Waterfield N.R., LePage R.W., Wilson P.W., Wells J.M.;  
RT "The isolation of lactococcal promoters and their use in investigating  
bacterial luciferase synthesis in Lactococcus lactis.";  
RL Gene 165:9-15(1995).  
DR EMBL; Z48181; CAA88226.1; --.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1054 MW; 7098B2CEA6D3372B CRC64;

Query Match 40.0%; Score 2; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4  
DB 1 ME 2

RESULT 64  
Q8LPT5 PRELIMINARY; PRT; 9 AA.  
AC Q8LPT5;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Beta-expansin-like protein (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]\_TaxID=4577;  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. C123;  
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
Morgante M., Rafalski J.A.;  
RT "SNP frequency, haplotype structure and linkage disequilibrium in  
elite maize inbred lines.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY094310; AAM21836.1; --.  
FT NON\_TER 1 1  
SQ SEQUENCE 9 AA; 977 MW; 5C05B2D2CB1AAAA3 CRC64;

Query Match 40.0%; Score 2; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2  
DB 6 VV 7

RESULT 65  
Q92012 PRELIMINARY; PRT; 9 AA.  
AC Q92012;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE SLC12a4 (Fragment).  
GN SLC12A4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_TaxID=10090;  
RP SEQUENCE FROM N.A.  
RC STRAIN=12956/SvEvTac; TISSUE=Spleen;  
RA Bjoernleitt M.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF236367; AAL11037.1; --.  
FT NON\_TER 1 1  
SQ SEQUENCE 9 AA; 1037 MW; 78305041A042CB04 CRC64;

Query Match 40.0%; Score 2; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5  
DB 3 EV 4

RESULT 66.  
Q9ILX6 PRELIMINARY; PRT; 9 AA.  
AC Q9ILX6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE ORF 10-like protein (Fragment).  
OS Macaca nemestrina rhadinovirus 2.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Rhadinovirus.  
OX NCBI\_TaxID=123630;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mne442N;  
RX MEDLINE=20240083; PubMed=10775636;  
RA Schultz E.R., Rankin G.W. Jr., Blanc M.P., Raden B.W., Tsai C.C.,  
RA Rose T.M.;  
RT "Characterization of two divergent lineages of macaque rhadinoviruses  
RT related to Kaposi's sarcoma-associated herpesvirus.";  
RL J. Virol. 74:4919-4928(2000).  
DR EMBL; AF204167; AAF81665.1; -.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1003 MW; 41EBD5B7233AB2C7 CRC64;  
  
Query Match 40.0%; Score 2; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VW 2  
Db 8 VV 9  
  
RESULT 67  
Q47091 PRELIMINARY; PRT; 10 AA.  
ID Q47091  
AC Q47091;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Colicin E1 (Fragment).  
OS Escherichia coli.  
OG Plasmid ColE1.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86094231; PubMed=3936034;  
RA Waleh N.S., Johnson P.H.;  
RT "Structural and functional organization of the colicin E1 operon.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).  
DR EMBL; M12543; AAA23065.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1085 MW; 88F00B32CB144041 CRC64;  
  
Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 EV 5  
Db 6 EV 7  
  
RESULT 68  
ID P82588 PRELIMINARY; PRT; 10 AA.  
AC P82588  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unknown protein from 2D-page (Fragment).  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC STRAIN=JRS4;  
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,  
RA VanBogelen R.A.;  
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes  
RT proteins.";  
RL Submitted (MAY-2000) to the SWISS-PROT data bank.  
CC -1- MASS SPECTROMETRY; MW=23573.25; METHOD=ELECTROSPRAY.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1134 MW; 4D5A1DCB105695B7 CRC64;  
  
Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 EV 5  
Db 7 EV 8  
  
RESULT 69  
O00493 PRELIMINARY; PRT; 10 AA.  
ID O00493  
AC O00493;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MJD1 alt MS (Fragment).  
GN MJD1 INC 45.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RA Sugawara M., Toyoshima I., Takeda S., Imota T., Kato K., Wada C.,  
RA Masamune O.;  
RT "Genomic DNA containing the insertion that is seen in the alternative  
RT transcript of MJD1.";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; AB003802; BAA20388.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1161 MW; 9A6E507B1AB2CB05 CRC64;  
  
Query Match 40.0%; Score 2; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 EV 5  
Db 4 EV 5  
  
RESULT 70  
Q13318 PRELIMINARY; PRT; 10 AA.  
ID Q13318  
AC Q13318;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PU.1 (Fragment).  
GN SPI-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9603882; PubMed=7478579;
RA Chen H., Ray-Galliet D., Zhang P., Hetherington C.J., Gonzalez D.A.,
RA Zhang D.E., Moreau-Gachelin F., Tenen D.G.;
RT "PU.1 (Spi-1) autoregulates its expression in myeloid cells.";
RL Oncogene 11:1549-1560 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90265606; PubMed=1693183;
RA Ray D., Culine S., Ravitain A., Moreau-Gachelin F.;
RT "The human homologue of the putative proto-oncogene Spi-1:
RT characterization and expression in tumors [published erratum appears
RT in Oncogene 1990 Oct;5(10):1611-2].";
RL Oncogene 5:663-668 (1990).
DR EMBL; U34046; AAC50247.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1157 MW; C2EB4216933EBDC6 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
7 ME 8

RESULT 71
Q9UCQ8 PRELIMINARY; PRT; 10 AA.
AC Q9UCQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.B., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529 (1992).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1171 MW; 736F44577AF1B2CB CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
3 EV 4

RESULT 72
Q96QT9 PRELIMINARY; PRT; 10 AA.
AC Q96QT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein tyrosine phosphatase 1B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21326081; PubMed=11316810;
RA Fukada T., Tonks N.K.;
RT "The Reciprocal Role of Egr-1 and Sp Family Proteins in Regulation of
RT the Pp1B Promoter in Response to the p210 Bcr-Abl Oncoprotein-
RT tyrosine Kinase.";
RL J. Biol. Chem. 276:25512-25519 (2001).
DR EMBL; AY029236; AAK31734.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1314 MW; AC08E219CB133B16 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
1 ME 2

RESULT 73
Q8WTT4 PRELIMINARY; PRT; 10 AA.
AC Q8WTT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dystrophin (Fragment).
GN DYSTROPHIN OR DMD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ditta S.D., Klamut H.J., Ray P.N., Morton R.G.;
RT "The role of matrix attachment regions in transcriptional regulation
RT from the muscle-specific promoter in the dystrophin gene.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beggs A.H., Koenig M., Kunkel L.M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA den Dunnen J.T.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276053; AAL35752.1; -.
DR EMBL; AF213401; AAL61549.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1339 MW; 2B999202CB1B0363 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
6 EV 7

RESULT 74
Q81ZA2 PRELIMINARY; PRT; 10 AA.
AC Q81ZA2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cardiac troponin T (Fragment).
GN TNNT2.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Bahl A., Kubo T., Steffensen U., Steffensen M., McKenna W.J.,
RA Mogensen J.;
RT "Homo sapiens Troponin T (TNNT2) introns 6 and 7 and exon 7.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV160215; AAN71650.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1099 MW; AB24EC6325BB1B16 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred.No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
Db 3 ME 4

RESULT 75
P82384
ID P82384 PRELIMINARY; PRT; 10 AA.
AC P82384;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Larval cuticle Lcp9 protein (Fragment).
GN LCP9.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_
RP SEQUENCE.
RC STRAIN=OREGON-R; TISSUE=Larva;
RA Chihara C.J.;
RT "Third instar cuticle proteins.";
RL DIS 83:0-0(2000).
CC -!- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
DR FlyBase; FBgn0025578; Lcp9.
DR InterPro; IPR000618; Insect cuticle.
DR PROSITE; PS00233; CUTICLE; PARTIAL.
KW Cuticle; Structural protein.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1105 MW; 7EF84522D2CAADB CRC64;

Query Match 40.0%; Score 2; DB 5; Length 10;
Best Local Similarity 100.0%; Pred.No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 6 VV 7

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Search completed: November 25, 2003, 18:25:28  
 Job time : 15.0979 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 16.1968 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-9  
Perfect score: 5  
Sequence: 1 VNEV 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03:\*

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- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5	100.0	5	22 AAB72254	Colostrinin derive
2	5	100.0	5	22 AAB72508	Colostrinin peptid
3	5	100.0	5	22 AAB72540	Colostrinin peptid
4	5	100.0	5	22 AAB59321	Ewe colostrinin pe
5	5	100.0	5	23 AAE20236	Colostrinin consti
6	5	100.0	5	23 AAW51044	Colostrinin consti
7	5	100.0	5	23 AA014585	Neural cell regula
8	5	100.0	5	22 AAE59351	Ewe colostrinin pe
9	4	80.0	9	22 AAY46069	Immunogenic peptid

10	4	80.0	9	15	AAV38335	MAGE-derived HLA-b
11	4	80.0	9	15	AAV38333	Antigen fragment 1
12	4	80.0	9	16	AAV65122	MAGE 1 immunogenic
13	4	80.0	9	20	AAV45916	Immunogenic peptid
14	4	80.0	9	20	AAV46133	Immunogenic peptid
15	4	80.0	9	20	AAV46358	Immunogenic peptid
16	4	80.0	9	20	AAV47189	Immunogenic peptid
17	4	80.0	9	20	AAV47274	Immunogenic peptid
18	4	80.0	9	20	AAV47275	Immunogenic peptid
19	4	80.0	10	15	AAV38327	MAGE-derived HLA-b
20	4	80.0	10	15	AAV47332	HLA-A1 MAGE 1 anti
21	4	80.0	10	15	AAV45908	Immunogenic peptid
22	4	80.0	10	20	AAV46049	Immunogenic peptid
23	4	80.0	10	20	AAV46105	Immunogenic peptid
24	4	80.0	10	20	AAV46106	Immunogenic peptid
25	4	80.0	11	20	AAV46073	Immunogenic peptid
26	4	80.0	11	20	AAV47431	Immunogenic peptid
27	4	80.0	11	20	AAV47558	Immunogenic peptid
28	4	80.0	11	21	AAV12653	Immunogenic peptid
29	4	80.0	16	16	AAV83269	Protein kinase pep
30	3	60.0	4	12	AAV15779	HIV principal neut
31	3	60.0	4	12	AAV15650	Farnesyl-protein t
32	3	60.0	4	15	AAV49744	Ras protein inhibi
33	3	60.0	4	16	AAV77806	Farnesyltransferas
34	3	60.0	4	17	AAV04436	Farnesyl transfera
35	3	60.0	4	20	AAV18380	N-Ras geranylgeran
36	3	60.0	4	20	AAV18367	N-Ras geranylgeran
37	3	60.0	4	20	AAV18350	N-Ras geranylgeran
38	3	60.0	4	20	AAV18337	N-Ras geranylgeran
39	3	60.0	4	20	AAV18324	N-Ras geranylgeran
40	3	60.0	4	20	AAV13426	Human N-Ras peptid
41	3	60.0	4	20	AAV17051	Human N-Ras peptid
42	3	60.0	4	20	AAV02235	"CAAXG" motif from
43	3	60.0	4	20	AAV99755	CAAX-G motif pepti
44	3	60.0	4	21	AAV99740	CAAX-G motif pepti
45	3	60.0	4	21	AAV03979	N-Ras C-terminal P
46	3	60.0	4	21	AAV92850	CAAX-F motif from
47	3	60.0	4	22	AAV34980	Chimpanzee erythro
48	3	60.0	4	23	AAV29301	Chimpanzee erythro
49	3	60.0	5	16	AAV82999	M. prolifera fucos
50	3	60.0	5	16	AAV69999	High affinity Ige
51	3	60.0	5	16	AAV70276	VIM-containing pep
52	3	60.0	5	16	AAV70277	VIM-containing pep
53	3	60.0	5	16	AAV70275	Thrombospondin 1 (
54	3	60.0	5	17	AAV05024	Thrombospondin-der
55	3	60.0	5	19	AAV87390	Peptide determined
56	3	60.0	5	23	AAV59311	Peptide #56 for us
57	3	60.0	5	24	ABU57836	Thrombospondin 1 r
58	3	60.0	5	24	ABU57837	Thrombospondin 1 c
59	3	60.0	5	24	ABU57838	Thrombospondin 1 c
60	3	60.0	6	16	AAV70272	Thrombospondin 1 (
61	3	60.0	6	17	AAV77518	Cytochrome-P450-lp
62	3	60.0	6	17	AAV05018	Thrombospondin-der
63	3	60.0	6	17	AAV05022	Thrombospondin-der
64	3	60.0	6	17	AAV05023	Thrombospondin-der
65	3	60.0	6	18	AAV41047	6PI staurosporine
66	3	60.0	6	22	AAV45986	Transdominant effe
67	3	60.0	6	23	AAV22870	Carrot red leaf lu
68	3	60.0	6	23	ABV55686	Mutated protein Fe
69	3	60.0	6	24	ABU57569	HIV polypeptide ex
70	3	60.0	6	24	ABU57834	Thrombospondin 1 c
71	3	60.0	7	14	ABU14070	Transdominant effe
72	3	60.0	7	14	AAV35098	B. thuringiensis l
73	3	60.0	7	15	AAV26638	Myrotrophin trypti
74	3	60.0	7	16	AAV82905	X.luminescens flav
75	3	60.0	7	16	AAV78214	B. thuringiensis e
76	3	60.0	7	17	AAV05011	Thrombospondin-der
77	3	60.0	7	17	AAV05012	Thrombospondin-der
78	3	60.0	7	17	AAV05015	Thrombospondin-der
79	3	60.0	7	17	AAV05016	Thrombospondin-der
80	3	60.0	7	17	AAV05017	Thrombospondin-der
81	3	60.0	7	20	AAV50318	Neutrophil-activat
82	3	60.0	7	20	AAV67462	Human delta-sarcog

83 E. coli DP3B prote  
84 S. typhimurium DP3  
85 Protein fragment D  
86 Protein fragment D  
87 Human delta melano  
88 Human Breast cance  
89 Human cell death p  
90 Rabbit delta-sarco  
91 Protein sequence b  
92 Human MAGE-A2 clas  
93 Hepatitis C virus  
94 Enterokinase recog  
95 Mutated protein Fe  
96 G-protein coupled  
97 G-protein coupled  
98 Proteome analysis  
99 C-terminal prenyl  
100 Subpeptide 4N1-1 o

3 60.0 7 21 AAW90753  
3 60.0 7 21 AAW90754  
3 60.0 7 21 AAW90755  
3 60.0 7 21 AAW90756  
3 60.0 7 21 AAY80505  
3 60.0 7 22 AAU68305  
3 60.0 7 22 AAG98675  
3 60.0 7 22 AAE00528  
3 60.0 7 22 AAB20127  
3 60.0 7 23 ABG79014  
3 60.0 7 23 ABB07088  
3 60.0 7 23 AAU81667  
3 60.0 7 23 ABB55662  
3 60.0 7 24 ABJ37357  
3 60.0 7 24 ABJ37437  
3 60.0 7 24 ABP74813  
3 60.0 8 15 AAR63218  
3 60.0 8 16 AAR70288

## ALIGNMENTS

RESULT 1  
AAB72254  
ID AAB72254 standard; peptide; 5 AA.

XX AC AAB72254;  
DT 14-MAY-2001 (first entry)  
XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 9.

KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.

XX OS Synthetic.

XX PN WO200111937-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22818.

XX PR 17-AUG-1999; 99US-0149311.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -

XX PS Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX SQ Sequence 5 AA;  
Query Match 100.0%; Score 5; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVMEV 5

Db 1 VVMEV 5

RESULT 2

AAB72508

ID AAB72508 standard; Peptide; 5 AA.

XX AC AAB72508;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #9.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -

XX PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 22; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVMEV 5

Db 1 VVMEV 5

RESULT 3

AAB72540

ID AAB72540 standard; Peptide; 5 AA.

XX AC AAB72540;

XX DT 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #9.
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
XX Unidentified.
XX OS
XX WO200112651-A2.
XX PN
XX 22-FEB-2001.
XX PD
XX 17-AUG-2000; 2000WO-US22774.
XX PF
XX 17-AUG-1999; 99US-0149633.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Boldogh I;
XX PI
XX WPI; 2001-226545/23.
XX DR
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX PT
XX Claim 6; Page 21; 35pp; English.
XX PS
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX CC
XX
XX Query Match 100.0%; Score 5; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VVMEV 5
XX Db 1 VVMEV 5
XX
XX RESULT 4
XX AAB59321
XX ID AAB59321 standard; Peptide; 5 AA.
XX AC
XX AAB59321;
XX DT 21-MAR-2001 (first entry)
XX DE
XX Ewe colostrinin peptide fragment B-6.
XX DE
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX KW
XX Ovis sp.
XX OS
XX WO200075173-A2.
XX PN
XX 14-DEC-2000.
XX PD
XX 02-JUN-2000; 2000WO-GB02128.
XX PF
XX 02-JUN-1999; 99GB-0012852.
XX PR
XX (REGE-) REGEN THERAPEUTICS PLC.
XX PA
XX Georgiades JA;
XX PI
XX WPI; 2001-071058/08.
XX DR
XX Peptides having an N-terminal amino acid sequence isolated from
XX PT

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
XX PT characterized by amyloid plaques -
XX PS Claim 7; Page 27; 63pp; English.
XX CC
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX CC
XX Sequence 5 AA;
XX SQ
XX Query Match 100.0%; Score 5; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VVMEV 5
XX Db 1 VVMEV 5
XX
XX RESULT 5
XX AAE20236
XX ID AAE20236 standard; peptide; 5 AA.
XX AC
XX AAE20236;
XX XX
XX 18-JUN-2002 (first entry)
XX DT
XX Colostrinin constituent peptide #9.
XX DE
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX KW transplantation; implantation; dermatological; vulnerary.
XX KW
XX Unidentified.
XX OS
XX Key, Location/Qualifiers
XX FH Modified-site 5
XX FT /note= "Optionally C-terminal amide"
XX FT
XX WO200213850-A1.
XX PN
XX 21-FEB-2002.
XX PD
XX 17-AUG-2000; 2000WO-US22776.
XX PF
XX 17-AUG-2000; 2000WO-US22776.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Stanton GJ, Hughes TK, Boldogh I;
XX PI WPI; 2002-269151/31.
XX PN
XX Composition useful for the modulation of blood cell proliferation in a
XX PT patient comprises a blood cell regulator selected from colostrinin, its
XX PT constituent peptide and/or analog -
XX PS Claim 6; Page 25; 51pp; English.
XX CC
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress
XX level in a cell e.g. mammalian or human cell present in a cell culture,
XX CC tissue, organ, or organism; or for treating oxidative damage to the skin
XX of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 1 VVMEV 5  
 |||||  
 Db 1 VVMEV 5

#### RESULT 6

AA051044  
 ID AAM51044 standard; Peptide; 5 AA.

XX  
 AC AAM51044;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 5 /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. The peptide is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response, modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 1 VVMEV 5  
 |||||  
 Db 1 VVMEV 5

#### RESULT 7

AA014585

ID AAO14585 standard; peptide; 5 AA.

XX  
 AC AAO14585;

DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 9.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 5 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

```

CC the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVMEV 5
Db 1 VVMEV 5
|||||

RESULT 8
AAB59351
ID AAB59351 standard; Peptide; 9 AA.
XX
AC AAB59351;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment derived sequence #11.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REG-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
PS Claim 8; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVMEV 5
Db 5 VVMEV 9
|||||

RESULT 9
AAY46069
ID AAY46069 standard; Peptide; 8 AA.
XX

AC AAY46069;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #680.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment
PT and diagnosis of cancers and viral diseases -
XX
PS Claim 1; Page 55; 150pp; English.
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 8 AA;

Query Match 80.0%; Score 4; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVMEV 5
Db 1 VVMEV 4
|||||

RESULT 10
AAY38335
ID AAY38335 standard; Peptide; 9 AA.
XX
AC AAY38335;
XX
XX

```

DT 29-SEP-1999 (first entry)  
 XX MAGE-derived HLA-binding peptide.  
 XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral;  
 KW MHC; major histocompatibility complex; viral infection; anticancer;  
 KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.  
 XX Homo sapiens.  
 OS WO9403205-A1.  
 XX 17-FEB-1994.  
 XX 06-AUG-1993; 93WO-US07421.  
 XX 05-MAR-1993; 93US-0027746.  
 PR 07-AUG-1992; 92US-0926666.  
 XX (CYTE-) CYTEL CORP.  
 FA Celis E, Grey HM, Kubo RT, Sette A;  
 XX WPI; 1994-065403/08.  
 XX Peptide which specifically binds selected MHC allele - used to  
 PT induce an immune response for treatment or prevention of viral  
 PT infection or cancer, or for diagnosis  
 XX Disclosure; Page 112; 150pp; English.  
 XX The sequence is a specific example of a group of new immunogenic  
 CC peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding  
 CC motif. For example, the peptides having an HLA-A3.2 binding motif  
 CC each have 9-10 residues and contain, from the N-terminus to the  
 CC C-terminus, (a) a first conserved residue selected from L, M, I,  
 CC V, S, A, T, F, C, G, D and E and (b) a second conserved residue of  
 CC K, R, Y, H or F, where the first and second conserved residues are  
 CC separated by 6-7 residues. The peptides are capable of binding  
 CC selected MHC molecules and inducing an immune response. They can be  
 CC used to treat and/or prevent viral infection and cancer, e.g. prostate  
 CC cancer, lymphoma, hepatitis or AIDS. They can also be used to produce  
 CC antibodies for use as diagnostic or therapeutic agents. The peptides  
 CC can also be used as diagnostic agents.  
 XX SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 DB 2 VMEV 5  
 RESULT 11  
 AAR73833  
 ID AAR73833 standard; peptide; 9 AA.  
 XX AC AAR73833;  
 XX 25-MAR-2003 (updated)  
 DT 22-JUN-1995 (first entry)  
 XX Antigen fragment 149, from MAGE1(a) has binding affinity for HLA-2.1.  
 XX antigen; epitope; immunogenic target protein; PSA; HBVc; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;

KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PIP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; M1; LCMV.  
 XX Homo sapiens.  
 OS WO9420127-A1.  
 XX 15-SEP-1994.  
 XX 04-MAR-1994; 94WO-US02353.  
 XX 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX (CYTE-) CYTEL CORP.  
 XX Grey HM, Kast WM, Sette A, Sidney J;  
 XX WPI; 1994-302678/37.  
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX Disclosure; Page 85; 138pp; English.  
 XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from MAGE1(a) has a  
 CC binding value of 0.0410. The peptides of the invention can induce  
 CC cytotoxic T lymphocytes which can react with target cells. They can  
 CC be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 DB 6 VMEV 9  
 RESULT 12  
 AAR65122  
 ID AAR65122 standard; peptide; 9 AA.  
 XX AC AAR65122;  
 XX 25-MAR-2003 (updated)  
 DT 09-OCT-1995 (first entry)  
 XX MAGE 1 immunogenic peptide 219-227.  
 DE MAGE 1; immunogenic peptide 219-227; cytotoxic C cells;  
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;  
 KW fungal infections; tuberculosis; hepatitis.  
 XX Homo sapiens.  
 OS WO9504817-A1.  
 XX 16-FEB-1995.  
 XX 01-AUG-1994; 94WO-US08672.  
 PF

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PR 06-AUG-1993; 93US-0103401.
PA (CYTE-) CYTEL CORP.
XX
XX Celis E, Kubo R, Serira H, Tsai V, Wentworth P;
XX WPI; 1995-090895/12.
XX
XX In vitro activation of cytotoxic T cells for selected killing of
XX target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
XX incubating them with antigen presenting cells loaded with
XX appropriate immunogenic peptide
XX
XX Example 3; Page 35; 53pp; English.
XX
XX AAR65109-R65145 are immunogenic peptides, they are used in a new
XX method for the in vitro activation of cytotoxic T cells (CTC).
XX This is achieved by incubating the CTCs with antigen presenting
XX cells loaded with an appropriate immunogenic peptide (e.g. one
XX of the above peptides). By selecting the peptides used the
XX following diseases and infections can be treated; cancer, AIDS,
XX hepatitis, other viral and bacterial infections, malaria and
XX tuberculosis.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 9 AA;
SQ
Query Match 80.0%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VMEV 5
Db 2 VMEV 5
|||||
2 VMEV 5

RESULT 13
AAY45916
ID AAY45916 standard; Peptide; 9 AA.
XX
XX AAY45916;
AC
DT 01-DEC-1999 (first entry)
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #527.
DE
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9945954-A1.
XX
XX 16-SEP-1999.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX
XX Claim 1; Page 46; 150pp; English.

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XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
XX Sequence 9 AA;
SQ
Query Match 80.0%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VMEV 5
Db 2 VMEV 5
|||||
2 VMEV 5

RESULT 14
AAY46133
ID AAY46133 standard; Peptide; 9 AA.
XX
XX AAY46133;
AC
DT 01-DEC-1999 (first entry)
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #744.
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9945954-A1.
XX
XX 16-SEP-1999.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX
XX Claim 1; Page 58; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides

```





CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 XX  
 SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 Db |||||  
 4 VMEV 7  
 RESULT 17  
 AAY47274  
 ID AAY47274 standard; Peptide; 9 AA.  
 XX  
 AC AAY47274;  
 XX  
 DT 01-DEC-1999 (first entry)  
 XX  
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1885.  
 DE  
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9945954-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 13-MAR-1998; 98WO-US05039.  
 XX  
 PR 13-MAR-1998; 98WO-US05039.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;  
 XX  
 DR WPI; 1999-551214/46.  
 XX  
 PT New immunogenic peptides with HLA binding motif, useful in treatment  
 PT and diagnosis of cancers and viral diseases -  
 XX  
 PS Claim 1; Page 101; 150pp; English.  
 XX  
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and

CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 XX  
 SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 Db |||||  
 6 VMEV 9  
 RESULT 18  
 AAY47275  
 ID AAY47275 standard; Peptide; 9 AA.  
 XX  
 AC AAY47275;  
 XX  
 DT 01-DEC-1999 (first entry)  
 XX  
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1886.  
 DE  
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9945954-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 13-MAR-1998; 98WO-US05039.  
 XX  
 PR 13-MAR-1998; 98WO-US05039.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;  
 XX  
 DR WPI; 1999-551214/46.  
 XX  
 PT New immunogenic peptides with HLA binding motif, useful in treatment  
 PT and diagnosis of cancers and viral diseases -  
 XX  
 PS Claim 1; Page 101; 150pp; English.  
 XX  
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and

CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.

SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMEV 5  
 ||||  
 Db 6 VMEV 9

## RESULT 19

AAV38327  
 ID AAV38327 standard; Peptide; 10 AA.

XX AAV38327;

XX 29-SEP-1999 (first entry)

XX MAGE-derived HLA-binding peptide.

XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral;  
 KW MHC; major histocompatibility complex; viral infection; anticancer;  
 KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.

XX Homo sapiens.

XX WO9403205-A1.

XX 17-FEB-1994.

XX 06-AUG-1993; 93WO-US07421.

XX 05-MAR-1993; 93US-0027746.

XX 07-AUG-1992; 92US-0926666.

XX (CYTE-) CYTEL CORP.

XX Celis E, Grey HM, Kubo RT, Sette A;

XX WPI; 1994-065403/08.

XX Peptide which specifically binds selected MHC allele - used to  
 PT induce an immune response for treatment or prevention of viral  
 PT infection or cancer, or for diagnosis

XX Disclosure; Page 112; 150pp; English.

XX The sequence is a specific example of a group of new immunogenic  
 CC peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding  
 CC motif. For example, the peptides having an HLA-A3.2 binding motif  
 CC each have 9-10 residues and contain, from the N-terminus to the  
 CC C-terminus, (a) a first conserved residue selected from L, M, I,  
 CC V, S, A, T, F, C, G, D and E and (b) a second conserved residue of  
 CC K, R, Y, H or F, where the first and second conserved residues are  
 CC separated by 6-7 residues. The peptides are capable of binding  
 CC selected MHC molecules and inducing an immune response. They can be  
 CC used to treat and/or prevent viral infection and cancer, e.g. prostate  
 CC cancer, lymphoma, hepatitis or AIDS. They can also be used to produce  
 CC antibodies for use as diagnostic or therapeutic agents. The peptides

CC can also be used as diagnostic agents.

SQ Sequence 10 AA;

Query Match 80.0%; Score 4; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMEV 5  
 ||||  
 Db 3 VMEV 6

## RESULT 20

AAV47332  
 ID AAV47332 standard; Protein; 10 AA.

XX AAV47332;

XX 14-MAY-2003 (updated)

XX 25-MAR-2003 (updated)

XX 31-AUG-1994 (first entry)

XX HLA-A1 MAGE 1 antigen peptide fragment 215-224.

XX Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;  
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;  
 KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.

XX Synthetic.

XX WO9403205-A1.

XX 17-FEB-1994.

XX 06-AUG-1993; 93WO-US07421.

XX 07-AUG-1992; 92US-0926666.

XX 05-MAR-1993; 93US-0027746.

XX (CYTE-) CYTEL CORP.

XX Celis E, Grey HM, Kubo RT, Sette A;

XX WPI; 1994-065403/08.

XX Peptide which specifically binds selected MHC allele - used to  
 PT induce an immune response for treatment or prevention of viral  
 PT infection or cancer, or for diagnosis

XX Example 8; Page 52; 150pp; English.

XX The sequences given in AAR47304-33 and AAR49201-44 are immunogenic  
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.  
 CC These peptides may be used in the composition of the invention.  
 CC These peptides are capable of binding selected MHC molecules and  
 CC inducing an immune response. They can be used to treat and/or  
 CC prevent viral infection and cancer, eg prostate cancer, lymphoma,  
 CC hepatitis or AIDS. They can also be used to produce antibodies for  
 CC use as diagnostic or therapeutic agents. The peptides can also be  
 CC used as diagnostic agents.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 14-MAY-2003 to correct PS field.)

XX Sequence 10 AA;

Query Match 80.0%; Score 4; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMEV 5  
 ||||  
 Db 6 VMEV 9

```

RESULT 21
AAV45908
ID AAY45908 standard; Peptide; 10 AA.
XX AC
XX AAY45908;
XX DT
XX 01-DEC-1999 (first entry)
XX DE
XX Immunogenic peptide having a human leukocyte antigen binding motif #519.
XX KW
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX OS
XX Synthetic.
XX OS
XX Homo sapiens.
XX PN
XX WO9945954-A1.
XX XX
XX PD
XX 16-SEP-1999.
XX PF
XX 13-MAR-1998; 98WO-US05039.
XX XX
XX PR
XX 13-MAR-1998; 98WO-US05039.
XX XX
XX PA
XX (EPIM-) EPIIMUNE INC.
XX PI
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX DR
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX PT
XX and diagnosis of cancers and viral diseases -
XX PS
XX Claim 1; Page 46; 150pp; English.
XX CC
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX SQ
XX Sequence 10 AA;
XX
XX Query Match 80.0%; Score 4; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 VMEV 5
XX |||||
XX 3 VMEV 6
XX Db

```

```

RESULT 22
AAV46049
ID AAY46049 standard; Peptide; 10 AA.
XX AC
XX AAY46049;
XX DT
XX 01-DEC-1999 (first entry)
XX DE
XX Immunogenic peptide having a human leukocyte antigen binding motif #660.
XX KW
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX OS
XX Synthetic.
XX OS
XX Homo sapiens.
XX PN
XX WO9945954-A1.
XX XX
XX PD
XX 16-SEP-1999.
XX PF
XX 13-MAR-1998; 98WO-US05039.
XX XX
XX PR
XX 13-MAR-1998; 98WO-US05039.
XX XX
XX PA
XX (EPIM-) EPIIMUNE INC.
XX PI
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX DR
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX PT
XX and diagnosis of cancers and viral diseases -
XX PS
XX Claim 1; Page 54; 150pp; English.
XX CC
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX SQ
XX Sequence 10 AA;
XX
XX Query Match 80.0%; Score 4; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 VMEV 5
XX |||||
XX 6 VMEV 9
XX Db

```

RESULT 23  
AAY46105

ID AAY46105 standard; Peptide; 10 AA.  
 AC AAY46105;  
 XX  
 DT 01-DEC-1999 (first entry)  
 XX  
 DE Immunogenic peptide having a human leukocyte antigen binding motif #716.  
 XX  
 DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 XX immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9945954-A1.  
 PN  
 XX 16-SEP-1999.  
 PD  
 XX 13-MAR-1998; 98WO-US05039.  
 PF  
 XX 13-MAR-1998; 98WO-US05039.  
 PR  
 XX (EPIM-) EPIMMUNE INC.  
 PA  
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;  
 PI WPI; 1999-551214/46.  
 XX  
 DR New immunogenic peptides with HLA binding motif, useful in treatment  
 PT and diagnosis of cancers and viral diseases -  
 PT  
 XX Claim 1; Page 56; 150pp; English.  
 PS  
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 Db ||||  
 3 VMEV 6  
 RESULT 24  
 AAY46106  
 ID AAY46106 standard; Peptide; 10 AA.  
 XX

AC AAY46106;  
 XX  
 DT 01-DEC-1999 (first entry)  
 XX  
 DE Immunogenic peptide having a human leukocyte antigen binding motif #717.  
 XX  
 DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9945954-A1.  
 PN  
 XX 16-SEP-1999.  
 PD  
 XX 13-MAR-1998; 98WO-US05039.  
 PF  
 XX 13-MAR-1998; 98WO-US05039.  
 PR  
 XX (EPIM-) EPIMMUNE INC.  
 PA  
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;  
 PI WPI; 1999-551214/46.  
 XX  
 DR New immunogenic peptides with HLA binding motif, useful in treatment  
 PT and diagnosis of cancers and viral diseases -  
 PT  
 XX Claim 1; Page 56; 150pp; English.  
 PS  
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 Db ||||  
 1 VMEV 4  
 RESULT 25  
 AAY46073  
 ID AAY46073 standard; Peptide; 11 AA.  
 XX  
 AC AAY46073;  
 XX

```

DT 01-DEC-1999 (first entry)
DE Immunogenic peptide having a human leukocyte antigen binding motif #684.
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX Synthetic.
XX Homo sapiens.
XX WO9945954-A1.
XX 16-SEP-1999.
XX 13-MAR-1998; 98WO-US05039.
XX 13-MAR-1998; 98WO-US05039.
XX 13-MAR-1998; 98WO-US05039.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX Claim 1; Page 55; 150pp; English.
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
XX Sequence 11 AA;
XX
XX Query Match 80.0%; Score 4; DB 20; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 31;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 VMEV 5
XX Db |||||
XX 7 VMEV 10
XX
XX RESULT 26
XX AAY47431
XX ID AAY47431 standard; Peptide; 11 AA.
XX AC AAY47431;
XX 01-DEC-1999 (first entry)
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #2169.
XX

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```

DE Immunogenic peptide having a human leukocyte antigen binding motif #2042.
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX Synthetic.
XX Homo sapiens.
XX WO9945954-A1.
XX 16-SEP-1999.
XX 13-MAR-1998; 98WO-US05039.
XX 13-MAR-1998; 98WO-US05039.
XX 13-MAR-1998; 98WO-US05039.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX Claim 1; Page 108; 150pp; English.
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX
XX Sequence 11 AA;
XX
XX Query Match 80.0%; Score 4; DB 20; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 31;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 VMEV 5
XX Db |||||
XX 8 VMEV 11
XX
XX RESULT 27
XX AAY47558
XX ID AAY47558 standard; Peptide; 11 AA.
XX AC AAY47558;
XX 01-DEC-1999 (first entry)
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #2169.
XX

```

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 XX vaccine; immunisation.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9945954-A1.  
 XX  
 XX 16-SEP-1999.  
 PD  
 XX  
 XX 13-MAR-1998; 98WO-US05039.  
 PF  
 XX 13-MAR-1998; 98WO-US05039.  
 PR  
 XX (EPIM-) EPIMUNE INC.  
 PA  
 PI Sette A, Kubo RT, Sidney J, Cellis E, Grey HM, Southwood S;  
 XX WPI; 1999-551214/46.  
 DR  
 XX New immunogenic peptides with HLA binding motif, useful in treatment  
 PT and diagnosis of cancers and viral diseases -  
 PT  
 XX Claim 1; Page 114; 150pp; English.  
 PS  
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VMEV 5  
 DB 8 VMEV 11  
 ||||  
 RESULT 28  
 AAB12653  
 ID AAB12653 standard; peptide; 11 AA.  
 XX  
 AC AAB12653;  
 XX  
 DT 13-NOV-2000 (first entry)  
 XX  
 DE Protein kinase peptide INSR human.  
 XX  
 KW Protein kinase; P38-gamma; crystallised P38 complex; structure;  
 KW Protein co-ordinate data; inhibitor; identification.

XX Homo sapiens.  
 OS WO200036096-A1.  
 XX  
 XX 22-JUN-2000.  
 PD  
 XX  
 XX 08-DEC-1999; 99WO-US29096.  
 PF  
 XX 16-DEC-1998; 98US-0112354.  
 PR  
 XX 03-NOV-1999; 99US-0163373.  
 XX  
 XX (VERT-) VERTEX PHARM INC.  
 PA  
 XX  
 XX Bellon S, Bemis G, Wilson K, Fitzgibbon M;  
 PI WPI; 2000-548618/50.  
 XX  
 DR  
 XX Crystallized protein-kinase ligand complexes and their structural  
 PT coordinates useful for designing and identifying protein kinase  
 PT inhibitors -  
 PT  
 XX Claim 5; Page 33; 179pp; English.  
 PS  
 XX The present invention describes crystallised protein-kinase ligand  
 CC complexes (especially P38-ligand complexes) and their structure  
 CC coordinates (SCs). The key structural features of the proteins,  
 CC especially the shape of the substrate binding site, are useful in  
 CC methods for designing and/or identifying selective inhibitors of  
 CC protein kinases and in solving the structures of other proteins with  
 CC similar features. The SCs may be displayed on a computer for graphical  
 CC 3 dimensional representation of the structure and for computer aided  
 CC molecular design of new inhibitors. The SCs are based on the structure  
 CC of the phosphorylated P38-gamma complex which has been solved and which  
 CC reveals new structural information useful for understanding the  
 CC activated states of other, related kinase proteins. The present sequence  
 CC represents a protein kinase peptide sequence which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 80.0%; Score 4; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVWE 4  
 DB 5 VVWE 8  
 ||||  
 RESULT 29  
 AAR83269  
 ID AAR83269 standard; peptide; 16 AA.  
 XX  
 AC AAR83269;  
 XX  
 DT 18-APR-1996 (first entry)  
 XX  
 DE HIV principal neutralisation epitope binding to 447 antibody.  
 XX  
 KW SPNE; selected principal neutralisation epitope; vaccine; HIV;  
 KW outer membrane proteosome; Neisseria; OMPC; AIDS; 447 antibody.  
 XX  
 OS Synthetic.  
 XX  
 XX GB2282378-A.  
 PN  
 XX 05-APR-1995.  
 PD  
 XX 23-SEP-1994; 94GB-0019253.  
 PF  
 XX 30-SEP-1993; 93US-0130111.  
 PR  
 XX

```

PA (MERI ) MERCK & CO INC.
XX
XX Arnold BA, Conley AJ, Keller PM, Shaw AR;
XX WPI; 1995-125265/17.
XX
XX New antigenic conjugate useful as vaccine for AIDS - comprising HIV
XX principal neutralisation epitope covalently linked to outer membrane
XX proteosome of Neisseria
XX
XX Claim 14; Page 8; 73pp; English.
XX
XX An antigenic conjugate, useful as a vaccine for AIDS, has the formula
XX (SPNE)n-(OMPC), where SPNE is a selected principal neutralisation
XX epitope of HIV, which is one of 27 specified polypeptides (including the
XX present sequence) or their fragments containing at least 5 amino acids
XX and including the GPCR loop region or its homologue; OMPC is purified
XX outer membrane proteosome of Neisseria (pref. N. meningitidis); and n
XX is 1-200, indicating the number of SPNE moieties covalently linked to
XX the OMPC. The conjugates may be substituted by anions, and conjugation
XX may be via a biogenic spacer. The SPNE polypeptides bind an HIV broadly
XX neutralising monoclonal antibody (447 antibody) in a competition assay
XX in the presence of natural HIV antigen such as gp120, and were
XX originally identified in the screening of phage epitope libraries having
XX randomly or semi-randomly generated epitope polypeptides accessible to
XX the antibody. The sequences of these polypeptides were deduced from
XX their corresponding DNA sequence, in turn determined by PCR.
XX
XX Sequence 16 AA;
XX
XX Query Match 80.0%; Score 4; DB 16; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 VMEV 5
XX ||||
XX Db 11 VMEV 14
XX
XX
XX RESULT 30
XX AAR15779
XX ID AAR15779 standard; Protein; 4 AA.
XX
XX AC AAR15779;
XX
XX DT 25-MAR-2003 (updated)
XX DT 09-JAN-2003 (updated)
XX DT 29-JAN-1992 (first entry)
XX
XX DE Farnesyl-protein transferase inhibitor (32).
XX
XX KW Farnesyl; transferase; FT; inhibitor; p21ras; rat.
XX
XX OS Synthetic.
XX
XX PN WO9116340-A.
XX
XX PD 31-OCT-1991.
XX
XX PF 18-APR-1991; 91WO-US02650.
XX
XX PR 20-NOV-1990; 90US-0615715.
XX PR 18-APR-1990; 90US-0510706.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Brown MS, Goldstein JL, Reiss Y;
XX
XX WPI; 1991-339750/46.
XX
XX Compsn. comprising purified farnesyl-protein transferase - used
XX to inhibit attachment of farnesyl moiety to RAS protein in
XX malignant cells and to treat cancer
XX
XX Claim 25; Page 68; 87pp; English.
XX
XX This peptide or the peptides represented in AAR15751-81, AAR14723 and
XX AAR14711 inhibit the rat FTs represented in AAR14712-22. They show FT
XX inhibition at an IC50 of 0.01-10 microm. The most potent inhibitors are
XX ones in which phenylalanine occurs at the third position of a
XX tetrapeptide whose N-terminus is cysteine. The inhibitors have a
XX farnesyl acceptor or inhibitor sequence within its structure and are
XX capable of inhibiting the farnesylation of p21ras by FT.
XX See also AAR14711-23 and AAQ14541-47.
XX (Updated on 09-JAN-2003 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 60.0%; Score 3; DB 12; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VVM 3
XX |||
XX Db 2 VVM 4
XX
XX
XX RESULT 31
XX AAR15650
XX ID AAR15650 standard; Protein; 4 AA.
XX
XX AC AAR15650;
XX
XX DT 25-MAR-2003 (updated)
XX DT 17-MAR-1992 (first entry)
XX
XX DE Ras protein inhibitor tetrapeptide.
XX
XX KW Plasma membrane; cancer; transformation.
XX
XX OS Synthetic.
XX
XX PN EP461869-A.
XX
XX PD 18-DEC-1991.
XX
XX PF 12-JUN-1991; 91EP-0305283.
XX
XX PR 17-MAY-1991; 91US-0700232.
XX PR 12-JUN-1990; 90US-0536840.
XX
XX PA (MERI ) MERCK & CO INC.
XX PA (GIBB/) GIBBS J B.
XX
XX PI Gibbs JB, Dixon RAF, Garsky VM, Schrabar MD;
XX
XX WPI; 1991-370840/51.
XX
XX New tetrapeptide inhibitors of Ras protein farnesylation -
XX prevent the transformation of normal cells into cancer cells
XX
XX Claim 5; Page 7; 7pp; English.
XX
XX The amino acid sequence is that of a tetrapeptide which inhibits
XX plasma membrane localisation and prevents transformation of normal
XX cells into cancer cells. It can also be used for inhibiting
XX farnesylation of Ras protein and is an inhibitor of farnesyl-protein
XX transferase. Admin. of the peptide not only decreases the amt. of
XX Ras in the membrane but also generates a cytosolic pool of Ras.
XX See also AAR15648 and AAR15649.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 60.0%; Score 3; DB 12; Length 4;

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```
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4

RESULT 32
AAR49744
ID AAR49744 standard; Peptide; 4 AA.
XX
AC AAR49744;
XX
DT 25-MAR-2003 (updated)
DT 08-AUG-1994 (first entry)
XX
DE Farnesyltransferase-inhibitor.
XX
KW Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
KW ras protein; farnesylation; cancer therapy.
XX
OS Synthetic.
XX
PN WO9404561-AL.
XX
PD 03-MAR-1994.
XX
PF 24-AUG-1993; 93WO-US08062.
XX
PR 24-AUG-1992; 92US-0935087.
XX
PA (GETH ) GENENTECH INC.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, Marsters JC, Reiss Y;
XX
DR WPI; 1994-083105/10.
XX
PT New farnesyl-transferase inhibitors - used for inhibiting
PT attachment of a farnesyl moiety to a p21ras protein in malignant
PT cells
XX
PS Disclosure; Page 33; 183pp; English.
XX
CC Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which
CC include a family of tetrapeptides based on the recognition site
CC (AAR49776) of farnesyltransferase (FT), are potential anticancer agents
CC that inhibit FT, thereby preventing expression of p21ras.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 4 AA;
Query Match 60.0%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4

RESULT 33
AAR77806
ID AAR77806 standard; Protein; 4 AA.
XX
AC AAR77806;
XX
DT 25-MAR-2003 (updated)
DT 23-JAN-1996 (first entry)
XX
DE Farnesyl transferase inhibitor tetrapeptide, CVWM.
XX

Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4

RESULT 34
AAW04436
ID AAW04436 standard; peptide; 4 AA.
XX
AC AAW04436;
XX
DT 30-JUL-1997 (first entry)
XX
DE Farnesyl transferase peptide inhibitor used in cancer treatment.
XX
KW Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification.
XX
OS Synthetic.
XX
PN WO9634113-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-US05969.
XX
PR 27-APR-1995; 95US-0429964.
XX

Farnesyl transferase; inhibitor; cancer; ras; p21.
Synthetic.
US5420245-A.
30-MAY-1995.
03-APR-1992; 92US-0863169.
16-JAN-1992; 92US-0822011.
18-APR-1990; 90US-0510706.
20-NOV-1990; 90US-0615715.
03-APR-1992; 92US-0863169.
(TEXA ) UNIV TEXAS.
Brown MS, Goldstein JL, Reiss Y;
WPI; 1995-206308/27.
New farnesyl transferase inhibitor peptide(s) - based on farnesyl
acceptor substrate carboxy terminal sequences, used for the
treatment of cancer
Claim 2; Column 61; 55pp; English.
AAR77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl
transferase. They all obey a generic formula for the C-terminal
sequence of 4-10 amino acid inhibitory peptides; the formula is
-CAAX, where C= cysteine, A= any aliphatic, aromatic or hydroxy
amino acid and X= any normal amino acid. Farnesyl transferase is
involved in the farnesylation of various cellular proteins
including the cancer related ras proteins. The transforming
activity of ras is dependent on the localisation of the protein
to membranes, a property which is thought to be dependent upon
the addition of farnesyl groups. The peptide inhibitors are
useful for treating cancers and ras-related cancers in particular.
(Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 4 AA;
Query Match 60.0%; Score 3; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Brown MS, Goldstein JL, James GL;  
 XX WPI; 1996-497642/49.  
 XX  
 PT Assay for farnesyl transferase activity - by determining ability to  
 PT transfer farnesyl moiety to K-Ras B protein, partic. useful for  
 PT identifying inhibitors  
 XX  
 XX Example 1; Page 33; 257pp; English.  
 XX  
 CC AA04433-W04465 are peptide inhibitors of farnesyl transferase (FT)  
 CC activity. The peptides block the attachment of prenyl groups to ras  
 CC proteins in malignant cells of patients suffering from cancer or a  
 CC precancerous state and as such are used to treat cancer. The peptides  
 CC were identified by determining the ability of candidate substances to  
 CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety  
 CC to a K-RasB protein.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 17; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVM 3  
 Db |||  
 2 VVM 4  
 RESULT 35  
 AAY18380  
 ID AAY18380 standard; peptide; 4 AA.  
 XX  
 AC AAY18380;  
 XX  
 DT 20-AUG-1999 (first entry)  
 XX  
 DE N-Ras geranylgeranylated CAAX motif.  
 XX  
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;  
 KW cancer; proliferative disorder; restenosis; hepatitis delta virus;  
 KW neurofibromin benign proliferative disorder; polycystic kidney disease;  
 KW fused azacyclic ring system; therapy; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9927928-A1.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 30-NOV-1998; 98WO-US25325.  
 XX  
 PR 06-APR-1998; 98GB-0007364.  
 PR 04-DEC-1997; 97US-0067552.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Ciccarone TM, Desolms SJ;  
 XX  
 XX WPI; 1999-394825/33.  
 XX  
 PT New bicyclic pyridine derivative peptide and peptidomimetic farnesyl  
 PT protein transferase inhibitors, used for treating cancer and other  
 PT proliferative disorders  
 XX  
 PS Disclosure; Page 62; 131pp; English.  
 XX  
 CC This sequence represents a CAAX motif.  
 CC The invention relates to peptides and peptidomimetics (I), containing a  
 CC bicyclic pyridine derivative ring system. The peptides and peptidomimetics (I), containing a

CC peptidomimetics can be used for treating cancer. (I) are also useful for  
 CC the treatment of other proliferative disorders, including neurofibromin  
 CC benign proliferative disorder, blindness related to retinal  
 CC vascularisation, infections by hepatitis delta and related viruses,  
 CC restenosis and polycystic kidney disease. They may also be useful in  
 CC treatment of fungal infections; and in qualitative and quantitative  
 CC assays for farnesyl protein transferase. (I) are selective, non-thiol,  
 CC farnesyl protein transferase inhibitors.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVM 3  
 Db |||  
 2 VVM 4  
 RESULT 36  
 AAY18367  
 ID AAY18367 standard; peptide; 4 AA.  
 XX  
 AC AAY18367;  
 XX  
 DT 20-AUG-1999 (first entry)  
 XX  
 DE N-Ras geranylgeranylated CAAX motif.  
 XX  
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;  
 KW cancer; proliferative disorder; restenosis; hepatitis delta virus;  
 KW neurofibromin benign proliferative disorder; polycystic kidney disease;  
 KW fused azacyclic ring system; therapy; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9927929-A1.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 30-NOV-1998; 98WO-US25324.  
 XX  
 PR 04-DEC-1997; 97US-0984732.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Halczenko W, Stump CA;  
 XX  
 DR WPI; 1999-394826/33.  
 XX  
 PT New fused aza-cyclic peptide and peptidomimetic compound farnesyl  
 PT protein transferase inhibitors, used for treating cancer and other  
 PT proliferative disorders  
 XX  
 PS Disclosure; Page 72; 141pp; English.  
 XX  
 CC This sequence represents a CAAX motif.  
 CC The invention relates to peptides and peptidomimetics (I), containing a  
 CC fused azacyclic ring system. The peptides and peptidomimetics can be used  
 CC for treating cancer. (I) are also useful for the treatment of other  
 CC proliferative disorders, including neurofibromin benign proliferative  
 CC disorder, blindness related to retinal vascularisation, infections by  
 CC hepatitis delta and related viruses, restenosis and polycystic kidney  
 CC disease. They may also be useful in treatment of fungal infections; and  
 CC in qualitative and quantitative assays for farnesyl protein transferase.  
 CC (I) are selective, non-thiol, farnesyl protein transferase inhibitors.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 Db |||  
 2 VVM 4

RESULT 37  
 AAY18350  
 ID AAY18350 standard; peptide; 4 AA.  
 AC AAY18350;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX  
 DE N-Ras geranylgeranylated CAAX motif.  
 XX  
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;  
 KW piperidine ring; homopiperidine ring; cancer; proliferative disorder;  
 KW neurofibromin benign proliferative disorder; hepatitis delta virus;  
 KW infection; polycystic kidney disease; restenosis; therapy.  
 OS Synthetic.  
 XX  
 PN WO9927933-A1.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 30-NOV-1998; 98WO-US25348.  
 XX  
 PR 04-DEC-1997; 97US-0985124.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Desolms SJ;  
 XX  
 DR WPI; 1999-385315/32.  
 XX  
 XX New piperidine or homopiperidine derivative peptide or  
 PT peptidomimetic compound farnesyl protein transferase inhibitors,  
 PT used for treating cancer and other proliferative disorders  
 XX  
 PS Disclosure; Page 79; 145pp; English.  
 XX  
 CC This sequence represents a CAAX motif.  
 CC The invention relates to peptides and peptidomimetics (I), containing a  
 CC piperidine or homopiperidine ring. The peptides and peptidomimetics can  
 CC be used for treating cancer. (I) are also useful for the treatment of  
 CC other proliferative disorders, including neurofibromin benign  
 CC proliferative disorder, blindness related to retinal vascularisation,  
 CC infections by hepatitis delta and related viruses, restenosis and  
 CC polycystic kidney disease. They may also be useful in treatment of fungal  
 CC infections; and in qualitative and quantitative assays for farnesyl  
 CC protein transferase.  
 XX  
 SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 Db |||  
 2 VVM 4

RESULT 38  
 AAY18337  
 ID AAY18337 standard; peptide; 4 AA.  
 AC AAY18337;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX

DE N-Ras geranylgeranylated CAAX motif.  
 XX  
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;  
 KW cancer; proliferative disorder; restenosis; hepatitis delta virus;  
 KW neurofibromin benign proliferative disorder; polycystic kidney disease;  
 KW tetrahydrobenzazepine ring system; therapy; tetrahydroisoquinoline;  
 KW infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9928314-A1.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 30-NOV-1998; 98WO-US25383.  
 XX  
 PR 04-DEC-1997; 97US-0985337.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Ciccarone TM, Desolms SJ;  
 XX  
 DR WPI; 1999-385349/32.  
 XX  
 XX New benzo-heterocyclic peptide and peptidomimetic compound farnesyl  
 PT protein transferase inhibitors, used for treating cancer and other  
 PT proliferative disorders  
 XX  
 PS Disclosure; Page 92; 184pp; English.  
 XX  
 CC This sequence represents a CAAX motif.  
 CC The invention relates to peptides and peptidomimetics (I), linked to a  
 CC tetrahydroisoquinoline or tetrahydrobenzazepine ring system. The peptides  
 CC and peptidomimetics can be used for treating cancer. (I) are also useful  
 CC for the treatment of other proliferative disorders, including  
 CC neurofibromin benign proliferative disorder, blindness related to retinal  
 CC vascularisation, infections by hepatitis delta and related viruses,  
 CC restenosis and polycystic kidney disease. They may also be useful in  
 CC treatment of fungal infections; and in qualitative and quantitative  
 CC assays for farnesyl protein transferase.  
 XX  
 SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 Db |||  
 2 VVM 4

RESULT 39  
 AAY18324  
 ID AAY18324 standard; peptide; 4 AA.  
 XX  
 AC AAY18324;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX  
 DE N-Ras geranylgeranylated CAAX motif.  
 XX  
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;  
 KW fused aza-bicyclic system; cancer; proliferative disorder; restenosis;  
 KW neurofibromin benign proliferative disorder; hepatitis delta virus;  
 KW infection; polycystic kidney disease; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9928313-A1.  
 XX  
 PD 10-JUN-1999.  
 XX

PF 30-NOV-1998; 98WO-US25352.  
XX  
PR 04-DEC-1997; 97US-0985320.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Ciccarone TM, Halczenko W, Hutchinson JH, Lumma WC;  
PI Stokker GE, Stump CA, Williams TM;  
XX WPI; 1999-385348/32.  
DR  
XX  
XX New aza-bicyclic peptide and peptidomimetic compound farnesyl  
PT protein transferase inhibitors, used for treating cancer or other  
PT proliferative disorders  
XX  
XX Disclosure; Page 85; 201pp; English.  
XX  
XX This sequence represents a CAAX motif.  
CC  
CC The invention relates to peptides and peptidomimetics (I), containing a  
CC fused aza-bicyclic system. The peptides and peptidomimetics can be used  
CC for treating cancer. (I) are also useful for the treatment of other  
CC proliferative disorders, including neurofibromin benign proliferative  
CC disorder, blindness related to retinal vascularisation, infections by  
CC hepatitis delta and related viruses, restenosis and polycystic kidney  
CC disease. They may also be useful in treatment of fungal infections; and  
CC in qualitative and quantitative assays for farnesyl protein transferase.  
XX  
XX  
SQ Sequence 4 AA;  
Query Match 60.0%; Score 3; DB 20; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VWM 3  
Db |||  
2 VWM 4  
  
RESULT 40  
AAV13426  
ID AAY13426 standard; peptide; 4 AA.  
XX  
AC AAY13426;  
XX  
XX 26-JUL-1999 (first entry)  
DT  
XX Human N-Ras peptide used in farnesyl-protein transferase assays.  
DE  
XX Diazabicyclo compound; farnesyl-protein transferase; Ffase; cancer;  
KW farnesylation; oncogene; Ras; chemotherapeutic agent; infection;  
KW neurofibromin benign proliferative disorder; blindness; hepatitis;  
KW retinal vascularisation; polycystic kidney disease; restenosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9920609-A1.  
PN  
XX 29-APR-1999.  
PD  
XX 13-OCT-1998; 98WO-US21599.  
PF  
XX 25-MAR-1998; 98GB-0006432.  
PR 17-OCT-1997; 97US-0064342.  
XX  
XX (MERI ) MERCK & CO INC.  
PA  
XX Bergman JM, Dinsmore C, Graham SL;  
PI WPI; 1999-326580/27.  
DR  
XX New diazabicyclo farnesyl-protein transferase inhibitors for  
PT treating e.g. cancer  
PT  
XX

PS Disclosure; Page 66; 138pp; English.  
XX  
XX The invention relates to diazabicyclo farnesyl-protein transferase  
CC (Ffase) inhibitors. The inhibitors are used for inhibiting Ffase and  
CC the farnesylation of the oncogene protein Ras. They are useful as  
CC chemotherapeutic agents for treating cancer, neurofibromin benign  
CC proliferative disorder, blindness related to retinal vascularisation,  
CC infections due to hepatitis delta and related viruses, polycystic kidney  
CC disease and for preventing restenosis.  
XX  
XX  
SQ Sequence 4 AA;  
Query Match 60.0%; Score 3; DB 20; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VWM 3  
Db |||  
2 VWM 4  
  
RESULT 41  
AAV17051  
ID AAY17051 standard; peptide; 4 AA.  
XX  
AC AAY17051;  
XX  
XX 20-JUL-1999 (first entry)  
DT  
XX Human N-Ras peptide used in farnesyl-protein transferase assays.  
DE  
XX Bicyclic compound; inhibitor; prenyl-protein transferase; prenylation;  
KW oncogene; Ras; tumour angiogenesis; vision deficit; oncogenic mutation;  
KW retinal vascularisation; proliferative disease; viral; fungal; infection;  
KW hepatitis infection; restenosis; polycystic kidney disease; assay;  
KW arteriosclerosis; diabetic vascular pathology.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9918096-A1.  
PN  
XX 15-APR-1999.  
PD  
XX 01-OCT-1998; 98WO-US20525.  
PF  
XX 14-APR-1998; 98GB-0007948.  
PR 02-OCT-1997; 97US-0060871.  
XX  
XX (MERI ) MERCK & CO INC.  
PA  
XX Desolms SJ, Lumma WC, Shaw AW, Sisko JT, Tucker TJ;  
PI WPI; 1999-312433/26.  
DR  
XX Novel chemotherapeutic bicyclic compounds  
PT  
XX  
XX Examples; Page 85; 178pp; English.  
PS  
XX The invention relates to novel bicyclic compounds that inhibit prenyl-  
CC protein transferase and the prenylation of the oncogene protein Ras.  
CC The bicyclic compounds may also inhibit tumour angiogenesis, thereby  
CC affecting the growth of tumours. They may also be useful in the treatment  
CC of certain forms of vision deficit related to retinal vascularisation.  
CC The compounds are also useful for inhibiting other proliferative  
CC diseases, both benign and malignant, in which Ras proteins are aberrantly  
CC activated as a result of oncogenic mutation in other genes. They may also  
CC be used in the treatment of certain viral infections, in particular in  
CC the treatment of hepatitis delta and related viruses. The compounds are  
CC useful in the prevention of restenosis after percutaneous transluminal  
CC coronary angioplasty by inhibiting neointimal formation. They may also be  
CC used in the treatment and prevention of polycystic kidney disease, fungal  
CC infections, arteriosclerosis and diabetic vascular pathologies.  
XX

SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3  
 Db 2 VWM 4  
 |||

RESULT 42  
 AAY02235  
 ID AAY02235 standard; peptide; 4 AA.  
 XX AC AAY02235;  
 DT 07-JUL-1999 (first entry)  
 XX DE "CAAXG" motif from human N-Ras protein.  
 XX KW CAAXG motif; prenyl-protein transferase; farnesylation;  
 KW oncogene protein Ras; tumour angiogenesis; tumour growth;  
 KW vision deficit; retinal vascularisation; proliferative disease;  
 KW oncogene mutation; viral infection; hepatitis delta; restenosis;  
 KW percutaneous transluminal coronary angioplasty; neointimal formation;  
 KW polycystic kidney disease; fungal infection; arteriosclerosis;  
 KW diabetic vascular pathology.  
 XX OS Homo sapiens.  
 XX FN WO991777-A1.  
 XX PD 15-APR-1999.  
 XX PF 07-OCT-1998; 98WO-US21063.  
 XX PR 08-OCT-1997; 97US-0062660.  
 XX PA (MERI ) MERCK & CO INC.  
 XX PI Ciccarone TM, Desolms SJ, Graham SL, Hutchinson JH;  
 PI Shaw AW;  
 XX DR WPI; 1999-277200/23.  
 XX PT New small molecule phenyl-containing compounds  
 XX PS Disclosure; Page 71; 200pp; English.  
 XX CC AAY02233-43 represent "CAAXG" motif from various human proteins. The  
 CC specification describes small molecule phenyl-containing compounds  
 CC which inhibit a prenyl-protein transferase and the farnesylation of  
 CC the oncogene protein Ras. The compounds inhibit tumour angiogenesis,  
 CC thereby affecting the growth of tumours. They may therefore be useful  
 CC in the treatment of certain forms of vision deficit related to  
 CC retinal vascularisation. The compounds are also useful for inhibiting  
 CC other proliferative diseases, both benign and malignant, in which Ras  
 CC proteins are aberrantly activated as a result of oncogenic mutation in  
 CC other genes, and for the treatment of certain viral infections,  
 CC particularly hepatitis delta and related viruses. The compounds are  
 CC also useful in the prevention of restenosis after percutaneous  
 CC transluminal coronary angioplasty by inhibiting neointimal formation.  
 CC The compounds may also be useful in the treatment and prevention of  
 CC polycystic kidney disease, fungal infections, arteriosclerosis and  
 CC diabetic vascular pathologies.

SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3  
 Db 2 VWM 4  
 |||

RESULT 43  
 AAW99755  
 ID AAW99755 standard; peptide; 4 AA.  
 XX AC AAW99755;  
 XX DT 03-JUN-1999 (first entry)  
 XX DE CAAX-G motif peptide N-Ras.  
 XX KW Cancer; prenyl-protein transferase inhibitor; GGTase-I; Ras protein;  
 KW geranylgeranyl-protein transferase type I; farnesyl-protein transferase;  
 KW proliferative disorder; benign; malignant; oncogenic mutation;  
 KW neurofibromatosis; restenosis; polycystic kidney disease; angiogenesis;  
 KW retinal vascularisation; arteriosclerosis; fungal infection;  
 KW diabetic vascular pathology.  
 XX OS Synthetic.  
 XX FN WO9910524-A1.  
 XX PD 04-MAR-1999.  
 XX PF 26-AUG-1998; 98WO-US17698.  
 XX PR 06-APR-1998; 98GB-0007361.  
 XX PR 27-AUG-1997; 97US-0057228.  
 XX PA (MERI ) MERCK & CO INC.  
 XX PI Burkhardt AL, Buser-Doepner CA, Huang PS, Kobian KS;  
 PI Kohl NE, Lobell RB;  
 XX DR WPI; 1999-204676/17.  
 XX PT Inhibition of prenyl-protein transferases, e.g. for cancer therapy  
 PT - using a compound which inhibits cellular processing of a protein  
 PT substrate of one or both of geranylgeranyl-protein transferase and  
 PT farnesyl-protein transferase  
 XX PS Disclosure; Page 9; 177pp; English.  
 XX CC A method has been developed for inhibiting prenyl-protein transferases,  
 CC for cancer therapy. The method uses a compound which inhibits cellular  
 CC processing of a protein substrate of one or both of geranylgeranyl-  
 CC protein transferase and farnesyl-protein transferase. Methods and  
 CC products from the present invention can be used for identifying  
 CC compounds for treating cancer and other proliferative disorders, both  
 CC benign and malignant, in which Ras proteins are aberrantly activated as a  
 CC result of oncogenic mutation in other genes. They can be used for e.g.  
 CC treating neurofibromatosis, preventing restenosis after percutaneous  
 CC transluminal coronary angioplasty by inhibiting neointimal formation,  
 CC preventing polycystic kidney disease, for inhibiting for inhibiting  
 CC angiogenesis in the treatment of certain forms of vision deficit related  
 CC to retinal vascularisation, in the treatment of hepatitis delta and  
 CC related viruses, in the prevention and therapy of arteriosclerosis and  
 CC diabetic vascular pathologies, and fungal infections. The dual FTP and  
 CC GPT-1 inhibitors can inhibit the growth of cancer cells at  
 CC concentrations that do not cause mechanism based toxicity in rapidly  
 CC proliferating tissues, e.g. bone marrow. The present sequence represents  
 CC a CAAX-G motif peptide for use in the method of the invention.

SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



CC transferase (FPPase), geranylgeranyl-protein transferase type I  
 CC (GGPase-I) and geranylgeranyl-protein transferase type II  
 CC (GGPase-II, also called Rab GGPase). Each of these enzymes  
 CC selectively uses farnesyl diphosphate (FPP) or geranyl geranyl  
 CC diphosphate as the isoprenoid donor and selectively recognises the  
 CC protein substrate. The therapeutic effect of the new treatment  
 CC method is treatment of cancer and comprises inhibition of cancerous  
 CC tumour growth and regression of cancerous tumours. The cancer is  
 CC especially related to cells that express enzymatically active PSA,  
 CC particularly prostate cancer. This peptide is a C-terminus motif  
 CC that is geranylated by geranylgeranyl-protein transferase type I.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 |||  
 Db 2 VVM 4  
 |||  
 RESULT 46  
 AAY92850  
 ID AAY92850 standard; peptide; 4 AA.  
 AC AAY92850;  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE C-terminus; H-ras; farnesylated; farnesyl-protein transferase;  
 KW inhibitor; CHAX-F motif; cytostatic; gynecological; endometriosis;  
 KW prenyl-protein transferase; geranyl-geranyl-protein transferase.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000025789-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 25-OCT-1999; 99WO-US25001.  
 XX  
 PR 29-OCT-1998; 98US-0106179.  
 PR 05-JAN-1999; 99GB-0000160.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Oliff AI, Gibbs JB;  
 XX  
 DR WPI; 2000-387113/33.  
 XX  
 PT Treating e.g. dysfunctional uterine bleeding and endometrial  
 PT hyperplasia comprises administration of a prenyl-protein transferase  
 PT inhibitor e.g. 2-(S)-butyl-1-(2,3-diaminoprop-1-yl)-1-(1-naphthoyl)-  
 PT piperazine  
 XX  
 PS Example 12; Page 5; 365pp; English.  
 XX  
 CC AAY92848-53 are C-terminal peptide motifs that are farnesylated by  
 CC farnesyl-protein transferase. Selective inhibitors of farnesyl-protein  
 CC transferase are characterized by an IC-50 of less than about 100 nM  
 CC against transfer of a farnesyl residue to a protein or peptide substrate  
 CC comprising a CHAX-F motif by farnesyl-protein transferase. Treating  
 CC endometriosis, uterine fibroids, dysfunctional uterine bleeding and  
 CC endometrial hyperplasia comprises administration of a prenyl-protein  
 CC transferase inhibitor and optionally a HMG-CoA reductase inhibitor or an  
 CC anti-hormonal compound, a GnRH antagonist compound a GnRH agonist  
 CC compound, an anti-estrogen compound, an anti-progesterone compound or a  
 CC selective oestrogen receptor modulator and a prenyl-protein transferase  
 CC inhibitor.

XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 |||  
 Db 2 VVM 4  
 |||  
 RESULT 47  
 AAB34980  
 ID AAB34980 standard; Peptide; 4 AA.  
 XX  
 AC AAB34980;  
 XX  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE Chimpanzee erythropoietin fragment SEQ ID NO: 6.  
 XX  
 KW Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;  
 KW mapping; therapeutic agent.  
 XX  
 OS Pan sp.  
 XX  
 PN WO2000068376-A1.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PF 05-MAY-2000; 2000WO-US12370.  
 XX  
 PR 07-MAY-1999; 99US-0307307.  
 PR 28-MAR-2000; 2000US-0307307.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Desauvage F, Henner DJ;  
 XX  
 DR WPI; 2001-007393/01.  
 XX  
 PT Nucleic acids encoding chimpanzee erythropoietin, useful for treatment  
 PT of e.g. anemia, also derived proteins, antibodies and modulators -  
 XX  
 PS Disclosure; Page 7; 109pp; English.  
 XX  
 CC The present invention provides the coding and protein sequences of  
 CC chimpanzee erythropoietin (EPO). These sequences can be used in gene  
 CC therapy, to block the activity of EPO, as hybridisation probes, in  
 CC genetic and chromosome mapping and as therapeutic agents.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 |||  
 Db 1 MEV 3  
 |||  
 RESULT 48  
 AAE29301  
 ID AAE29301 standard; peptide; 4 AA.  
 XX  
 AC AAE29301;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE Chimpanzee erythropoietin (CHEPO) peptide #1.  
 XX

KW Chimpanzee; erythropoietin; gene therapy; blood disorder; immunoadhesin;  
 KW chromosome identification; tissue typing; antianemic; CHEFO.  
 XX  
 OS Pan troglodytes.  
 XX  
 PN WO200274807-A2.  
 XX  
 XX 26-SEP-2002.  
 XX  
 PF 14-FEB-2002; 2002WO-US04773.  
 XX  
 PR 20-MAR-2001; 2001US-0813775.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Desauvage F, Henner DJ;  
 PI  
 XX NPI; 2002-759880/82.  
 DR  
 XX  
 XX New immunoadhesin comprising a chimpanzee erythropoietin (CHEPO)  
 PT polypeptide, useful for the treatment of blood disorders with low or  
 PT defective red blood cell production -  
 XX  
 PS Disclosure; Page 100; 120pp; English.  
 XX  
 CC The invention relates to immunoadhesins comprising chimpanzee  
 CC erythropoietin (CHEPO) polypeptide. The invention further relates to  
 CC methods using and compositions comprising CHEPO immunoadhesins. The  
 CC methods and compositions of the present invention are useful for the  
 CC treatment of blood disorders characterised by low or defective red  
 CC blood cell production. The CHEPO polypeptides may also be used as  
 CC molecular weight markers, tissue typing and chromosome identification.  
 CC CHEPO DNA is used in gene therapy. The present sequence is chimpanzee  
 CC erythropoietin peptide.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 DB ||||  
 1 MEV 3  
 RESULT 49  
 AAR82999  
 ID AAR82999 standard; peptide; 5 AA.  
 AC AAR82999;  
 XX  
 DT 02-MAY-1996 (first entry)  
 XX  
 DE M. prolifera fucose contg. proteoglycan trypsin digest peptide.  
 XX  
 KW Proteoglycan; trypsin digest; marine sponge; fucose;  
 KW immunostimulants; cancer; viral infection; natural killer; cells;  
 KW gamma/delta-T; metastases; retro-viral; immunosuppressants.  
 XX  
 XX Microciona prolifera.  
 OS  
 XX WO9525745-A1.  
 PN  
 XX 28-SEP-1995.  
 PD  
 XX 24-MAR-1995; 95WO-IB00208.  
 PF  
 XX 24-MAR-1994; 94GB-0005846.  
 PR  
 XX (MISE/) MISEVIC G.  
 PA  
 XX Misevic G;  
 PI

XX  
 DR WPI; 1995-344588/44.  
 XX  
 PT Fucose contg. proteoglycan and acidic glycan cpds - with  
 PT immunostimulating activity, partic for treating cancer and viral  
 PT infections, includes new cpds isolated from sponges and sea  
 PT urchin(s)  
 XX  
 XX Example 1; Page 8; 27pp; English.  
 PS  
 XX M. prolifera (a marine sponge) derived fucose contg. proteoglycans  
 CC (PGs) have the trypsin digest protein backbone peptides AAR82999-03.  
 CC The PGs stimulate the proliferation of natural killer (NK) and/or  
 CC gamma/delta-T cells, useful in the treatment of cancer, esp.  
 CC metastases and (retro)viral infections, they may also be used to  
 CC screen for immunosuppressant cpds.. Monovalent forms of the PGs  
 CC inhibit the activation of NK and gamma/delta-T cells, and are  
 CC therefore useful as immunosuppressants.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 DB ||||  
 2 VVM 4  
 RESULT 50  
 AAR69999  
 ID AAR69999 standard; Protein; 5 AA.  
 XX  
 AC AAR69999;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 21-OCT-1995 (first entry)  
 XX  
 DE High affinity Ige receptor beta-subunit variant.  
 XX  
 KW Ige receptor; mutation; polymorphism; atopy diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 2 /note= "Ile-181 in wt"  
 FT  
 XX  
 PN WO9505481-A1.  
 XX  
 XX 23-FEB-1995.  
 PD  
 XX  
 PF 17-AUG-1994; 94WO-GB01801.  
 XX  
 PR 18-AUG-1993; 93GB-0017185.  
 PR 27-MAY-1994; 94GB-0010669.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX  
 XX Cookson WOCM, Hopkin JM, Shirakawa T;  
 PI  
 XX WPI; 1995-098778/13.  
 DR N-PSDB; AAQ80599.  
 XX  
 PT Diagnostic method for atopy - comprises detecting presence of  
 PT mutation or polymorphism in gene encoding beta-subunit of high  
 PT affinity Igs receptor.  
 XX  
 PS Claim 4; Page 33; 48pp; English.  
 XX  
 CC The sequence corresponds to mutant high affinity Ige receptor  
 CC (180-184). The mutation at AA 181 arises from mutations

CC in exon 6 of the gene found on chromosome-11q. The mutations  
 CC can be detected in a method for the diagnosis of atopy or  
 CC predisposition to atopy.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
 ||||  
 Db 3 VVM 5

RESULT 51

AAR70276  
 ID AAR70276 standard; peptide; 5 AA.

XX  
 AC AAR70276;

XX  
 DT 14-NOV-1995 (first entry)

XX VVM-containing peptide, non-thrombospondin binding.

XX Thrombospondin 1; TSI; receptor; inactive; cell-adhesion.

XX Synthetic.

XX US5399667-A.

XX 21-MAR-1995.

XX 05-MAR-1993; 93US-0029333.

XX 05-MAR-1993; 93US-0029333.

XX (UNIW ) UNIV WASHINGTON.

XX Frazier WA, Kosfeld MD;

XX WPI; 1995-130736/17.

XX Thrombospondin receptor binding peptide(s) - comprise tri:peptide  
 sequence Val-Val-Met (VVM)

XX Example 1; Column 8; 25pp; English.

XX AAR70276-78 are synthetic peptides containing the tri-peptide VVM which  
 CC are incapable of binding to the thrombospondin 1 (TS1) receptor cell-  
 CC binding domain (CBD).

XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
 ||||  
 Db 3 VVM 5

RESULT 52

AAR70277  
 ID AAR70277 standard; peptide; 5 AA.

XX  
 AC AAR70277;

XX 14-NOV-1995 (first entry)

XX VVM-containing peptide, non-thrombospondin binding.

XX Thrombospondin 1; TSI; receptor; inactive; cell-adhesion.  
 XX Synthetic.  
 XX US5399667-A.  
 XX 21-MAR-1995.  
 XX 05-MAR-1993; 93US-0029333.  
 XX 05-MAR-1993; 93US-0029333.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Frazier WA, Kosfeld MD;  
 XX WPI; 1995-130736/17.  
 XX Thrombospondin receptor binding peptide(s) - comprise tri:peptide  
 sequence Val-Val-Met (VVM)  
 XX Example 1; Column 8; 25pp; English.  
 XX AAR70276-78 are synthetic peptides containing the tri-peptide VVM which  
 CC are incapable of binding to the thrombospondin 1 (TS1) receptor cell-  
 CC binding domain (CBD).

XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
 ||||  
 Db 3 VVM 5

RESULT 53

AAR70275  
 ID AAR70275 standard; peptide; 5 AA.

XX  
 AC AAR70275;

XX 14-NOV-1995 (first entry)

XX Thrombospondin 1 (TS1) receptor binding peptide.

XX Thrombospondin 1; TSI; receptor; inhibition; cell-adhesion.

XX Synthetic.

XX US5399667-A.

XX 21-MAR-1995.

XX 05-MAR-1993; 93US-0029333.

XX 05-MAR-1993; 93US-0029333.

XX (UNIW ) UNIV WASHINGTON.

XX Frazier WA, Kosfeld MD;

XX WPI; 1995-130736/17.

XX Thrombospondin receptor binding peptide(s) - comprise tri:peptide  
 sequence Val-Val-Met (VVM)

XX Claim 1; Column 29; 25pp; English.

XX AAR70271-75 are synthetic peptides containing the tri-peptide VVM which



CC are capable of binding to the thrombospondin 1 (TSP1) receptor cell-  
 CC binding domain (CBD). These peptides are useful in preventing cell-  
 CC adhesion of several normal and transformed cell lines.

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 |||  
 Db 3 VVM 5

RESULT 54

AAW05024  
 ID AAW05024 standard; peptide; 5 AA.

AC AAW05024;

DT 03-DEC-1996 (first entry)

XX Thrombospondin-derived, homotypic platelet aggregation inducer #17.  
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;  
 KW antagonist; RGD peptide; thrombus formation; receptor binding.

XX Synthetic.

XX WO9611942-A1.

XX 25-APR-1996.

XX 17-OCT-1995; 95WO-AU006683.

XX 18-OCT-1994; 94AU-0008858.

XX (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.

XX Burns GF;

XX WPI; 1996-221937/22.

XX Identifying platelet aggregation antagonists - using  
 PT thrombospondin-derived octa-peptide or its mutants, derivatives or  
 PT modified forms, some of which are new

PS Claim 4; Page 24; 38pp; English.

CC A peptide derived from the region of thrombospondin (TSP) which  
 CC binds to the carboxy terminal receptor on platelets and which induces  
 CC homotypic platelet aggregation even in the presence of RGD peptides  
 CC or their mimetics has been identified previously. The peptide has  
 CC the sequence RFYVVMWK and was disclosed by Kosfeld and Frazier in  
 CC J.Biol.Chem.268:8808-8814 (1993) where it was designated "peptide  
 CC 4N1-1". Peptides able to induce homotypic platelet aggregation and  
 CC which differ by at least 1 amino acid from the sequence of peptide  
 CC 4N1-1 are claimed. The present peptide is a preferred example.

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 17; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 |||  
 Db 1 VVM 3

RESULT 55

AAW87390

ID AAW87390 standard; peptide; 5 AA.

AC AAW87390;

XX 09-FEB-1999 (first entry)

XX Peptide determined by the method of the invention.

XX Amino acid determination; molecular mass; fragmentation spectrum;  
 KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.

XX Synthetic.

XX GB2325465-A.

XX 25-NOV-1998.

XX 22-MAY-1998; 98GB-0011196.

XX 22-MAY-1997; 97GB-0010582.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Parekh RB, Prime SB, Townsend RR, Wedd NS;

XX WPI; 1998-571195/49.

XX Peptide sequence determination used in e.g. DNA cloning - by  
 PT comparing mass spectra of the unknown peptide with a library of  
 PT linear chain known peptide sequences

XX Example 3; Page 24; 40pp; English.

XX The invention relates to a method for determination of the amino acid  
 CC sequence of an unknown peptide. The method comprises (a) determining  
 CC the molecular mass and an experimental fragmentation spectrum for the  
 CC peptide; (b) comparing the experimental fragmentation spectrum of the  
 CC unknown peptide with a theoretical fragmentation spectra calculated for  
 CC a peptide library composed of all possible linear sequences of amino  
 CC acids having a total mass that corresponds to the molecular mass of the  
 CC unknown peptide; and (c) identifying a peptide in the library with a  
 CC theoretical fragmentation spectrum that most closely matches the  
 CC fragmentation spectrum of the unknown peptide. The method is useful in  
 CC DNA cloning, anti-body production, identification of recombinant  
 CC products, and the study of post-translational modifications. It allows  
 CC the sequence of unknown peptides or proteins with no sub-sequences  
 CC identity, to be characterised using mass spectrometry. Sequences  
 CC AAW87377 to AAW87444 represent linear peptides constructed to exemplify  
 CC the method.

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 |||  
 Db 3 VVM 5

RESULT 56

AAU85931

ID AAU85931 standard; peptide; 5 AA.

AC AAU85931;

XX 08-MAY-2002 (first entry)

XX Peptide #56 for use in cell culture media.

XX Cell-growth affecting peptide; cellular protein production;  
 KW bacterial cell growth; Clostridium perfringens; beta-toxin;

KW cell culture media; rapid identification of biologically active compound;  
 KW peptide library; concatamer-based recombinant expression method;  
 XX large-scale recombinant production method; antibacterial.  
 OS Synthetic.  
 XX WO200202591-A2.  
 PN 10-JAN-2002.  
 XX 04-JUN-2001; 2001WO-US17943.  
 XX 30-JUN-2000; 2000US-0608892.  
 XX (BECT ) BECTON DICKINSON & CO.  
 XX Haaland PD, Sherman DB, Campbell RL, Stewart WW, Lloyd SA;  
 PI Erickson BW;  
 XX WPI; 2002-195744/25.  
 DR Novel synthetic peptides which include cell-growth affecting peptides  
 PT and peptides which enhance or inhibit cellular protein production.  
 PT useful for enhancing or inhibiting cell growth or cellular protein  
 PT production -  
 XX Claim 1; Page 9; 4lpp; English.  
 XX The present invention relates to synthetic peptides which include  
 CC cell-growth affecting peptides and peptides which enhance or inhibit  
 CC cellular protein production. The peptides of the invention are useful  
 CC for enhancing or inhibiting cell growth of bacteria, particularly  
 CC Clostridium perfringens, or cellular protein production of beta-toxins,  
 CC in cell culture. They are also useful in a peptide library for the rapid  
 CC identification of biologically active compounds which affect the  
 CC properties of cells in culture media. The peptide can be used in  
 CC concatamer-based recombinant expression methods or in large-scale,  
 CC economical recombinant production methods. The peptides reduce the  
 CC number and quantity of undefined components in culture media, reduce  
 CC the need for animal-derived components, improve media consistency and  
 CC quality control, and provide a method for precisely controlling and  
 CC adjusting the performance of the cell culture.  
 CC AAU85876-AAU85969 represent the synthetic peptides of the invention.  
 XX  
 XX SQ Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 VME 4  
 Db |||  
 2 VME 4  
 RESULT 57  
 ABUS7836  
 ID ABUS7836 standard; Peptide; 5 AA.  
 AC  
 XX ABUS7836;  
 XX 10-APR-2003 (first entry)  
 XX Thrombospondin 1 receptor cell binding domain peptide C7.  
 XX Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;  
 KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.  
 XX Homo sapiens.  
 OS Mus sp.  
 XX US6469138-B1.  
 PN  
 XX

PD 22-OCT-2002.  
 XX 21-FEB-1995; 95US-0391820.  
 XX 05-MAR-1993; 93US-0029333.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Frazier WA, Kosfeld MD;  
 XX WPI; 2003-196751/19.  
 XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe  
 PT sequence in computer search of all available databases -  
 XX Examples; Column 7; 25pp; English.  
 XX This invention relates to a novel peptide that binds to the  
 CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which  
 CC acts to promote cell adhesion and is involved in platelet aggregation,  
 CC wound healing and tumour cell migration. Also disclosed in the  
 CC invention is Laminin peptides which have been shown to be able to  
 CC substitute for TS-1 peptides. Preferably the peptides of  
 CC the invention share a tripeptide motif VVM and are useful as probe  
 CC sequences in a computer search of all available databases for  
 CC similar receptor binding motif peptides. The present sequence  
 CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain  
 CC peptide of the invention.  
 XX SQ Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 24; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVM 3  
 Db |||  
 3 VVM 5  
 RESULT 58  
 ABUS7837  
 ID ABUS7837 standard; Peptide; 5 AA.  
 AC  
 XX ABUS7837;  
 XX 10-APR-2003 (first entry)  
 XX Thrombospondin 1 cell binding domain peptide #1.  
 XX Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;  
 KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.  
 XX Synthetic.  
 OS  
 XX US6469138-B1.  
 XX 22-OCT-2002.  
 XX 21-FEB-1995; 95US-0391820.  
 XX 05-MAR-1993; 93US-0029333.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Frazier WA, Kosfeld MD;  
 XX WPI; 2003-196751/19.  
 XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe  
 PT sequence in computer search of all available databases -  
 XX Examples; Column 8; 25pp; English.  
 PS

XX This invention relates to a novel peptide that binds to the  
CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which  
CC acts to promote cell adhesion and is involved in platelet aggregation,  
CC wound healing and tumour cell migration. Also disclosed in the  
CC invention is laminin peptides which have been shown to be able to  
CC substitute for TS-1 peptides. Preferably the peptides of  
CC the invention share a tripeptide motif VVM and are useful as probe  
CC sequences in a computer search of all available databases for  
CC similar receptor binding motif peptides. The present sequence  
CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain  
CC peptide of the invention.  
XX SQ Sequence 5 AA;  
XX  
XX Query Match 60.0%; Score 3; DB 24; Length 5;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 VVM 3  
XX |||  
XX Db 3 VVM 5  
XX  
XX RESULT 59  
XX ABUS7838  
XX ID ABUS7838 standard; Peptide; 5 AA.  
XX AC ABUS7838;  
XX XX  
XX DT 10-APR-2003 (first entry)  
XX XX  
XX DE Thrombospondin 1 cell binding domain peptide 7N3-1.  
XX KW Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;  
XX KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.  
XX OS Synthetic.  
XX XX  
XX FN US6469138-B1.  
XX XX  
XX PD 22-OCT-2002.  
XX XX  
XX PF 21-FEB-1995; 95US-0391820.  
XX XX  
XX PR 05-MAR-1993; 93US-0029333.  
XX XX  
XX PA (UNIW ) UNIV WASHINGTON.  
XX XX  
XX PI Frazier WA, Kosfeld MD;  
XX XX  
XX DR WPI; 2003-196751/19.  
XX XX  
XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe  
XX sequence in computer search of all available databases -  
XX  
XX Examples; Column 8; 25pp; English.  
XX  
XX This invention relates to a novel peptide that binds to the  
XX thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which  
XX acts to promote cell adhesion and is involved in platelet aggregation,  
XX wound healing and tumour cell migration. Also disclosed in the  
XX invention is laminin peptides which have been shown to be able to  
XX substitute for TS-1 peptides. Preferably the peptides of  
XX the invention share a tripeptide motif VVM and are useful as probe  
XX sequences in a computer search of all available databases for  
XX similar receptor binding motif peptides. The present sequence  
XX represents a thrombospondin-1 (TS-1) or Laminin cell binding domain  
XX peptide of the invention.  
XX SQ Sequence 5 AA;  
XX  
XX Query Match 60.0%; Score 3; DB 24; Length 5;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 VVM 3  
XX |||  
XX Db 3 VVM 5  
XX  
XX RESULT 60  
XX AAR70272  
XX ID AAR70272 standard; peptide; 6 AA.  
XX XX  
XX AC AAR70272;  
XX XX  
XX DT 14-NOV-1995 (first entry)  
XX XX  
XX DE Thrombospondin 1 (TS1) receptor binding peptide.  
XX KW Thrombospondin 1; TS1; receptor; inhibition; cell-adhesion.  
XX OS Synthetic.  
XX XX  
XX PN US5399667-A.  
XX XX  
XX PD 21-MAR-1995.  
XX XX  
XX PF 05-MAR-1993; 93US-0029333.  
XX XX  
XX PR 05-MAR-1993; 93US-0029333.  
XX XX  
XX PA (UNIW ) UNIV WASHINGTON.  
XX XX  
XX PI Frazier WA, Kosfeld MD;  
XX XX  
XX DR WPI; 1995-130736/17.  
XX XX  
XX PT Thrombospondin receptor binding peptide(s) - comprise tri:peptide  
XX sequence Val-Val-Met (VVM)  
XX XX  
XX Claim 1; Column 29; 25pp; English.  
XX XX  
XX AAR70271-75 are synthetic peptides containing the tri-peptide VVM which  
XX are capable of binding to the thrombospondin 1 (TS1) receptor cell-  
XX binding domain (CBD). These peptides are useful in preventing cell-  
XX adhesion of several normal and transformed cell lines.  
XX SQ Sequence 6 AA;  
XX  
XX Query Match 60.0%; Score 3; DB 16; Length 6;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 VVM 3  
XX |||  
XX Db 4 VVM 6  
XX  
XX RESULT 61  
XX AAR77518  
XX ID AAR77518 standard; Peptide; 6 AA.  
XX XX  
XX AC AAR77518;  
XX XX  
XX DT 27-MAR-1996 (first entry)  
XX XX  
XX DE Cytochrome-P450-lpr N-terminal peptide.  
XX KW Cytochrome P450-lpr; P450-monoxygenase; insecticide;  
XX KW biological control; pesticide degradation; bioremediation;  
XX KW transgenic plant; crop improvement; insect resistance; housefly;  
XX KW PCR; primer; polymerase chain reaction.  
XX OS Musca domestica Learn-PyR.

Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVM 3  
|||  
Db 3 VVM 5  
RESULT 60  
AAR70272  
ID AAR70272 standard; peptide; 6 AA.  
XX  
XX AC AAR70272;  
XX  
XX DT 14-NOV-1995 (first entry)  
XX  
XX DE Thrombospondin 1 (TS1) receptor binding peptide.  
XX KW Thrombospondin 1; TS1; receptor; inhibition; cell-adhesion.  
XX OS Synthetic.  
XX  
XX PN US5399667-A.  
XX  
XX PD 21-MAR-1995.  
XX  
XX PF 05-MAR-1993; 93US-0029333.  
XX  
XX PR 05-MAR-1993; 93US-0029333.  
XX  
XX PA (UNIW ) UNIV WASHINGTON.  
XX  
XX PI Frazier WA, Kosfeld MD;  
XX  
XX DR WPI; 1995-130736/17.  
XX  
XX PT Thrombospondin receptor binding peptide(s) - comprise tri:peptide  
XX sequence Val-Val-Met (VVM)  
XX  
XX Claim 1; Column 29; 25pp; English.  
XX  
XX AAR70271-75 are synthetic peptides containing the tri-peptide VVM which  
XX are capable of binding to the thrombospondin 1 (TS1) receptor cell-  
XX binding domain (CBD). These peptides are useful in preventing cell-  
XX adhesion of several normal and transformed cell lines.  
XX SQ Sequence 6 AA;  
XX  
XX Query Match 60.0%; Score 3; DB 16; Length 6;  
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 VVM 3  
XX |||  
XX Db 4 VVM 6  
XX  
XX RESULT 61  
XX AAR77518  
XX ID AAR77518 standard; Peptide; 6 AA.  
XX  
XX AC AAR77518;  
XX  
XX DT 27-MAR-1996 (first entry)  
XX  
XX DE Cytochrome-P450-lpr N-terminal peptide.  
XX KW Cytochrome P450-lpr; P450-monoxygenase; insecticide;  
XX KW biological control; pesticide degradation; bioremediation;  
XX KW transgenic plant; crop improvement; insect resistance; housefly;  
XX KW PCR; primer; polymerase chain reaction.  
XX OS Musca domestica Learn-PyR.

XX WO9530745-A1.  
 XX 16-NOV-1995.  
 XX 08-MAY-1995; 95WO-US05758.  
 XX 10-MAY-1994; 94US-0241388.  
 XX (CORR ) CORNELL RES FOUND INC.  
 XX Scott JG, Tomita T;  
 XX WPI; 1995-404112/51.  
 DR N-PSDB; AAT05519.  
 XX DNA encoding cytochrome P450-lpr - used for insect control,  
 PT bioremediation of insecticides or reducing crop sensitivity to  
 PT pesticides  
 XX  
 PS Example 8; Page 30; 87pp; English.  
 XX A peptide (AAR77518) corresponding to a fragment of housefly cytochrome  
 CC P450-lpr was used to design degenerate primer AS3 (AAT05519), used for  
 CC the PCR amplification of internal sequences of P450-lpr cDNA.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 16; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VME 4  
 DB 2 VME 4  
 RESULT 62  
 AAW05018  
 ID AAW05018 standard; peptide; 6 AA.  
 XX  
 AC AAW05018;  
 XX  
 DT 03-DEC-1996 (first entry)  
 XX  
 DE Thrombospondin-derived, homotypic platelet aggregation inducer #9.  
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;  
 KW antagonist; RGD peptide; thrombus formation; receptor binding.  
 XX  
 CS Synthetic.  
 XX  
 XX WO9611942-A1.  
 PN  
 PD 25-APR-1996.  
 XX  
 PF 17-OCT-1995; 95WO-AU00683.  
 XX  
 PR 18-OCT-1994; 94AU-0008858.  
 XX  
 PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.  
 XX  
 PI Burns GF;  
 XX  
 DR WPI; 1996-221937/22.  
 XX  
 PT Identifying platelet aggregation antagonists - using  
 PT thrombospondin-derived octa-peptide or its mutants, derivatives or  
 PT modified forms, some of which are new  
 XX  
 PS Claim 3; Page 24; 38pp; English.  
 XX  
 XX A peptide derived from the region of thrombospondin (TSP) which  
 binds to the carboxy terminal receptor on platelets and which induces  
 homotypic platelet aggregation even in the presence of RGD peptides  
 or their mimetics has been identified previously. The peptide has  
 the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in  
 J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide  
 4N1-1". Peptides able to induce homotypic platelet aggregation and  
 CC which differ by at least 1 amino acid from the sequence of peptide  
 CC 4N1-1 are claimed. The present peptide is a preferred example.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 DB 4 VVM 6  
 RESULT 63  
 AAW05022  
 ID AAW05022 standard; peptide; 6 AA.  
 XX  
 AC AAW05022;  
 XX  
 DT 03-DEC-1996 (first entry)  
 XX  
 DE Thrombospondin-derived, homotypic platelet aggregation inducer #13.  
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;  
 KW antagonist; RGD peptide; thrombus formation; receptor binding.  
 XX  
 CS Synthetic.  
 XX  
 XX WO9611942-A1.  
 PN  
 PD 25-APR-1996.  
 XX  
 PF 17-OCT-1995; 95WO-AU00683.  
 XX  
 PR 18-OCT-1994; 94AU-0008858.  
 XX  
 PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.  
 XX  
 PI Burns GF;  
 XX  
 DR WPI; 1996-221937/22.  
 XX  
 PT Identifying platelet aggregation antagonists - using  
 PT thrombospondin-derived octa-peptide or its mutants, derivatives or  
 PT modified forms, some of which are new  
 XX  
 PS Claim 3; Page 24; 38pp; English.  
 XX  
 XX A peptide derived from the region of thrombospondin (TSP) which  
 binds to the carboxy terminal receptor on platelets and which induces  
 homotypic platelet aggregation even in the presence of RGD peptides  
 or their mimetics has been identified previously. The peptide has  
 the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in  
 J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide  
 4N1-1". Peptides able to induce homotypic platelet aggregation and  
 CC which differ by at least 1 amino acid from the sequence of peptide  
 CC 4N1-1 are claimed. The present peptide is a preferred example.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 DB 4 VVM 6

CC binds to the carboxy terminal receptor on platelets and which induces  
 CC homotypic platelet aggregation even in the presence of RGD peptides  
 CC or their mimetics has been identified previously. The peptide has  
 CC the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in  
 CC J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide  
 CC 4N1-1". Peptides able to induce homotypic platelet aggregation and  
 CC which differ by at least 1 amino acid from the sequence of peptide  
 CC 4N1-1 are claimed. The present peptide is a preferred example.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 DB 4 VVM 6  
 RESULT 63  
 AAW05022  
 ID AAW05022 standard; peptide; 6 AA.  
 XX  
 AC AAW05022;  
 XX  
 DT 03-DEC-1996 (first entry)  
 XX  
 DE Thrombospondin-derived, homotypic platelet aggregation inducer #13.  
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;  
 KW antagonist; RGD peptide; thrombus formation; receptor binding.  
 XX  
 CS Synthetic.  
 XX  
 XX WO9611942-A1.  
 PN  
 PD 25-APR-1996.  
 XX  
 PF 17-OCT-1995; 95WO-AU00683.  
 XX  
 PR 18-OCT-1994; 94AU-0008858.  
 XX  
 PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.  
 XX  
 PI Burns GF;  
 XX  
 DR WPI; 1996-221937/22.  
 XX  
 PT Identifying platelet aggregation antagonists - using  
 PT thrombospondin-derived octa-peptide or its mutants, derivatives or  
 PT modified forms, some of which are new  
 XX  
 PS Claim 3; Page 24; 38pp; English.  
 XX  
 XX A peptide derived from the region of thrombospondin (TSP) which  
 binds to the carboxy terminal receptor on platelets and which induces  
 CC homotypic platelet aggregation even in the presence of RGD peptides  
 CC or their mimetics has been identified previously. The peptide has  
 CC the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in  
 CC J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide  
 CC 4N1-1". Peptides able to induce homotypic platelet aggregation and  
 CC which differ by at least 1 amino acid from the sequence of peptide  
 CC 4N1-1 are claimed. The present peptide is a preferred example.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVM 3  
 DB 4 VVM 6

```

Db      .      2 VVM 4

RESULT 64
AAW05023
ID AAW05023 standard; peptide; 6 AA.
XX
AC AAW05023;
XX
DT 03-DEC-1996 (first entry)
XX
DE Thrombospondin-derived, homotypic platelet aggregation inducer #14.
XX
KW Thrombospondin; TSP; platelet aggregation; induction; activation;
KW antagonist; RGD peptide; thrombus formation; receptor binding.
XX
OS Synthetic.
XX
PN WO9611942-A1.
XX
PD 25-APR-1996.
XX
PF 17-OCT-1995; 95WO-AU00683.
XX
PR 18-OCT-1994; 94AU-0008858.
XX
PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
XX
PI Burns GF;
XX
DR WPI; 1996-221937/22.
XX
PT Identifying platelet aggregation antagonists - using
PT thrombospondin-derived octa-peptide or its mutants, derivatives or
PT modified forms, some of which are new
XX
PS Claim 3; Page 24; 38pp; English.
XX
CC A peptide derived from the region of thrombospondin (TSP) which
CC binds to the carboxy terminal receptor on platelets and which induces
CC homotypic platelet aggregation even in the presence of RGD peptides
CC or their mimetics has been identified previously. The peptide has
CC the sequence RFRVNMWK and was disclosed by Kosfeld and Frazier in
CC J.Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
CC 4N1-1". Peptides able to induce homotypic platelet aggregation and
CC which differ by at least 1 amino acid from the sequence of peptide
CC 4N1-1 are claimed. The present peptide is a preferred example.
XX
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
DB 2 VVM 4

RESULT 65
AAW41047
ID AAW41047 standard; Protein; 6 AA.
XX
AC AAW41047;
XX
DT 12-MAY-1998 (first entry)
XX
DE 6P1 staurosporine selected clone.
XX
KW Transdominant bioactive agent; phenotype alteration; signalling pathway;
KW antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis;
KW obesity; neurodegeneration; bone disease; infection; allergy; therapy;
KW staurosporine selected clone.

XX OS Synthetic.
XX PN WO9727213-A1.
XX PD 31-JUL-1997.
XX PF 23-JAN-1997; 97WO-US01048.
XX PR 23-JAN-1996; 96US-0589911.
XX PR 23-JAN-1996; 96US-0589109.
XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX PI Noaln GP, Rothenberg SM;
XX DR WPI; 1997-393612/36.
XX DR N-PSDB; AAV03821.
XX PT Screening for trans-dominant active agents able to alter cell
XX PT anti-tumour activity
XX PS Example 3; Page 72; 91pp; English.
XX
CC This sequence is a staurosporine selected clone identified using the
CC method of the invention. The method is for screening for transdominant
CC bioactive agents (A) able to alter the phenotype of a cell comprises:
CC (a) introducing a library of different randomised nucleic acids (I) into
CC cells; and (b) screening the cells for altered phenotype due to presence
CC of (A). (A) are potential pharmaceuticals, from their effect on
CC signalling pathways. A particular application is to identify peptides,
CC encoded by (I), that have antitumour activity or are able to increase
CC sensitivity to, or reduce toxicity of, known antitumour agents. More
CC generally the method can identify agents for treatment of many other
CC conditions, e.g. cardiovascular diseases, angiogenesis, atherosclerosis,
CC obesity, neurodegeneration, bone disease, viral and other infections,
CC allergy etc.
XX
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
DB 1 MEV 3

RESULT 66
AAB45986
ID AAB45986 standard; Peptide; 6 AA.
XX
AC AAB45986;
XX
DT 02-APR-2001 (first entry)
XX
DE Transdominant effector peptide associated screening peptide #65.
XX
KW Intracellular transdominant bioactive agent; screening; cell phenotype;
KW effector peptide.
XX
OS Unidentified.
XX
PN US6153380-A.
XX
PD 28-NOV-2000.
XX
PF 23-JAN-1997; 97US-0789333.
XX
PR 23-JAN-1996; 96US-0589108.
PR 23-JAN-1996; 96US-0589911.

```

XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (RIGE-) RIGEL PHARM INC.  
 XX  
 PI Rothenberg SM, Nolan GP;  
 XX  
 DR WPI; 2001-060084/07.  
 XX  
 XX Methods for screening intracellular transdominant effector peptides and  
 PT RNA molecules comprise delivering random oligonucleotides to cells,  
 PT which are then screened for an altered phenotype -  
 XX  
 PS Example 3; Column 97-98; 57pp; English.  
 XX  
 CC This invention describes novel in vitro screening methods (I) for a  
 CC transdominant intracellular bioactive agent capable of altering the  
 CC phenotype of a cell. (I) comprises: (a) introducing a molecular library  
 CC of randomized candidate nucleic acids into several cells; and (b)  
 CC screening the cells for a cell exhibiting an altered phenotype, where the  
 CC altered phenotype is due to the presence of a transdominant bioactive  
 CC agent. The methods are particularly useful for screening intracellular  
 CC transdominant effector peptides and RNA molecules selected inside living  
 CC cells from randomized pools. (I) is also useful for introducing random  
 CC libraries into cells to screen for bioactive compounds. The methods allow  
 CC rapid and highly efficient screening of large numbers of random  
 CC oligonucleotides and their corresponding expression products in a single  
 CC step. In addition, the methods allow screening in the absence of  
 CC significant prior characterization of the cellular defect.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 DB 1 MEV 3  
 RESULT 67  
 AAE22870  
 ID AAE22870 standard; peptide; 6 AA.  
 XX  
 AC AAE22870;  
 XX  
 DT 09-AUG-2002 (first entry)  
 XX  
 DE Carrot red leaf luteovirus (CRLV) peptide motif #3.  
 XX  
 KW Carrot red leaf luteovirus; CRLV; potato leaf roll polerovirus; PLRV;  
 KW barley yellow dwarf virus; BYDV; beet Western yellow virus; BWYV;  
 KW luteovirus detection.  
 XX  
 OS Carrot red leaf luteovirus.  
 XX  
 PN WO200222868-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-GE04053.  
 XX  
 PR 14-SEP-2000; 2000GB-0022505.  
 XX  
 PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.  
 XX  
 PI Cooper JI, Naylor M;  
 XX  
 DR WPI; 2002-393973/42.  
 XX  
 PT Primer useful in diagnosing the presence of luteovirus sequences in  
 PT plant tissue, is capable of hybridizing to conserved regions of nucleic  
 PT acid for e.g. carrot red leaf luteovirus and barley yellow dwarf virus

PT  
 XX  
 PS  
 XX Claim 7; Page 17; 29pp; English.  
 XX  
 CC The invention relates to a method for detecting luteoviruses and primers  
 CC capable of hybridizing to conserved regions of nucleic acids of  
 CC carrot red leaf luteovirus (CRLV), potato leaf roll polerovirus (PLRV),  
 CC barley yellow dwarf virus (BYDV) and beet Western yellow virus (BWYV).  
 CC These primers are useful for diagnosing the presence of a luteovirus  
 CC sequence in a plant tissue nucleic acid sample. The method comprises  
 CC treating the nucleic acid with a first polymerase chain reaction (PCR)  
 CC primer, preferably CL2, to obtain a DNA product, treating the DNA  
 CC product with one or more second PCR primers, preferably a mixture of  
 CC CL1 and CL2 to obtain a PCR product, and comparing the nucleotide  
 CC sequence or corresponding amino acid sequence of the PCR product with  
 CC a known nucleotide sequence or corresponding amino acid sequence  
 CC characteristics of the luteovirus. The primers of the invention are  
 CC also useful for diagnosing the presence of CRLV or PLRV sequences in  
 CC a plant tissue, where the second PCR primers used are CL1 and CL3.  
 CC The present sequence is CRLV peptide motif.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 3; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 DB 4 MEV 6  
 RESULT 68  
 ABB55686  
 ID ABB55686 standard; Peptide; 6 AA.  
 XX  
 AC ABB55686;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Mutated protein Fes fragment #5.  
 XX  
 KW Enzyme inhibitor; wild-type enzyme; mutant; muten; cytostatic;  
 KW osteopathic; immunomodulatory; antiallergic; protein kinase; cancer;  
 KW allergy; transplant rejection; osteoporosis.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 PN WO200198530-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 17-MAY-2001; 2001WO-EP05661.  
 XX  
 PR 17-MAY-2000; 2000DE-1024174.  
 XX  
 PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.  
 XX  
 PI Warmuth M, Mathes R, Hallek M;  
 XX  
 DR WPI; 2002-055716/07.  
 XX  
 PT Selecting enzyme inhibitors active against wild type, but not mutant  
 PT enzyme, useful for treating or preventing diseases such as cancer,  
 PT allergy and osteoporosis -  
 XX  
 PS Disclosure; Fig 7; 56pp; German.  
 XX  
 CC The present invention relates to a method of selecting inhibitors which  
 CC are active against wild-type enzymes but not against mutant enzymes.  
 CC These inhibitors can be used particularly to inhibit disease-associated  
 CC enzymes, especially protein kinases, and are useful in the treatment of

CC cancer, allergies, transplant rejection and osteoporosis. The present  
CC sequence is a peptide fragment described in the exemplification of the  
CC invention.

XX  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
|||  
Db 3 VME 5

RESULT 69  
ABU57569  
ID ABU57569 standard; Peptide; 6 AA.  
XX  
AC ABU57569;  
XX  
XX 09-APR-2003 (first entry)  
XX HIV polypeptide expression related polypeptide.  
XX  
XX Immunoassay; human immunodeficiency virus; HIV; antibody;  
KW gag antigen; acquired immunodeficiency syndrome; AIDS; HIV infection;  
KW vaccine; gene therapy; protein expression system.  
XX  
XX Synthetic.  
XX  
XX US6458527-B1.  
XX  
XX 01-OCT-2002.  
XX  
XX 28-JUN-1993; 93US-0083391.  
XX  
XX 24-DEC-1987; 87US-0138894.  
XX 17-AUG-1992; 92US-0931191.  
XX 31-OCT-1984; 84US-0667501.  
XX 30-JAN-1985; 85US-0696534.  
XX 06-SEP-1985; 85US-0773447.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Luciw PA, Dina D, Steimer K, Pescador RS, George-Nascimento C;  
XX Parkes D, Hallelwell R, Barr PJ, Truett M;  
XX  
XX WPI; 2003-182063/18.  
XX N-PSDB; ABX77347.  
XX  
XX Immunoassay for detecting the presence of antibodies to a human  
PT immunodeficiency virus (HIV) for diagnosing, treating or preventing HIV  
PT infection, comprises contacting the sample with an HIV gag antigen -  
XX  
XX Disclosure; Column 55; 101pp; English.

CC The invention describes an immunoassay for detecting the presence of  
CC antibodies to a human immunodeficiency virus (HIV) in a sample by:  
CC contacting the sample with an HIV gag antigen that binds anti-HIV  
CC antibodies in an acquired immunodeficiency syndrome (AIDS) patient sera;  
CC and determining binding, where the improvement comprises employing as  
CC the gag antigen either a synthetic polypeptide or a recombinant  
CC polypeptide. The method is used for detecting the presence of antibodies  
CC to a human immunodeficiency virus (HIV) in a human sample. The  
CC method is used in the preparation of a medicament for diagnosing,  
CC treating or preventing HIV infection e.g. a vaccine or for gene  
CC therapy. This is the amino acid sequence of a peptide associated with  
CC the creation of systems to express proteins encoded by HIV.

XX  
XX  
XX Sequence 6 AA;

Query Match 60.0%; Score 3; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5  
|||  
Db 1 MEV 3

RESULT 70  
ABU57834  
ID ABU57834 standard; Peptide; 6 AA.  
XX  
AC ABU57834;  
XX  
XX 10-APR-2003 (first entry)  
XX Thrombospondin 1 cell binding domain peptide fragment.  
XX  
XX Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;  
KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.  
XX  
XX Synthetic.  
XX OS  
XX US6469138-B1.  
XX PN  
XX 22-OCT-2002.  
XX PD  
XX 21-FEB-1995; 95US-0391820.  
XX PF  
XX 05-MAR-1993; 93US-0029333.  
XX PR  
XX (UNIW ) UNIV WASHINGTON.  
XX PA  
XX Frazier WA, Kosfeld MD;  
XX PI  
XX WPI; 2003-196751/19.  
XX DR  
XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe  
PT sequence in computer search of all available databases -  
XX  
XX Disclosure; Column 2; 25pp; English.

CC This invention relates to a novel peptide that binds to the  
CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which  
CC acts to promote cell adhesion and is involved in platelet aggregation,  
CC wound healing and tumour cell migration. Also disclosed in the  
CC invention is laminin peptides which have been shown to be able to  
CC substitute for TS-1 peptides. Preferably the peptides of  
CC the invention share a tripeptide motif VVM and are useful as probe  
CC sequences in a computer search of all available databases for  
CC similar receptor binding motif peptides. The present sequence  
CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain  
CC peptide of the invention.

XX  
XX  
XX Sequence 6 AA;

Query Match 60.0%; Score 3; DB 24; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
|||  
Db 4 VVM 6

RESULT 71  
ABU14070  
ID ABU14070 standard; Peptide; 6 AA.  
XX  
XX AC ABU14070;  
XX AC  
XX 27-FEB-2003 (first entry)  
XX DT  
XX

DE Transdominant effector peptide screening related peptide #15.  
 XX Transdominant effector peptide; screening; cell phenotype;  
 KW transdominant bioactive agent; disease pathogenesis; drug discovery;  
 KW signal system regulation.  
 XX Synthetic.  
 OS US6455247-B1.  
 XX  
 XX  
 XX  
 PD 24-SEP-2002.  
 XX  
 PF 23-JAN-1997; 97US-0787738.  
 XX  
 PR 23-JAN-1996; 96US-0589109.  
 PR 23-JAN-1996; 96US-0589311.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (RIGB-) RIGEL PHARM INC.  
 XX  
 PI Nolan GP, Rothenberg SM;  
 XX  
 XX WPI; 2003-110187/10.  
 DR N-PSDB; ABX64339.  
 XX  
 XX Screening for a transdominant bioactive agent that alters the phenotype  
 PT of a cell by introducing a molecular library of randomized candidate  
 PT nucleic acids each operably linked to a nucleic acid encoding a  
 PT secretion signal into first cells -  
 XX Example 3; Column 50; 56pp; English.  
 XX  
 XX The invention describes a method of screening for a transdominant  
 CC bioactive agent that alters the phenotype of a cell. The method is  
 CC useful for screening for transdominant effector peptides and RNA  
 CC molecules. These peptides and RNA molecules are useful in disease  
 CC pathogenesis, and discovering chemical drugs that regulate signal  
 CC systems. This sequence represents a peptide associated with the method  
 CC of identifying transdominant effector peptides described in the  
 CC invention.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 60.0%; Score 3; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 MEV 5  
 DB |||  
 1 MEV 3  
 RESULT 72  
 AAR35098  
 ID AAR35098 standard; Protein; 7 AA.  
 XX  
 AC AAR35098;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 05-AUG-1993 (first entry)  
 XX  
 XX B. thuringiensis lepidopteran toxin probe (i) design peptide.  
 DE  
 XX Probe; Bacillus thuringiensis; Bt; insecticidal; active; endotoxin;  
 KW lepidoptera; diptera; coleoptera.  
 XX  
 OS Synthetic.  
 XX  
 XX US5204237-A.  
 PN  
 XX  
 PD 20-APR-1993.  
 XX  
 XX 26-JUL-1991; 91US-0737569.

XX 25-OCT-1989; 89US-0427068.  
 PR 26-JUL-1991; 91US-0737569.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 XX Gaertner FH, Schwab GE, Sick AJ;  
 PI WPI; 1993-143952/17.  
 DR  
 XX  
 XX Gene probe for identifying endotoxin sequences in Bacillus  
 PT thuringiensis - are universal, type specific or gene specific,  
 PT for rapid detection and characterisation of insecticidal activity  
 XX  
 XX Disclosure; Column 2; 5pp; English.  
 CC  
 CC The sequences given in AAR35090-100 and AAR34628-32 are peptides which  
 CC were used to design the probes given in AAQ0219-34. These probes can  
 CC be used to identify Bacillus thuringiensis (Bt) DNA which encodes  
 CC insecticidally active endotoxin. Probe (a) identifies genes encoding  
 CC a toxin effective against any sort of insect. Sequences (b) and (e)-  
 CC (1) are specific for toxins against lepidoptera; sequences (c), (m)  
 CC and (n) for toxins active against diptera and sequence (d), (o) and  
 CC (p) for toxins active against coleoptera.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 60.0%; Score 3; DB 14; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VME 4  
 DB |||  
 2 VME 4  
 RESULT 73  
 AAR52638  
 ID AAR52638 standard; peptide; 7 AA.  
 XX  
 AC AAR52638;  
 XX  
 DT 11-JUL-1994 (first entry)  
 XX  
 XX Myrotrophin tryptic peptide.  
 DE  
 XX Myrotrophin; tryptic peptide; soluble protein factor;  
 KW myocardial hypertrophy; hypertension.  
 XX  
 OS Rattus sp.  
 XX  
 XX US5284932-A.  
 PN  
 XX 08-FEB-1994.  
 PD  
 XX 07-SEP-1990; 90US-0578935.  
 PF  
 PR 07-SEP-1990; 90US-0578935.  
 XX  
 XX (CLEV-) CLEVELAND CLINIC FOUND.  
 PA  
 XX Sen S;  
 PI  
 XX WPI; 1994-056404/07.  
 DR  
 XX Myotrophin partially characterised soluble protein factor -  
 PT purified from hypertrophied heart, regulates myocardial  
 PT hypertrophy in hypertension  
 XX  
 XX Disclosure; Page 12; 21pp; English.  
 XX  
 XX Rat hypertrophied heart myotrophin peptides (AAR52637-42) were



CC obtained by carboxymethylation of purified myrotrophin, followed by  
CC trypsin digestion. Purification of myrotrophin peptides may lead to  
CC the development of peptide analogs and/or antagonists for use in  
CC the control of cardiac hypertrophy.

XX  
XX  
SQ Sequence 7 AA;  
Query Match 60.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
Db 5 MEV 7

RESULT 74  
AAR82905  
ID AAR82905 standard; Protein; 7 AA.  
AC AAR82905;  
XX  
XX  
DT 13-DEC-1995 (first entry)  
XX  
XX x.luminescens flavin reductase peptide for primer synthesis.  
DE  
XX  
KW Flavon reductase; Vibrio fischeri; primer; PCR; amplification; probe;  
KW Xenorhabdus luminescens; expression plasmid; FMN reducing activity;  
KW E.coli; ss.  
XX  
XX Synthetic.  
OS  
XX  
FN JP07079783-A.  
XX  
XX 28-MAR-1995.  
PD  
XX  
PF 28-JUN-1993; 93JP-0181850.  
XX  
PR 28-JUN-1993; 93JP-0181850.  
XX  
XX (CHCC ) CHISSO CORP.  
XX  
XX WPI; 1995-157853/21.  
DR  
DR N-PSDB; AAT01084.  
XX  
XX Flavon reductase gene from Vibrio fischeri - useful for production  
PT of enzyme with FMN reducing activity  
XX  
XX Example 1; Fig 1; 10pp; Japanese.  
PS  
XX  
XX The sequence of a peptide from the Xenorhabdus luminescens flavin  
CC reductase protein which was used to generate the primer AAT01084. The  
CC primers AAT01084-5 were used to amplify the gene encoding flavin  
CC reductase (fr) from Vibrio fischeri strain ATCC-7744 (see AAQ88282-4).  
CC The resultant fragment was cloned into pUC8 and used as a probe to obtain  
CC the full length gene sequence (AAQ88284) of the V.fischeri fr gene from  
CC a lambda phage library. The gene was inserted into the expression plasmid  
CC pUC13 and transformed into E.coli D1210. The resultant transformant  
CC E.coli D1210/pfFR1 was used for the IPTG-inducible expression of the fr  
CC gene. The gene encodes a protein with FMN reducing activity.

XX  
SQ Sequence 7 AA;  
Query Match 60.0%; Score 3; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
Db 5 VVM 7

RESULT 75

AAR78214  
ID AAR78214 standard; Peptide; 7 AA.  
XX  
AC AAR78214;  
XX  
XX  
DT 25-MAR-2003 (updated)  
DT 22-FEB-1996 (first entry)  
XX  
XX B. thuringiensis endotoxin derived peptide.  
DE  
XX  
KW Endotoxin; probe; microbes; peptide; detection; lepidopteran.  
XX  
XX Bacillus thuringiensis.  
OS  
XX  
XX US5430137-A.  
PN  
XX  
XX 04-JUL-1995.  
PD  
XX  
PF 30-OCT-1992; 92US-0968781.  
XX  
XX 30-OCT-1992; 92US-0968781.  
PR  
PR 25-OCT-1989; 89US-0427068.  
PR 26-JUL-1991; 91US-0737569.  
XX  
XX (MYCO ) MYCOGEN CORP.  
PA  
XX  
XX Gaertner FH, Narva KE, Schnepf HE, Schwab GE, Sick AJ;  
PI Thompson M;  
PI  
XX  
XX WPI; 1995-245777/32.  
DR  
XX  
XX Nucleotide sequence used as probes to identify Bacillus  
PT thuringiensis - are derived from the B.thuringiensis endotoxin  
PT genes, for identifying microbes which encode toxins  
XX  
XX Example 2; Columns 43-44; 30pp; English.  
PS  
XX  
XX The nucleotide sequences which encode AAR78210-R78217, B.  
CC thuringiensis (B.t.) endotoxin derived peptides, specify the probes  
CC AAQ94859-Q94866 respectively. The probes can be used for the detection  
CC of endotoxin producing B.t. microbes. The probes aid in the search  
CC for useful microbes hosting toxin encoding genes, specifically from  
CC lepidopteran species.  
CC  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
|||  
Db 2 VME 4

Search completed: November 25, 2003, 18:15:51  
Job time : 18.1968 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 9.94681 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-9

Perfect score: 5

Sequence: 1 VVNEV 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5	100.0	5	15	US-10-281-652-9
2	5	100.0	12	11	US-09-994-595-121
3	4	80.0	8	12	US-10-137-867-330
4	3	60.0	3	12	US-10-137-867-540
5	3	60.0	4	11	US-09-813-775C-6
6	3	60.0	5	11	US-09-731-092-4
7	3	60.0	6	10	US-09-916-940-91
8	3	60.0	6	12	US-10-095-550-91
9	3	60.0	7	10	US-09-922-261-140
10	3	60.0	7	10	US-09-884-767A-134
11	3	60.0	8	9	US-09-110-716-4
12	3	60.0	8	12	US-10-022-066-238
13	3	60.0	8	14	US-10-042-991-5
14	3	60.0	8	15	US-10-046-801-18
15	3	60.0	9	12	US-10-022-066-190
16	3	60.0	9	12	US-10-022-066-190
17	3	60.0	9	12	US-10-022-066-190
18	3	60.0	9	12	US-10-022-066-190
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21	3	60.0	9	12	US-10-022-066-190
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93	3	60.0	9	12	US-10-022-066-190
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96	3	60.0	9	12	US-10-022-066-190
97	3	60.0	9	12	US-10-022-066-190
98	3	60.0	9	12	US-10-022-066-190
99	3	60.0	9	12	US-10-022-066-190
100	3	60.0	9	12	US-10-022-066-190

Sequence 294, Appl  
Sequence 76, Appl  
Sequence 24, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 26, Appl  
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Sequence 56, Appl  
Sequence 58, Appl  
Sequence 59, Appl  
Sequence 60, Appl  
Sequence 13, Appl  
Sequence 8, Appl  
Sequence 269, Appl  
Sequence 20, Appl  
Sequence 59, Appl  
Sequence 315, Appl  
Sequence 607, Appl  
Sequence 49, Appl  
Sequence 42, Appl  
Sequence 2, Appl  
Sequence 295, Appl  
Sequence 7, Appl  
Sequence 14, Appl  
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Sequence 142, Appl  
Sequence 269, Appl  
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Sequence 104, Appl  
Sequence 25, Appl  
Sequence 30, Appl  
Sequence 268, Appl  
Sequence 30, Appl  
Sequence 35, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
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Sequence 300, Appl  
Sequence 84, Appl  
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Sequence 808, Appl  
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Sequence 84, Appl  
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Sequence 2, Appl  
Sequence 13, Appl  
Sequence 181, Appl  
Sequence 20, Appl  
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Sequence 18, Appl  
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Sequence 23, Appl  
Sequence 2230, Appl  
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Sequence 24, Appl  
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89 Sequence 809, App  
90 Sequence 139, App  
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93 Sequence 16, Appl  
94 Sequence 809, App  
95 Sequence 139, App  
96 Sequence 8, Appl  
97 Sequence 11, Appl  
98 Sequence 117, Appl  
99 Sequence 62, Appl  
100 Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-10-281-652-9  
; Sequence 9, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-9

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMEV 5  
Db 1 VMEV 5

RESULT 2  
US-09-994-595-121  
; Sequence 121, Application US/09994595  
; Publication No. US20030039981A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhattacherjee, J.  
; APPLICANT: Suvarna, Kalavati  
; APPLICANT: Bhattacherjee, Vasker  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN  
; TITLE OF INVENTION: A BIOLOGICAL SAMPLE  
; FILE REFERENCE: 96,247-A  
; CURRENT APPLICATION NUMBER: US/09/994,595  
; CURRENT FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 08/650,809  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Microsoft Word 97  
; SEQ ID NO 121  
; LENGTH: 12

; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide segment of GR5B\_1BACB shown in Figure 4.  
US-09-994-595-121  
Query Match 100.0%; Score 5; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VMEV 5  
Db 8 VMEV 12

RESULT 3  
US-10-137-867-330  
; Sequence 330, Application US/10137867  
; Publication No. US20030207349A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C146  
; CURRENT APPLICATION NUMBER: US/10/137,867  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 330  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-867-330

Query Match 80.0%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5  
Db 1 VMEV 4

RESULT 4  
US-10-137-867-540  
; Sequence 540, Application US/10137867  
; Publication No. US20030207349A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

```
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 540
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-540

Query Match          60.0%; Score 3; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3

RESULT 5
US-09-813-775C-6
; Sequence 6, Application US/09813775C
; Publication No. US20030054494A1
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. US20030054494A1 chimpanzee erythropoietin
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057C52
; CURRENT APPLICATION NUMBER: US/09/813,775C
; CURRENT FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/552265
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-813-775C-6

Query Match          60.0%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3

RESULT 6
US-09-731-092-4
; Sequence 4, Application US/09731092
; Publication No. US20030082621A1
; GENERAL INFORMATION:
; APPLICANT: MISEVIC, GRADIMIR
; TITLE OF INVENTION: FUCOSE CONTAINING PROTEOGLYCAN OR ACIDIC GLYCAN AND
; TITLE OF INVENTION: THEIR PHARMACEUTICAL USE
; FILE REFERENCE: MISE-001
; CURRENT APPLICATION NUMBER: US/09/731,092
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; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 08/704,777
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/IB95/00208
; PRIOR FILING DATE: 1995-03-24
; PRIOR APPLICATION NUMBER: GB94-05 846.8
; PRIOR FILING DATE: 1994-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-731-092-4

Query Match          60.0%; Score 3; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VWM 3
Db      2 VWM 4

RESULT 7
US-09-916-940-91
; Sequence 91, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020127564Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64260-6/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-916-940-91

Query Match          60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3

RESULT 8
US-10-096-550-91
; Sequence 91, Application US/10096550
; Publication No. US20030170641A1
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; GENERAL INFORMATION:
; APPLICANT: No. US20030170641A1an, Garry P
; APPLICANT: Rothenburg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64259-1 correction
; CURRENT APPLICATION NUMBER: US/10/096,550
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 08/787,738
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-096-550-91

Query Match      60.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 9
US-09-922-261-140
; Sequence 140, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-140

Query Match      60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 10
US-09-884-767A-134
; Sequence 134, Application US/09884767A
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; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-134

Query Match      60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VME 4
Db      1 VME 3

RESULT 11
US-09-110-716-4
; Sequence 4, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:
; APPLICANT: Lehrner, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT APPLICATION NUMBER: US/09/110,716A
; CURRENT FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unidentified
US-09-110-716-4

Query Match      60.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      2 MEV 4

RESULT 12
US-10-022-066-238
; Sequence 238, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
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; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 238
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-238

```

```

Query Match          60.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VME 4
        |||
Db       1 VME 3

```

```

RESULT 13
US-10-042-991-5
; Sequence 5, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Psidium Guajava (guava)
US-10-042-991-5

```

```

Query Match          60.0%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VVM 3
        |||
Db       4 VVM 6

```

```

RESULT 14
US-10-046-801-18
; Sequence 18, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448

```

```

; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1e1 Sequ
US-10-046-801-18

```

```

Query Match          60.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VVM 3
        |||
Db       4 VVM 6

```

```

RESULT 15
US-10-022-066-190
; Sequence 190, Application US/10022066
; Publication No. US2003016057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: BRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-190

```

```

Query Match          60.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VME 4
        |||
Db       2 VME 4

```

```

RESULT 16
US-10-239-313A-294
; Sequence 294, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM

```

; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 294  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-294

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
|||  
Db 7 VME 9

## RESULT 17

US-10-119-536A-76  
; Sequence 76, Application US/10119536A  
; Publication No. US20030199438A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaw, Allan Christian  
; APPLICANT: Vandahl, Brian Berg  
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria  
; FILE REFERENCE: 4305/1J091US1  
; CURRENT APPLICATION NUMBER: US/10/119,536A  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: DK PA 200100581  
; PRIOR FILING DATE: 2001-04-09  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 76  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: CPN0796 immunogenic peptide  
US-10-119-536A-76

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
|||  
Db 2 VVM 4

## RESULT 18

US-10-136-145-24  
; Sequence 24, Application US/10136145  
; Publication No. US20030216559A1  
; GENERAL INFORMATION:  
; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.  
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide, epitopes thereof and vaccine against melanoma.  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav  
; STREET: Philips van Leydenlaan 25  
; CITY: Nijmegen  
; STATE: Brabant

; COUNTRY: the Netherlands  
; ZIP: 6525 EX  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/136,145  
; FILING DATE: 01-May-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,852B  
; FILING DATE: February 15, 1995  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-136-145-24

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5  
|||  
Db 7 MEV 9

## RESULT 19

US-10-026-001-5  
; Sequence 5, Application US/10026001  
; Publication No. US20020122791A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolette, Charles A.  
; TITLE OF INVENTION: ANTIGENIC CK-18 COMPOUNDS FOR THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS AND METHODS FOR USING SAME  
; FILE REFERENCE: GZ 210800  
; CURRENT APPLICATION NUMBER: US/10/026,001  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,820  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-026-001-5

Query Match 60.0%; Score 3; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5  
|||  
Db 7 MEV 9

## RESULT 20

US-10-114-091-5  
; Sequence 5, Application US/10114091  
; Publication No. US20020197243A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicolette, Charles A.  
; TITLE OF INVENTION: NOVEL p53BP2 COMPOUNDS FOR THERAPY AND DIAGNOSIS AND METHODS F  
; TITLE OF INVENTION: SAME  
; FILE REFERENCE: GZ 2106.00

; CURRENT APPLICATION NUMBER: US/10/114,091  
 ; CURRENT FILING DATE: 2002-06-04  
 ; PRIOR APPLICATION NUMBER: US 60/280,794  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: P53 BP2  
 US-10-114-091-5

Query Match 60.0%; Score 3; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
 ||||  
 Db 5 MEV 7

RESULT 21  
 US-10-195-117-26  
 ; Sequence 26, Application US/10195117  
 ; Publication No. US20030092083A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: In2Gen Co., Ltd.  
 ; APPLICANT: Jeoung, Doo-il  
 ; APPLICANT: Cho, Bomsoo  
 ; APPLICANT: Lim, Yoon  
 ; APPLICANT: Park, Saeyoung  
 ; APPLICANT: Lee, Daeyeon  
 ; APPLICANT: Bang, Yung-Jue  
 ; APPLICANT: Yang, Hankwang  
 ; APPLICANT: Kim, Dae-Ke  
 ; TITLE OF INVENTION: CAGE Antigen  
 ; FILE REFERENCE: S9258-00002  
 ; CURRENT APPLICATION NUMBER: US/10/195,117  
 ; CURRENT FILING DATE: 2002-07-11  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 26  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(9)  
 ; OTHER INFORMATION:  
 US-10-195-117-26

Query Match 60.0%; Score 3; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 ||||  
 Db 1 VVM 3

RESULT 22  
 US-08-344-824-54  
 ; Sequence 54, Application US/08344824  
 ; Publication No. US20030152580A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SETTE, Alessandro  
 ; APPLICANT: SIDNEY, John  
 ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
 ; NUMBER OF SEQUENCES: 399  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: One Market Plaza, Steuart Street Tower, 20th  
 ; STREET: Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/08/344,824  
 ; APPLICATION NUMBER: US/08/344,824  
 ; FILING DATE: 23-NOV-1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/278,634  
 ; FILING DATE: 21-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bastian, Kevin L.  
 ; REGISTRATION NUMBER: 34,774  
 ; REFERENCE/DOCKET NUMBER: 14137-80-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 543-3600  
 ; TELEFAX: (415) 543-5043  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 US-08-344-824-54

Query Match 60.0%; Score 3; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
 ||||  
 Db 4 VME 6

RESULT 23  
 US-08-344-824-55  
 ; Sequence 55, Application US/08344824  
 ; Publication No. US20030152580A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SETTE, Alessandro  
 ; APPLICANT: SIDNEY, John  
 ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
 ; NUMBER OF SEQUENCES: 399  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew  
 ; STREET: One Market Plaza, Steuart Street Tower, 20th  
 ; STREET: Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/344,824  
 ; FILING DATE: 23-NOV-1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/278,634  
 ; FILING DATE: 21-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:



NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-344-824-55

Query Match 60.0%; Score 3; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 VME 4  
Db 4 VME 6

RESULT 24  
US-08-344-824-56  
Sequence 56, Application US/08344824  
Publication No. US20030152580A1  
GENERAL INFORMATION:  
APPLICANT: SETTE, Alessandro  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower, 20th  
FLOOR  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-344-824-56

Query Match 60.0%; Score 3; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 VME 4  
Db 4 VME 6

RESULT 25  
US-08-344-824-58  
Sequence 58, Application US/08344824  
Publication No. US20030152580A1  
GENERAL INFORMATION:  
APPLICANT: SETTE, Alessandro  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower, 20th  
FLOOR  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-344-824-58

Query Match 60.0%; Score 3; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
Db 4 VME 6

RESULT 26  
US-08-344-824-59  
Sequence 59, Application US/08344824  
Publication No. US20030152580A1  
GENERAL INFORMATION:  
APPLICANT: SETTE, Alessandro  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower, 20th  
FLOOR  
CITY: San Francisco

```

; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-344-824-59

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 4 VME 6

RESULT 27
US-08-344-824-60
; Sequence 60, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-344-824-60

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 4 VME 6

RESULT 28
US-09-012-135A-13
; Sequence 13, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide

```

US-09-012-135A-13

Query Match 60.0%; Score 3; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
Db 1 VME 3

RESULT 29

US-09-923-831-8  
; Sequence 8, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923.831  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-8

Query Match 60.0%; Score 3; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5  
Db 1 MEV 3

RESULT 30

US-09-071-838-269  
; Sequence 269, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071.838  
; FILING DATE: 01-May-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 269:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-269

Query Match 60.0%; Score 3; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VME 3  
Db 6 VME 8

RESULT 31

US-09-766-889A-20  
; Sequence 20, Application US/09766889A  
; Patent No. US20020164654A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: Schultz, Erwin  
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
; FILE REFERENCE: L0461/7104  
; CURRENT APPLICATION NUMBER: US/09/766.889A  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/177,242  
; PRIOR FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: US 60/243,212  
; PRIOR FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-766-889A-20

Query Match 60.0%; Score 3; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5  
Db 1 MEV 3

RESULT 32

US-09-766-889A-59  
; Sequence 59, Application US/09766889A  
; Patent No. US20020164654A1  
; GENERAL INFORMATION:  
; APPLICANT: Luiten, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: Schultz, Erwin  
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
; FILE REFERENCE: L0461/7104  
; CURRENT APPLICATION NUMBER: US/09/766.889A

```

; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-59

Query Match 60.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 33
US-09-983-802-315
; Sequence 315, Application US/09983802
; Publication No. US20030032185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948

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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 315
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-315

Query Match 60.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 6 MEV 8

RESULT 34
US-10-022-066-607
; Sequence 607, Application US/10022066
; Publication No. US20030186057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680,034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

```

```

; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (10)
; OTHER INFORMATION: Unknown amino acid
US-10-022-066-607

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 7 VME 9

RESULT 35
US-10-170-832-49
; Sequence 49, Application US/10170832
; Publication No. US20030170792A1
; GENERAL INFORMATION:
; APPLICANT: Chauv. Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-49

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 36
US-10-293-580-42
; Sequence 42, Application US/10293580
; Publication No. US20030170767A1
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; APPLICANT: Cubitt, Andrew B.
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AURO1270 (08366/031001)
; CURRENT APPLICATION NUMBER: US/10/293,580
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/129,192
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: cytomegalovirus assemblin
US-10-293-580-42

```

```

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 2 VVM 4

RESULT 37
US-10-332-282-2
; Sequence 2, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Miller, Julie
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Titball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-332-282-2

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 38
US-10-239-313A-295
; Sequence 295, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 295
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-295

```

Query Match 60.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
|||  
DB 7 VME 9

RESULT 39  
US-10-192-869-7  
; Sequence 7, Application US/10192869  
; Publication No. US20030022265A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Woo-Jim  
; APPLICANT: Kim, Sung-Yun  
; APPLICANT: Park, Dae-Ho  
; TITLE OF INVENTION: Method for Determining Substrate Specificity of Protease  
; FILE REFERENCE: HYLEE68.001AUS  
; CURRENT APPLICATION NUMBER: US/10/192,869  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: KR 10-2001-0041011  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq 4.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide substrate for kex2

US-10-192-869-7  
Query Match 60.0%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
DB 1 VVM 3

RESULT 40  
US-10-201-386-14  
; Sequence 14, Application US/10201386  
; Publication No. US20030091567A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN  
; TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF  
; FILE REFERENCE: 28967/34140A  
; CURRENT APPLICATION NUMBER: US/10/201,386  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: US/09/534,376  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 09/355,700  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: PCT/US98/01973  
; PRIOR FILING DATE: 1998-02-02  
; PRIOR APPLICATION NUMBER: 08/795,430  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: PCT/FI96/00427  
; PRIOR FILING DATE: 1996-08-01  
; PRIOR APPLICATION NUMBER: 08/671,573  
; PRIOR FILING DATE: 1996-06-28  
; PRIOR APPLICATION NUMBER: 08/601,132  
; PRIOR FILING DATE: 1996-02-14  
; PRIOR APPLICATION NUMBER: 08/585,895  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: 08/510,133  
; PRIOR FILING DATE: 1995-08-01  
; PRIOR APPLICATION NUMBER: 08/340,011

Query Match 60.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
|||  
DB 7 VME 9

RESULT 39  
US-10-192-869-7  
; Sequence 7, Application US/10192869  
; Publication No. US20030022265A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Woo-Jim  
; APPLICANT: Kim, Sung-Yun  
; APPLICANT: Park, Dae-Ho  
; TITLE OF INVENTION: Method for Determining Substrate Specificity of Protease  
; FILE REFERENCE: HYLEE68.001AUS  
; CURRENT APPLICATION NUMBER: US/10/192,869  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: KR 10-2001-0041011  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq 4.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide substrate for kex2

US-10-192-869-7  
Query Match 60.0%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
DB 1 VVM 3

RESULT 40  
US-10-201-386-14  
; Sequence 14, Application US/10201386  
; Publication No. US20030091567A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN  
; TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF  
; FILE REFERENCE: 28967/34140A  
; CURRENT APPLICATION NUMBER: US/10/201,386  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: US/09/534,376  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 09/355,700  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: PCT/US98/01973  
; PRIOR FILING DATE: 1998-02-02  
; PRIOR APPLICATION NUMBER: 08/795,430  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: PCT/FI96/00427  
; PRIOR FILING DATE: 1996-08-01  
; PRIOR APPLICATION NUMBER: 08/671,573  
; PRIOR FILING DATE: 1996-06-28  
; PRIOR APPLICATION NUMBER: 08/601,132  
; PRIOR FILING DATE: 1996-02-14  
; PRIOR APPLICATION NUMBER: 08/585,895  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: 08/510,133  
; PRIOR FILING DATE: 1995-08-01  
; PRIOR APPLICATION NUMBER: 08/340,011

Query Match 60.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
|||  
DB 7 VME 9

RESULT 39  
US-10-192-869-7  
; Sequence 7, Application US/10192869  
; Publication No. US20030022265A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Woo-Jim  
; APPLICANT: Kim, Sung-Yun  
; APPLICANT: Park, Dae-Ho  
; TITLE OF INVENTION: Method for Determining Substrate Specificity of Protease  
; FILE REFERENCE: HYLEE68.001AUS  
; CURRENT APPLICATION NUMBER: US/10/192,869  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: KR 10-2001-0041011  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq 4.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide substrate for kex2

US-10-192-869-7  
Query Match 60.0%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
DB 1 VVM 3

RESULT 40  
US-10-201-386-14  
; Sequence 14, Application US/10201386  
; Publication No. US20030091567A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN  
; TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF  
; FILE REFERENCE: 28967/34140A  
; CURRENT APPLICATION NUMBER: US/10/201,386  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: US/09/534,376  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 09/355,700  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: PCT/US98/01973  
; PRIOR FILING DATE: 1998-02-02  
; PRIOR APPLICATION NUMBER: 08/795,430  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: PCT/FI96/00427  
; PRIOR FILING DATE: 1996-08-01  
; PRIOR APPLICATION NUMBER: 08/671,573  
; PRIOR FILING DATE: 1996-06-28  
; PRIOR APPLICATION NUMBER: 08/601,132  
; PRIOR FILING DATE: 1996-02-14  
; PRIOR APPLICATION NUMBER: 08/585,895  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: 08/510,133  
; PRIOR FILING DATE: 1995-08-01  
; PRIOR APPLICATION NUMBER: 08/340,011

Query Match 60.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
|||  
DB 7 VME 9

RESULT 39  
US-10-192-869-7  
; Sequence 7, Application US/10192869  
; Publication No. US20030022265A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Woo-Jim  
; APPLICANT: Kim, Sung-Yun  
; APPLICANT: Park, Dae-Ho  
; TITLE OF INVENTION: Method for Determining Substrate Specificity of Protease  
; FILE REFERENCE: HYLEE68.001AUS  
; CURRENT APPLICATION NUMBER: US/10/192,869  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: KR 10-2001-0041011  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq 4.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide substrate for kex2

US-10-192-869-7  
Query Match 60.0%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
DB 1 VVM 3

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
CTL IMMUNITY

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: Stewart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 83:

US-10-128-711-83

Query Match 60.0%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5

Db 8 MEV 10

RESULT 43

US-10-128-711-142

Sequence 142, Application US/10128711

Publication No. US20030099634A1

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.

CHESTNUT, Robert W.

SETTE, Alessandro D.

CELLIS, Esteban

GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING

CTL IMMUNITY

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: Stewart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 142:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 142:

US-10-128-711-142

Query Match 60.0%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5

Db 8 MEV 10

RESULT 44

US-10-213-512-269

Sequence 269, Application US/10213512

Publication No. US20030110536A1

GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.

APPLICANT: Ohad, Nir

APPLICANT: Kiyosue, Tomohiro

APPLICANT: Yadegari, Ramin

APPLICANT: Margossian, Linda

APPLICANT: Harada, John

APPLICANT: Goldberg, Robert B.

TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and

FILE REFERENCE: 021070-086110US

CURRENT APPLICATION NUMBER: US/10/213,512

CURRENT FILING DATE: 2002-08-06

PRIOR APPLICATION NUMBER: US/09/177,206

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: US 09/071,838

PRIOR FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 324

SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-269

Query Match
Best Local Similarity 60.0%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 6 VVM 8

RESULT 45
US-10-060-019-1
; Sequence 1, Application US/10060019
; Publication No. US20030003564A1
; GENERAL INFORMATION:
; APPLICANT: Tvers, Mike
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/10/060,019
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/177,165
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-060-019-1

Query Match
Best Local Similarity 60.0%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 46
US-09-954-385-400
; Sequence 400, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 400
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Binding peptide
US-09-954-385-400

Query Match
Best Local Similarity 60.0%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 6 MEV 8

RESULT 47
US-10-119-528-104
; Sequence 104, Application US/10119528
; Publication No. US20030175722A1
; GENERAL INFORMATION:
; APPLICANT: Mann, M.
; APPLICANT: Mortensen, P.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES
; FILE REFERENCE: MDSP-P01-004
; CURRENT APPLICATION NUMBER: US/10/119,528
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,551
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/285,362
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-119-528-104

Query Match
Best Local Similarity 60.0%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 3 VVM 5

RESULT 48
US-09-012-135A-25
; Sequence 25, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Florman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435

```



; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/005,268  
 ; FILING DATE: January 9, 1998  
 ; APPLICATION NUMBER: 08/755,728  
 ; FILING DATE: No. US20020081578A1ember 25, 1996  
 ; APPLICATION NUMBER: 60/023,943  
 ; FILING DATE: August 14, 1996  
 ; APPLICATION NUMBER: 60/008,809  
 ; FILING DATE: December 18, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 231/282  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-9440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; US-09-012-135A-25

Query Match 60.0%; Score 3; DB 9; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
 Db 5 VME 7

## RESULT 49

US-09-813-333-30  
 ; Sequence 30, Application US/0981333  
 ; Patent No. US20020119160A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeGroot, Anne S  
 ; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters  
 ; FILE REFERENCE: 17999-004 US  
 ; CURRENT APPLICATION NUMBER: US/09/813,333  
 ; CURRENT FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: 60/190,834  
 ; PRIOR FILING DATE: 2000-03-20  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 30  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; US-09-813-333-30

Query Match 60.0%; Score 3; DB 10; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 Db 5 VVM 7

## RESULT 50

US-10-137-867-268  
 ; Sequence 268, Application US/10137867  
 ; Publication No. US20030207349A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary B.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P330R1C146  
 ; CURRENT APPLICATION NUMBER: US/10/137,867  
 ; CURRENT FILING DATE: 2002-05-03  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 268  
 ; LENGTH: 493  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-137-867-268

Query Match 60.0%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 Db 1 VVM 3

## RESULT 51

US-10-044-703-30  
 ; Sequence 30, Application US/10044703  
 ; Publication No. US20020192233A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeGroot, Anne S  
 ; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters  
 ; FILE REFERENCE: 17999-004 US  
 ; CURRENT APPLICATION NUMBER: US/10/044,703  
 ; CURRENT FILING DATE: 2002-05-20  
 ; PRIOR APPLICATION NUMBER: 60/190,834  
 ; PRIOR FILING DATE: 2000-03-20  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 30  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; US-10-044-703-30

Query Match 60.0%; Score 3; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
 Db 5 VVM 7

## RESULT 52

US-09-229-173-35  
 ; Sequence 35, Application US/09229173  
 ; Publication No. US20030027296A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chatterjee, Deb K.  
 ; TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga  
 ; maritima and Mutants Thereof  
 ; NUMBER OF SEQUENCES: 47

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
;/ STREET: 1100 New York Ave., N.W., Suite 600  
;/ CITY: Washington  
;/ STATE: DC  
;/ COUNTRY: USA  
;/ ZIP: 20005-3934  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/229,173  
;/ FILING DATE: 13-JAN-1999  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/706,702  
;/ FILING DATE: 06-SEP-1996  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/689,807  
;/ FILING DATE: 14-AUG-1996  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/537,400  
;/ FILING DATE: 02-OCT-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/576,759  
;/ FILING DATE: 21-DEC-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/537,397  
;/ FILING DATE: 02-OCT-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/525,057  
;/ FILING DATE: 08-SEP-1995  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Millonig, Robert C.  
;/ REGISTRATION NUMBER: 34,395  
;/ REFERENCE/DOCKET NUMBER: 0942.2800008  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 202-371-2600  
;/ TELEFAX: 202-371-2540  
;/ INFORMATION FOR SEQ ID NO: 35:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 14 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: not relevant  
;/ MOLECULE TYPE: peptide  
;/ US-09-229-173-35

Query Match 60.0%; Score 3; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VVM 3  
DB 9 VVM 11

RESULT 53  
US-10-176-416-19  
;/ Sequence 19, Application US/10176416  
;/ Publication No. US20030186864A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Thorn, R.  
;/ APPLICANT: Lanzer, M.  
;/ APPLICANT: Moses, M.  
;/ APPLICANT: Wiederschain, D.  
;/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS, TO  
;/ TITLE OF INVENTION: FRAGMENTS AND HOMOLOGS THEREOF AND METHODS OF THEIR USE  
;/ TITLE OF INVENTION: INHIBIT ANGIOGENESIS  
;/ FILE REFERENCE: 8657-043  
;/ CURRENT APPLICATION NUMBER: US/10/176,416

;/ CURRENT FILING DATE: 2002-06-18  
;/ PRIOR APPLICATION NUMBER: 09/442,099  
;/ PRIOR FILING DATE: 1999-11-17  
;/ PRIOR APPLICATION NUMBER: 09/268,274  
;/ PRIOR FILING DATE: 1999-03-15  
;/ PRIOR APPLICATION NUMBER: 08/961,264  
;/ PRIOR FILING DATE: 1997-10-30  
;/ PRIOR APPLICATION NUMBER: 08/602,941  
;/ PRIOR FILING DATE: 1996-02-16  
;/ NUMBER OF SEQ ID NOS: 20  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 19  
;/ LENGTH: 14  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: tryptic peptide  
;/ US-10-176-416-19

Query Match 60.0%; Score 3; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 MEV 5  
DB 11 MEV 13

RESULT 54  
US-10-192-806-19  
;/ Sequence 19, Application US/10192806  
;/ Publication No. US20030083255A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Thorn, R.  
;/ APPLICANT: Lanzer, M.  
;/ APPLICANT: Moses, M.  
;/ APPLICANT: Wiederschain, D.  
;/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
;/ TITLE OF INVENTION: TROPONIN SUBUNITS, FRAGMENTS AND HOMOLOGS THEREOF AND  
;/ TITLE OF INVENTION: METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS  
;/ FILE REFERENCE: 8657-042-999  
;/ CURRENT APPLICATION NUMBER: US/10/192,806  
;/ CURRENT FILING DATE: 2002-07-09  
;/ PRIOR APPLICATION NUMBER: 09/612,421  
;/ PRIOR FILING DATE: 2000-07-07  
;/ PRIOR APPLICATION NUMBER: 09/268,274  
;/ PRIOR FILING DATE: 1999-03-15  
;/ PRIOR APPLICATION NUMBER: 08/961,264  
;/ PRIOR FILING DATE: 1997-10-30  
;/ PRIOR APPLICATION NUMBER: 08/602,941  
;/ PRIOR FILING DATE: 1996-02-16  
;/ NUMBER OF SEQ ID NOS: 20  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 19  
;/ LENGTH: 14  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: tryptic peptide  
;/ US-10-192-806-19

Query Match 60.0%; Score 3; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 MEV 5  
DB 11 MEV 13

RESULT 55  
US-10-120-604-124  
;/ Sequence 124, Application US/10120604

```

; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-124

Query Match      60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      10 VVM 12

RESULT 56
US-10-207-655-300
; Sequence 300, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 300
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 14 amino acids deleted from IGAH-T4 (so that total
; OF OTHER INFORMATION: of 18 amino acids deleted from wild type IGA CH3
US-10-207-655-300

Query Match      60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      8 VVM 10

RESULT 57
US-10-286-134-12
; Sequence 12, Application US/10286134
; Publication No. US20030119747A1
; GENERAL INFORMATION:
; APPLICANT: THORN, RICHARD M.
; APPLICANT: LANSER, MARC E.
; APPLICANT: MOSES, MARSHA A.
; APPLICANT: WIEDERSCHAIN, DMITRI G.

```

```

; TITLE OF INVENTION: METHODS OF USING PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: TROPONIN SUBUNITS AND HOMOLOGS THEREOF BEFORE, DURING, OR
; TITLE OF INVENTION: AFTER SURGICAL RESECTION OR RADIOLOGIC ABLATION OF A SOLID
; FILE REFERENCE: 057932-053421
; CURRENT APPLICATION NUMBER: US/10/286,134
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/335,133
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OF OTHER INFORMATION: tryptic peptide
US-10-286-134-12

```

```

Query Match      60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 MEV 5
Db      11 MEV 13

```

```

RESULT 58
US-09-759-143-808
; Sequence 808, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; OF OTHER INFORMATION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121,427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-808

```

```

Query Match      60.0%; Score 3; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VME 4
Db      3 VME 5

```

## RESULT 59

US-09-780-669-808  
; Sequence 808, Application US/09780669  
; Patent No. US20020051977A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C24  
; CURRENT APPLICATION NUMBER: US/09/780.669  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 943  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 808  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-669-808

Query Match 60.0%; Score 3; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
Db 3 VME 5

## RESULT 60

US-09-822-827-808  
; Sequence 808, Application US/09822827  
; Patent No. US20020081680A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822.827  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 808  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-822-827-808

Query Match 60.0%; Score 3; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
Db 3 VME 5

## RESULT 61

US-09-791-171-84  
; Sequence 84, Application US/09791171  
; Patent No. US20020094336A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSEN, Peter  
; APPLICANT: NIELSEN, Rikke  
; APPLICANT: OETTINGER, Thomas  
; APPLICANT: ROSENKRANDS, Ida  
; APPLICANT: WELDINGH, Karin  
; APPLICANT: FLORIO, Walter  
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS  
; FILE REFERENCE: 670001-2002.1  
; CURRENT APPLICATION NUMBER: US/09/791.171  
; CURRENT FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 09/050.739  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 0376/97  
; PRIOR FILING DATE: 1997-04-02  
; PRIOR APPLICATION NUMBER: 1277/97  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/044.624  
; PRIOR FILING DATE: 1997-04-18  
; PRIOR APPLICATION NUMBER: 60/070.488  
; PRIOR FILING DATE: 1998-01-05  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-09-791-171-84

Query Match 60.0%; Score 3; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
Db 12 VVM 14

## RESULT 62

US-09-945-249-88  
; Sequence 88, Application US/09945249  
; Patent No. US20020168748A1  
; GENERAL INFORMATION:  
; APPLICANT: BERLIN, VIVIAN  
; APPLICANT: DAMAGNEZ, VERONIQUE  
; APPLICANT: SMITH, SUSAN E.  
; TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,  
; FILE REFERENCE: MIV-074.06  
; CURRENT APPLICATION NUMBER: US/09/945.249  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 09/041.990  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: 08/771.212  
; PRIOR FILING DATE: 1996-12-20  
; PRIOR APPLICATION NUMBER: 08/631.319  
; PRIOR FILING DATE: 1996-04-11  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide that

; OTHER INFORMATION: corresponds to the C-termini of FTase or GGTase  
; OTHER INFORMATION: substrates  
US-09-945-249-88

Query Match 60.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VWM 3  
|||  
Db 13 VWM 15

## RESULT 63

US-09-895-793-808  
; Sequence 808, Application US/09895793  
; Publication No. US20020192763A1

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.534C2

; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 808

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-793-808

Query Match 60.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 VME 4  
|||  
Db 3 VME 5

## RESULT 64

US-09-895-814-808

; Sequence 808, Application US/09895814

; Publication No. US20020193296A1

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C26

; CURRENT APPLICATION NUMBER: US/09/895,814

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 990

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 808

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-814-808

Query Match 60.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 VME 4  
|||  
Db 3 VME 5

## RESULT 65

US-09-918-873-20

; Sequence 20, Application US/09918873

; Publication No. US20030032649A1

## GENERAL INFORMATION:

; APPLICANT: Goldsmith, Elizabeth J.

; APPLICANT: Radha, Akella

; APPLICANT: Gaynor, Richard B.

; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG

; TITLE OF INVENTION: DISCOVERY

; FILE REFERENCE: A33864 090495.0232

; CURRENT APPLICATION NUMBER: US/09/918,873

; CURRENT FILING DATE: 2002-07-31

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; DATABASE ACCESSION NUMBER: P47197

; DATABASE ENTRY DATE: 1996-06-01

US-09-918-873-20

Query Match 60.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 VME 4  
|||  
Db 3 VME 5

## RESULT 66

US-09-804-980-84

; Sequence 84, Application US/09804980

```

; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-84

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
      |||
Db      12 VVM 14

RESULT 67
US-10-144-678A-808
; Sequence 808, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retzer, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-808

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VME 4
      |||
Db      12 VVM 14

US-09-641-801-9.oligo.rapb

; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-84

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
      |||
Db      12 VVM 14

RESULT 68
US-10-199-820-273
; Sequence 273, Application US/10199820
; Publication No. US20030180739A1
; GENERAL INFORMATION:
; APPLICANT: Board of Trustees of the University of Illinois
; APPLICANT: Primiano, Thomas
; APPLICANT: Chang, Bey-dih
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating
; FILE REFERENCE: 99,216-U
; CURRENT APPLICATION NUMBER: US/10/199,820
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-820-273

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VME 4
      |||
Db      7 VME 9

RESULT 69
US-10-294-025-808
; Sequence 808, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-808

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VME 4
      |||
Db      3 VME 5

RESULT 70
US-10-012-896-808
; Sequence 808, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu

```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-808

Query Match      60.0%; Score 3; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VME 4
Db      3 VME 5

RESULT 71
US-10-060-019-2
; Sequence 2, Application US/10060019
; Publication No. US20030003564A1
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/10/060,019
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/177,165
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-060-019-2

Query Match      60.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
      |||

```

```

Db      2 MEV 4

RESULT 72
US-10-293-822-13
; Sequence 13, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-822-13

Query Match      60.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
      |||
Db      5 VVM 7

RESULT 73
US-08-424-550B-181
; Sequence 181, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207

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; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-181

Query Match          60.0%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      10 MEV 12

RESULT 74
US-09-813-333-20
; Sequence 20, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-20

Query Match          60.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
Db      2 VVM 4

RESULT 75
US-09-766-889A-57
; Sequence 57, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-57

Query Match          60.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3

Search completed: November 25, 2003, 20:25:36
Job time : 11.9468 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 5.45213 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-9

Perfect score: 5  
Sequence: 1 VMEV 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	4	US-09-641-803-9
2	5	100.0	12	4	US-09-106-568E-121
3	5	100.0	15	6	5252466-12
4	4	80.0	9	3	US-08-159-339A-603
5	4	80.0	10	3	US-08-159-339A-101
6	4	80.0	10	3	US-08-159-339A-596
7	3	60.0	4	1	US-08-062-287-7
8	3	60.0	4	2	US-08-464-203-7
9	3	60.0	4	2	US-08-429-964-18
10	3	60.0	4	3	US-09-195-578-3
11	3	60.0	4	3	US-09-140-557-3
12	3	60.0	4	3	US-09-170-951-3
13	3	60.0	4	3	US-09-164-482-3
14	3	60.0	4	3	US-09-167-180-3
15	3	60.0	4	4	US-09-552-265B-6
16	3	60.0	4	5	PCT-US93-08062-18
17	3	60.0	5	1	US-08-029-333-5
18	3	60.0	5	1	US-08-029-333-6
19	3	60.0	5	1	US-08-029-333-7
20	3	60.0	5	1	US-08-347-000-5
21	3	60.0	5	4	US-08-391-820-5
22	3	60.0	5	4	US-08-391-820-6
23	3	60.0	5	4	US-08-391-820-7
24	3	60.0	5	4	US-08-541-939-3
25	3	60.0	5	4	US-08-877-605-296
26	3	60.0	6	1	US-08-029-333-3
27	3	60.0	6	1	US-08-347-000-3

28	3	60.0	6	1	US-08-457-274A-14	Sequence 14, Appl
29	3	60.0	6	3	US-08-981-256A-1	Sequence 1, Appl
30	3	60.0	6	3	US-08-789-333F-91	Sequence 91, Appl
31	3	60.0	6	4	US-08-787-738B-91	Sequence 91, Appl
32	3	60.0	6	4	US-08-391-820-3	Sequence 3, Appl
33	3	60.0	6	5	PCT-US95-05758-14	Sequence 14, Appl
34	3	60.0	7	1	US-07-968-781A-67	Sequence 67, Appl
35	3	60.0	7	1	US-08-266-570A-8	Sequence 8, Appl
36	3	60.0	7	2	US-08-719-758-20	Sequence 20, Appl
37	3	60.0	7	3	US-09-119-827-20	Sequence 20, Appl
38	3	60.0	7	3	US-09-461-697-140	Sequence 140, App
39	3	60.0	7	4	US-09-354-147C-38	Sequence 38, Appl
40	3	60.0	8	1	US-08-029-333-2	Sequence 2, Appl
41	3	60.0	8	1	US-08-347-000-2	Sequence 2, Appl
42	3	60.0	8	3	US-08-993-165-18	Sequence 18, Appl
43	3	60.0	8	3	US-09-078-173A-5	Sequence 5, Appl
44	3	60.0	8	4	US-09-540-448-18	Sequence 18, Appl
45	3	60.0	8	4	US-08-391-820-2	Sequence 2, Appl
46	3	60.0	8	4	US-09-243-640-16	Sequence 16, Appl
47	3	60.0	8	4	US-08-929-847-18	Sequence 18, Appl
48	3	60.0	9	2	US-08-951-309-1	Sequence 1, Appl
49	3	60.0	9	2	US-08-951-309-2	Sequence 2, Appl
50	3	60.0	9	4	US-03-644-600-73	Sequence 73, Appl
51	3	60.0	9	4	US-08-388-852B-24	Sequence 24, Appl
52	3	60.0	10	1	US-08-331-398A-40	Sequence 40, Appl
53	3	60.0	10	1	US-08-331-398A-41	Sequence 41, Appl
54	3	60.0	10	1	US-08-331-398A-42	Sequence 42, Appl
55	3	60.0	10	1	US-08-347-000-7	Sequence 7, Appl
56	3	60.0	10	1	US-08-796-883-17	Sequence 17, Appl
57	3	60.0	10	1	US-08-796-883-29	Sequence 29, Appl
58	3	60.0	10	2	US-08-755-728-13	Sequence 13, Appl
59	3	60.0	10	2	US-09-036-582-5	Sequence 5, Appl
60	3	60.0	10	2	US-08-974-655-13	Sequence 13, Appl
61	3	60.0	10	2	US-08-531-864-17	Sequence 17, Appl
62	3	60.0	10	2	US-08-331-397B-40	Sequence 40, Appl
63	3	60.0	10	2	US-08-331-397B-41	Sequence 41, Appl
64	3	60.0	10	2	US-08-331-397B-42	Sequence 42, Appl
65	3	60.0	10	2	US-08-759-804A-40	Sequence 40, Appl
66	3	60.0	10	2	US-08-759-804A-41	Sequence 41, Appl
67	3	60.0	10	2	US-08-759-804A-42	Sequence 42, Appl
68	3	60.0	10	3	US-08-602-506A-17	Sequence 17, Appl
69	3	60.0	10	3	US-08-602-506A-29	Sequence 29, Appl
70	3	60.0	10	3	US-08-795-430-14	Sequence 14, Appl
71	3	60.0	10	3	US-08-613-557-12	Sequence 12, Appl
72	3	60.0	10	3	US-09-266-294-17	Sequence 17, Appl
73	3	60.0	10	3	US-09-283-011-13	Sequence 13, Appl
74	3	60.0	10	3	US-09-183-931-37	Sequence 37, Appl
75	3	60.0	10	3	US-09-177-249-269	Sequence 269, App
76	3	60.0	10	3	US-09-183-706-8	Sequence 8, Appl
77	3	60.0	10	3	US-09-227-693-40	Sequence 40, Appl
78	3	60.0	10	3	US-09-227-693-41	Sequence 41, Appl
79	3	60.0	10	3	US-09-227-693-42	Sequence 42, Appl
80	3	60.0	10	3	US-09-166-448-49	Sequence 49, Appl
81	3	60.0	10	4	US-09-567-995-8	Sequence 8, Appl
82	3	60.0	10	4	US-09-227-357-315	Sequence 315, App
83	3	60.0	10	4	US-09-355-700-14	Sequence 14, Appl
84	3	60.0	10	4	US-09-705-160-37	Sequence 37, Appl
85	3	60.0	10	4	US-09-165-863-5	Sequence 5, App
86	3	60.0	10	4	US-08-197-484-83	Sequence 83, Appl
87	3	60.0	10	4	US-08-197-484-142	Sequence 142, App
88	3	60.0	10	4	US-09-697-884-49	Sequence 49, Appl
89	3	60.0	10	4	US-09-123-192C-42	Sequence 42, Appl
90	3	60.0	10	4	US-09-289-350-5	Sequence 5, App
91	3	60.0	10	4	US-09-574-749B-5	Sequence 5, Appl
92	3	60.0	10	5	PCT-US95-02121-83	Sequence 83, Appl
93	3	60.0	10	5	PCT-US95-02121-142	Sequence 142, App
94	3	60.0	11	1	US-08-029-333-4	Sequence 4, Appl
95	3	60.0	11	1	US-08-029-333-30	Sequence 30, Appl
96	3	60.0	11	1	US-08-029-333-32	Sequence 32, Appl
97	3	60.0	11	1	US-08-029-333-33	Sequence 33, Appl
98	3	60.0	11	1	US-08-029-333-39	Sequence 39, Appl
99	3	60.0	11	1	US-08-029-333-40	Sequence 40, Appl
100	3	60.0	11	1	US-08-029-333-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-641-803-9  
; Sequence 9, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-9

Query Match 100.0%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMVEV 5  
Db 1 VMVEV 5

RESULT 2  
US-09-106-568E-121  
; Sequence 121, Application US/09106568E  
; Patent No. 6455248  
; GENERAL INFORMATION:  
; APPLICANT: Bhattacharjee, J.  
; APPLICANT: Suvarna, Kalavati  
; APPLICANT: Bhattacharjee, Vasker  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN  
; TITLE OF INVENTION: A BIOLOGICAL SAMPLE  
; FILE REFERENCE: 96,247-A  
; CURRENT APPLICATION NUMBER: US/09/106,568E  
; CURRENT FILING DATE: 1998-06-29  
; PRIOR APPLICATION NUMBER: 08/650,809  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Microsoft Word 97  
; SEQ ID NO 121  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide segment of GRSB\_1BACB shown in Figure 4.  
US-09-106-568E-121

Query Match 100.0%; Score 5; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMVEV 5  
Db 8 VMVEV 12

RESULT 3  
5252466-12  
; Patent No. 5252466  
; APPLICANT: CRONAN, JOHN E.  
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN  
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND  
; PURIFYING THEM  
; NUMBER OF SEQUENCES: 24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/525,568  
; FILING DATE: 18-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 354,266  
; FILING DATE: 19-MAY-1989  
; SEQ ID NO:12;  
; LENGTH: 15  
5252466-12

Query Match 100.0%; Score 5; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMVEV 5  
Db 10 VMVEV 14

RESULT 4  
US-08-159-339A-603  
; Sequence 603, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 603:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-603

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5  
Db 2 VMEV 5

RESULT 5  
US-08-159-339A-101  
; Sequence 101, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-101

Query Match 80.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5

Db  
||||  
6 VMEV 9

RESULT 6  
US-08-159-339A-596  
; Sequence 596, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 596:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-159-339A-596

Query Match 80.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5  
Db 3 VMEV 6

RESULT 7  
US-08-062-287-7  
; Sequence 7, Application US/08062287  
; Patent No. 5602098  
; GENERAL INFORMATION:  
; APPLICANT: SEBTLI, SAID  
; APPLICANT: HAMILTON, ANDREW  
; APPLICANT: SEONG, CHURL M.

;  
; TITLE OF INVENTION: INHIBITION OF FARNESYL TRANSFERASE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMNA  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/062,287  
; FILING DATE: 18-MAY-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 200385/6137  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-062-287-7

Query Match 60.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 VVM 3  
Db 2 VVM 4

RESULT 8  
US-08-464-203-7  
; Sequence 7, Application US/08464203  
; Patent No. 5856310  
; GENERAL INFORMATION:  
; APPLICANT: SEBTI, SAID  
; APPLICANT: HAMILTON, ANDREW  
; APPLICANT: SEONG, CHURL M.  
; TITLE OF INVENTION: INHIBITION OF FARNESYL TRANSFERASE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMNA  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,203  
; FILING DATE: 05-JUNE-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 200385/6137

;  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-464-203-7

Query Match 60.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 VVM 3  
Db 2 VVM 4

RESULT 9  
US-08-429-964-18  
; Sequence 18, Application US/08429964  
; Patent No. 5962243  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: REISS, YUVAL  
; APPLICANT: JAMES, GUY L.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE  
; STREET: P.O. BOX 4433  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 77210  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/429,964  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/021,625  
; FILING DATE: 16-FEB-1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/822,011  
; FILING DATE: ABANDONED  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: PCT/US/91/02650  
; FILING DATE: 18-APR-1991  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/615,715  
; FILING DATE: 20-NOV-1990  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/510,706  
; FILING DATE: 18-APR-1990 (ABANDONED)  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARKER, DAVID L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924



Query Match 60.0%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
Db 2 VVM 4

RESULT 14  
US-09-167-180-3  
; Sequence 3, Application US/09167180  
; Patent No. 6297239  
; GENERAL INFORMATION:  
; APPLICANT: deSolms, S. Jane  
; APPLICANT: Hutchinson, John H.  
; APPLICANT: Shaw, Anthony W.  
; APPLICANT: Graham, Samuel L.  
; APPLICANT: Ciccarone, Terrence M.  
; APPLICANT: Merck & Co., Inc.  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
; FILE REFERENCE: 19928Y  
; CURRENT APPLICATION NUMBER: US/09/167,180  
; CURRENT FILING DATE: 1998-10-06  
; EARLIER APPLICATION NUMBER: 60/062,660  
; EARLIER FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homosapien  
US-09-167-180-3

Query Match 60.0%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
Db 2 VVM 4

RESULT 15  
US-09-552-265B-6  
; Sequence 6, Application US/09552265B  
; Patent No. 6555343  
; GENERAL INFORMATION:  
; APPLICANT: DeSavauge, Frederick  
; APPLICANT: Henner, Dennis, J.  
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)  
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same  
; FILE REFERENCE: GENENT 057CP1  
; CURRENT APPLICATION NUMBER: US/09/552,265B  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: US 09/307307  
; PRIOR FILING DATE: 1999-05-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Pan troglodytes  
US-09-552-265B-6

Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
Db 1 MEV 3

RESULT 16  
PCT-US93-08062-18  
; Sequence 18, Application PC/TUS9308062  
; GENERAL INFORMATION:  
; APPLICANT:  
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.  
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.  
; SEQUENCE CHARACTERISTICS: REISS, YUVAL  
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.  
; ADDRESSEE: METHODS AND COMPOSITIONS FOR  
; ADDRESSEE: THE IDENTIFICATION,  
; ADDRESSEE: CHARACTERIZATION AND  
; ADDRESSEE: INHIBITION OF  
; ADDRESSEE: FARNESYLTRANSFERASE  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE  
; STREET: P.O. BOX 4433  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK/ASKII  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08062  
; FILING DATE: AUGUST 24, 1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/935,087  
; FILING DATE: 24 AUGUST 1992 (24.08.92)  
; NAME: UNKNOWN  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARKER, DAVID L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTFD377PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 512-474-7577  
; TELEX: NOT APPLICABLE  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US93-08062-18

Query Match 60.0%; Score 3; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
Db 2 VVM 4

RESULT 17  
US-08-029-333-5  
; Sequence 5, Application US/08029333  
; Patent No. 5399667  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Kosfeld, Minh D.  
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG

```
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-5

Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
Db      3 VVM 5

RESULT 18
US-08-029-333-6
; Sequence 6, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-7

Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
Db      3 VVM 5

RESULT 19
US-08-029-333-7
; Sequence 7, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-7

Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
Db      3 VVM 5

RESULT 20
US-08-347-000-5
; Sequence 5, Application US/08347000
; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
;
; PRIOR APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-347-000-5
;
; Query Match 60.0%; Score 3; DB 1; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 21
; US-08-391-820-5
; Sequence 5, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; US-08-391-820-6
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 22
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; US-08-391-820-6
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 23
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
```

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;
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
;
; US-08-391-820-5
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 22
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
; US-08-391-820-6
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 23
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
```



```
Db          3 VVM 5

RESULT 23
US-08-391-820-7
; Sequence 7, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-391-820-7

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 VVM 3
           |||
Db          3 VVM 5

RESULT 24
US-08-541-939-3
; Sequence 3, Application US/08541939
; Patent No. 6541238
; GENERAL INFORMATION:
; APPLICANT: Saxena, Inder M.
; APPLICANT: Lin, Fong C.
; APPLICANT: Brown, R. M.
; TITLE OF INVENTION: Recombinant Cellulose Synthase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/222,322
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSB:564/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-541-939-3

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 MEV 5
           |||
Db          1 MEV 3

RESULT 25
US-08-877-605-296
; Sequence 296, Application US/08877605
; Patent No. 6582965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Z Library
US-08-877-605-296

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 VVM 3
           |||
Db          3 VVM 5

RESULT 26
US-08-029-333-3
; Sequence 3, Application US/08029333
```

```
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24 (982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-029-333-3

Query Match 60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

; RESULT 27
; US-08-347-000-3
; Sequence 3, Application US/08347000
; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; Thrombospondins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-000-3

Query Match 60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

; RESULT 28
; US-08-457-274A-14
; Sequence 14, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
```

FILE REFERENCE: A642601DJBRMSDSS

STATE: Missouri  
COUNTRY: USA  
ZIP: 63167  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/391,820  
FILING DATE: 21-Feb-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/029,333  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyer, Scott J.  
REGISTRATION NUMBER: 25,275  
REFERENCE/DOCKET NUMBER: 07-24(1982)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)694-3117  
TELEFAX: (314)694-5435  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-391-820-3

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3  
|||  
Db 4 VWM 6

RESULT 33  
PCT-US95-05758-14  
Sequence 14, Application PC/TUS9505758  
GENERAL INFORMATION:  
APPLICANT: Cornell Research Foundation, Inc.  
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05758  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1304  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Musca domestica  
STRAIN: Learn-Pyr  
DEVELOPMENTAL STAGE: Adult  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Chromosome 1  
PCT-US95-05758-14

Query Match 60.0%; Score 3; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
|||  
Db 2 VME 4

RESULT 34  
US-07-968-781A-67  
Sequence 67, Application US/07968781A  
Patent No. 5430137  
GENERAL INFORMATION:  
APPLICANT: Gaertner, Frank H.  
APPLICANT: Sick, August J.  
APPLICANT: Thompson, Mark  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Schwab, George E.  
APPLICANT: Narva, Kenneth E.  
TITLE OF INVENTION: Probes for the Identification of Bacillus  
NUMBER OF INVENTION: thuringiensis Endotoxin Genes  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/968,781A  
FILING DATE: 19921030  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA44.FWCC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-968-781A-67

Query Match 60.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
|||  
Db 2 VME 4

## RESULT 35

US-08-266-570A-8  
; Sequence 8, Application US/08266570A  
; Patent No. 5484723  
; GENERAL INFORMATION:  
; APPLICANT: Zenno, Shuhei  
; APPLICANT: Saigo, Kaoru  
; TITLE OF INVENTION: FLAVIN REDUCTASE GENE FROM VIBRIO  
; TITLE OF INVENTION: FISCHERI  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
; STREET: 700 Thirteenth Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/266,570A  
; FILING DATE: 28-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 181850/1993  
; FILING DATE: 28-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rose, Herbert C.  
; REGISTRATION NUMBER: 29846  
; REFERENCE/DOCKET NUMBER: 60257/No. 5484723aka  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 737-6770  
; TELEFAX: (202) 737-6776  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acids  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-266-570A-8

Query Match 60.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
|||  
Db 5 VVM 7

## RESULT 36

US-08-719-758-20  
; Sequence 20, Application US/08719758  
; Patent No. 5837537  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Kevin P.  
; APPLICANT: Jung, Daniel  
; APPLICANT: Duclos, Franck  
; APPLICANT: Straub, Volker  
; TITLE OF INVENTION: k-SARCOSYLCAN NUCLEIC ACID SEQUENCES, AMINO  
; TITLE OF INVENTION: ACID SEQUENCES AND APPLICATIONS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/719,758  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: UIRF-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-719-758-20

Query Match 60.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4  
|||  
Db 3 VME 5

## RESULT 37

US-09-119-827-20  
; Sequence 20, Application US/09119827  
; Patent No. 6211340  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Kevin P.  
; APPLICANT: Jung, Daniel  
; APPLICANT: Duclos, Franck  
; APPLICANT: Straub, Volker  
; TITLE OF INVENTION: k-SARCOSYLCAN NUCLEIC ACID SEQUENCES, AMINO  
; TITLE OF INVENTION: ACID SEQUENCES AND APPLICATIONS  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/119,827  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: UIRF-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-119-827-20

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
|||  
Db 3 VME 5

RESULT 38  
US-09-461-697-140  
; Sequence 140, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; TITLE OF INVENTION: CELL DEATH  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-461-697-140

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
Db 1 MEV 3

RESULT 39  
US-09-354-147C-38  
; Sequence 38, Application US/09354147C  
; Patent No. 6573067  
; GENERAL INFORMATION:  
; APPLICANT: Dib-Hajj, Sulayman  
; APPLICANT: Waxman, Stephen G.  
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia  
; FILE REFERENCE: 44574-5004-01-US  
; CURRENT APPLICATION NUMBER: US/09/354,147C  
; CURRENT FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US 60/072,990  
; PRIOR FILING DATE: 1998-01-29  
; PRIOR APPLICATION NUMBER: US 60/109,402  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: PCT/US99/02008  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: protein seq.  
; OTHER INFORMATION: basis for rat Nan reverse primers  
; NAME/KEY: VARIANT  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa = Val or Asp  
US-09-354-147C-38

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
Db 5 MEV 7

RESULT 40  
US-08-029-333-2  
; Sequence 2, Application US/08029333  
; Patent No. 5399667  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Kosfeld, Minh D.  
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/029,333  
; FILING DATE: 19930305  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: 07-24 (982)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-029-333-2

Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
|||  
Db 4 VVM 6

RESULT 41  
US-08-347-000-2  
; Sequence 2, Application US/08347000

; Patent No. 5627265  
; GENERAL INFORMATION:  
; APPLICANT: Frazier, William A.  
; APPLICANT: Gao, Ai-Guo  
; TITLE OF INVENTION: Receptor for Cell-binding Domain of  
; TITLE OF INVENTION: Thrombospondins  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,000  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/029,333  
; FILING DATE: 05-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: WU-2848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-347-000-2

Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
Db 4 VVM 6

RESULT 42  
US-08-993-165-18  
; Sequence 18, Application US/08993165A  
; Patent No. 6123923  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C  
; APPLICANT: Wu, Yungiu  
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use  
; FILE REFERENCE: UNGR1224  
; CURRENT APPLICATION NUMBER: US/08/993,165A  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence  
US-08-993-165-18

Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVM 3  
Db 4 VVM 6

RESULT 43  
US-09-078-173A-5  
; Sequence 5, Application US/09078173A  
; Patent No. 6200794  
; GENERAL INFORMATION:  
; APPLICANT: Ian M. Whitehead  
; APPLICANT: Alan Slusarenko  
; APPLICANT: Duncan Gaskins  
; APPLICANT: Alan Brash  
; APPLICANT: Nathalie Tijet  
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE  
; TITLE OF INVENTION: LYASE AND USES THEREOF  
; FILE REFERENCE: 06027.0001  
; CURRENT APPLICATION NUMBER: US/09/078,173A  
; CURRENT FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Psidium Guajava (guava)  
US-09-078-173A-5

Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
Db 4 VVM 6

RESULT 44  
US-09-540-448-18  
; Sequence 18, Application US/09540448  
; Patent No. 6403056  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; TITLE OF INVENTION: Charged Lipids and Uses For The Same  
; FILE REFERENCE: UNGR1592  
; CURRENT APPLICATION NUMBER: US/09/540,448  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 08/925,353  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence  
US-09-540-448-18

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
Db 4 VVM 6

RESULT 45  
US-08-391-820-2  
; Sequence 2, Application US/08391820

```
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
;           Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-391-820-2

Query Match 60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

RESULT 46
US-09-243-640-16
; Sequence 16, Application US/09243640
; Patent No. 6521211
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: No. 6521211el Methods Of Imaging And Treatment With Targeted
; FILE REFERENCE: DUP-0463
; CURRENT APPLICATION NUMBER: US/09/243,640
; CURRENT FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 09/218,660
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 607/073,913
; PRIOR FILING DATE: 1998-02-06
```

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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
US-09-243-640-16

Query Match 60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

RESULT 47
US-08-929-847-18
; Sequence 18, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-18

Query Match 60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

RESULT 48
US-08-951-309-1
; Sequence 1, Application US/08951309
; Patent No. 5952473
; GENERAL INFORMATION:
; APPLICANT: COHEN, Louis H.
; APPLICANT: NIEUWENHUIZEN, Willem
; TITLE OF INVENTION: REAGENT AND KIT FOR DETERMINING
; TITLE OF INVENTION: ISOPRENYLATING ACTIVITY AND INHIBITION THEREOF
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Young & Thompson
; STREET: Second Floor, 745 S. 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,309
; FILING DATE:
```



```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,522
; FILING DATE: 20-APR-1994
; APPLICATION NUMBER: EP 93201146.3
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: BO 38354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/521-2297
; TELEFAX: 703/685-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-951-309-1
;
Query Match 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 7 VWM 9

RESULT 49
US-08-951-309-2
; Sequence 2, Application US/08951309
; Patent No. 5952473
; GENERAL INFORMATION:
; APPLICANT: COHEN, Louis H.
; APPLICANT: NIEUWENHUIZEN, Willem
; TITLE OF INVENTION: REAGENT AND KIT FOR DETERMINING
; FILE OF INVENTION: ISOPRENYLATING ACTIVITY AND INHIBITION THEREOF
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/o Young & Thompson
; STREET: Second Floor, 745 S. 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,522
; FILING DATE: 20-APR-1994
; APPLICATION NUMBER: EP 93201146.3
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: BO 38354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/521-2297
; TELEFAX: 703/685-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-951-309-2
;
Query Match 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 7 VWM 9

RESULT 50
US-09-644-600-73
; Sequence 73, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotsoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; FILE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 173-181 of the TADG-15 protein
; US-09-644-600-73
;
Query Match 60.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 6 VWM 8

RESULT 51
US-08-388-852B-24
; Sequence 24, Application US/08388852B
; Patent No. 6500919
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide.
; TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav
; STREET: Philips van Leydenlaan 25
; CITY: Nijmegen
; STATE: Brabant
; COUNTRY: the Netherlands
; ZIP: 6525 EX
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,852B
; FILING DATE: February 15, 1995
; INFORMATION FOR SEQ ID NO: 24:
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SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-388-852B-24

Query Match 60.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
DB 7 MEV 9

## RESULT 52

US-08-331-398A-40  
; Sequence 40, Application US/08331398A  
; Patent No. 5608039

GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: Fitzgerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pai, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TITLE OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US

TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-331-398A-40

Query Match 60.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
DB 1 MEV 3

## RESULT 54

US-08-331-398A-42  
; Sequence 42, Application US/08331398A  
; Patent No. 5608039

GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark

QY 3 MEV 5  
|||  
DB 1 MEV 3

## RESULT 53

US-08-331-398A-41  
; Sequence 41, Application US/08331398A  
; Patent No. 5608039

GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: Fitzgerald, David  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pai, Lee  
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
TITLE OF INVENTION: and Their Uses (as amended)  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US

TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-331-398A-41

Query Match 60.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
|||  
DB 1 MEV 3

```

; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-398A-42

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 6 VWM 8

RESULT 55
US-08-347-000-7
; Sequence 7, Application US/08347000
; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; TITLE OF INVENTION: Thrombospondins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 694-3117
; TELEFAX: (314) 694-5435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-000-7

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 5 VWM 7

RESULT 56
US-08-796-883-17
; Sequence 17, Application US/08796883
; Patent No. 5744353
; GENERAL INFORMATION:
; APPLICANT: Herman, Jean; Coullie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Luescher, Immanuel.
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By
; TITLE OF INVENTION: HLA-B*44 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,883
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,506
; FILING DATE: 20-FEBRUARY-1996
; APPLICATION NUMBER: 08/531,864
; FILING DATE: 21-SEPTEMBER-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5744353man D.
; REGISTRATION NUMBER: 30,946

```

REFERENCE/DOCKET NUMBER: LUD 5436  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Mage-3 peptide  
US-08-796-883-17

Query Match 60.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
Db 1 MEV 3

## RESULT 57

US-08-796-883-29  
Sequence 29, Application US/08796883  
Patent No. 5744353  
GENERAL INFORMATION:  
APPLICANT: Herman, Jean; Coullie, Pierre;  
APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;  
APPLICANT: Luescher, Immanuel.  
TITLE OF INVENTION: Tumor Rejection Antigens Presented By  
TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/796,883  
FILING DATE: 06-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,506  
FILING DATE: 20-FEBRUARY-1996  
APPLICATION NUMBER: 08/531,864  
FILING DATE: 21-SEPTEMBER-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,636  
FILING DATE: 17-JANUARY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253,503  
FILING DATE: 3-JUNE-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5744353man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5436  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

FEATURE:  
NAME/KEY: Mage-6/HLA-B44  
US-08-796-883-29

Query Match 60.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
Db 1 MEV 3

## RESULT 58

US-08-755-728-13  
Sequence 13, Application US/08755728  
Patent No. 5962312  
GENERAL INFORMATION:  
APPLICANT: Florman, Gregory  
APPLICANT: Mossie, Kevin  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1  
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/755,728  
FILING DATE: No. 5962312ember 25, 1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/008,809  
FILING DATE: December 18, 1995  
APPLICATION NUMBER: 60/023,943  
FILING DATE: August 14, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-755-728-13

Query Match 60.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4  
Db 1 VME 3

## RESULT 59

```
US-09-036-582-5
; Sequence 5, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human MAGE-3 peptide
US-09-036-582-5

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 60
US-09-74-655-13
; Sequence 13, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

US-09-036-655-13
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-974-655-13

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 MEV 4
Db      1 MEV 3

RESULT 61
US-08-531-864-17
; Sequence 17, Application US/08531864
; Patent No. 5977300
; GENERAL INFORMATION:
; APPLICANT: Coulie, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated No. 5977300a- and Decapeptides Which
; TITLE OF INVENTION: Bind to HLA-B44 Molecules And The Use Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,864
; FILING DATE: 21-September-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5977300man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5378.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-531-864-17

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 62
US-08-331-397B-40
; Sequence 40, Application US/08331397B
```

```
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-397B-40

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 63
US-08-331-397B-41
; Sequence 41, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-397B-41

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 64
US-08-331-397B-42
; Sequence 42, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-397B-42

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 6 VVM 8

;
; RESULT 65
; US-08-759-804A-40
; Sequence 40, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-759-804A-41

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

;
; RESULT 66
; US-08-759-804A-41
; Sequence 41, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-759-804A-41

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 MEV 5  
|||  
Db 1 MEV 3

## RESULT 67

US-08-759-804A-42  
; Sequence 42, Application US/08759804A  
; Patent No. 5990296  
; GENERAL INFORMATION:  
; APPLICANT: Fastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David J.  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/759,804A  
; FILING DATE: 03-DEC-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,398  
; FILING DATE: 28-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-126140US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-759-804A-42

Query Match 60.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3  
|||  
Db 6 VVM 8

## RESULT 68

US-08-602-506A-17  
; Sequence 17, Application US/08602506A  
; Patent No. 6060257  
; GENERAL INFORMATION:

; APPLICANT: Herman, Jean; Coulie, Pierre;  
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;  
; APPLICANT: Luescher, Immanuel.  
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By HLA-  
; TITLE OF INVENTION: B44 Molecules, And Uses Thereof  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,506A  
; FILING DATE: 20-FEBRUARY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/531,864  
; FILING DATE: 21-SEPTEMBER-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,636  
; FILING DATE: 17-JANUARY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/253,503  
; FILING DATE: 3-JUNE-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 6060257man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5436  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 938-3884  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Mage-3 peptide  
US-08-602-506A-17

Query Match 60.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5  
|||  
Db 1 MEV 3

## RESULT 69

US-08-602-506A-29  
; Sequence 29, Application US/08602506A  
; Patent No. 6060257  
; GENERAL INFORMATION:  
; APPLICANT: Herman, Jean; Coulie, Pierre;  
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;  
; APPLICANT: Luescher, Immanuel.  
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By HLA-  
; TITLE OF INVENTION: B44 Molecules, And Uses Thereof  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022



COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,506A  
FILING DATE: 20-FEBRUARY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/531,864  
FILING DATE: 21-SEPTEMBER-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,636  
FILING DATE: 17-JANUARY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/253,503  
FILING DATE: 3-JUNE-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6060257man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5436  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Wage-6/HLA-B44  
US-08-602-506A-29

Query Match 60.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
Db 1 MEV 3

RESULT 70  
US-08-795-430-14  
Sequence 14, Application US/08795430  
Patent No. 6130071  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33691  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-795-430-14

Query Match 60.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3  
Db 2 VVM 4

RESULT 71  
US-08-619-557-12  
Sequence 12, Application US/08619557  
Patent No. 6160087  
GENERAL INFORMATION:  
APPLICANT: Tomohiko OGAWA  
TITLE OF INVENTION: PEPTIDES HAVING AN AMINO ACID SEQUENCE FROM  
TITLE OF INVENTION: THE FIMBRIAL PROTEIN OF PORPHYROMONAS GINGIVALIS AND THEIR  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/619,557  
FILING DATE: March 27, 1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-619-557-12

Query Match 60.0%; Score 3; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3

|||

Db 4 VWM 6

## RESULT 72

US-09-266-294-17

Sequence 17, Application US/09266294

Patent No. 6171806

GENERAL INFORMATION:

APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated No. 6171806a- and Decapeptides Which

TITLE OF INVENTION: Bind to HLA-B44 Molecules And The Use Thereof

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe &amp; Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/266,294

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/531,864

FILING DATE: 21-September-1995

APPLICATION NUMBER: 08/373,636

FILING DATE: 17-JANUARY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/253,503

FILING DATE: 3-JUNE-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6171806man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5378.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-266-294-17

Query Match

Best Local Similarity 60.0%; Score 3; DB 3; Length 10;

Sequence 17, Application US/09183931C

Patent No. 6210886

GENERAL INFORMATION:

QY 3 MEV 5

|||

Db 1 MEV 3

## RESULT 73

US-09-283-011-13

Sequence 13, Application US/09283011

Patent No. 6207401

GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

APPLICANT: Mossie, Kevin

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1

TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/283,011

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/012,135

FILING DATE: January 22, 1998

APPLICATION NUMBER: 08/755,728

FILING DATE: No. 6207401ember 25, 1996

APPLICATION NUMBER: 60/023,943

FILING DATE: August 14, 1996

APPLICATION NUMBER: 60/008,809

FILING DATE: December 18, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 231/282

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-283-011-13

Query Match

Best Local Similarity 60.0%; Score 3; DB 3; Length 10;

Sequence 13, Application US/09183931C

Patent No. 6210886

GENERAL INFORMATION:

QY 2 VME 4

|||

Db 1 VME 3

## RESULT 74

US-09-183-931-37

Sequence 37, Application US/09183931C

Patent No. 6210886

GENERAL INFORMATION:

; APPLICANT: Van Baren, Nicolas  
; APPLICANT: Brasseur, Francis  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING  
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS  
; FILE REFERENCE: IJD 5527.1-JEL/ES  
; CURRENT APPLICATION NUMBER: US/09/183,931C  
; CURRENT FILING DATE: 2000-02-28  
; EARLIER APPLICATION NUMBER: US 09/018,422  
; EARLIER FILING DATE: 1998 - 02 - 04  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 37  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION:  
US-09-183-931-37

Query Match 60.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5  
Db 1 MEV 3

RESULT 75  
US-09-177-249-269  
; Sequence 269, Application US/09177249  
; Patent No. 6229064  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; TITLE OF INVENTION: Development in Plants  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/177,249  
; CURRENT FILING DATE: 1998-10-22  
; EARLIER APPLICATION NUMBER: US 09/071,838  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 269  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-269

Query Match 60.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3  
Db 6 VWM 8

Search completed: November 25, 2003, 20:16:05  
Job time : 6.45213 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 3.68085 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3	75.0	9	2	S77984	cytochrome-c oxida
2	3	75.0	12	2	E58502	43.2K bile stone p
3	3	75.0	12	2	S47363	T-cell antigen rec
4	3	75.0	14	2	S29209	avenin alpha-2 - o
5	3	75.0	15	2	S29207	avenin gamma-4 - o
6	3	75.0	15	4	I52698	hypothetical THRAL
7	3	75.0	20	2	C54052	phosphoribosyl-AMP
8	3	75.0	20	2	B46174	RNA-binding protei
9	2	50.0	4	2	I57745	D-mannosate hydrol
10	2	50.0	5	2	B37325	pap fibrial regul
11	2	50.0	5	2	D60274	major protein anti
12	2	50.0	5	2	B44823	synaptosomal-assoc
13	2	50.0	5	2	PT0610	T-cell receptor be
14	2	50.0	5	2	PT0535	T-cell receptor be
15	2	50.0	5	2	PT0684	T-cell receptor be
16	2	50.0	6	2	A61419	sarcosine dehydrot
17	2	50.0	6	2	T11779	phosphoglycerate t
18	2	50.0	6	2	S29637	jacalin beta-II ch
19	2	50.0	6	2	PT0648	T-cell receptor be
20	2	50.0	7	2	B39127	phosphotransferase
21	2	50.0	7	2	A44428	platelet aggregati
22	2	50.0	7	2	S71299	ICL2 protein - Par
23	2	50.0	7	2	PC1316	large granule L3 c
24	2	50.0	7	2	PT0283	Ig heavy chain CRD
25	2	50.0	7	2	PT0529	T-cell receptor be
26	2	50.0	7	2	PT0667	T-cell receptor be
27	2	50.0	7	2	PT0702	T-cell receptor be
28	2	50.0	7	2	A39690	neural cell adhesi
29	2	50.0	7	2	A58718	carnocin U149 - Ca

30	2	50.0	8	2	A32523	peptidyl-dipeptida
31	2	50.0	8	2	B24749	neuropeptide B - b
32	2	50.0	8	2	S43971	tumor-associated a
33	2	50.0	8	2	S43972	tumor-associated a
34	2	50.0	8	2	PT0030	inulinase (EC 3.2.
35	2	50.0	8	2	B27867	homeotic protein U
36	2	50.0	8	2	A14683	aspartate transami
37	2	50.0	8	2	PT0043	phosphatidylethano
38	2	50.0	8	2	PT0595	T-cell receptor be
39	2	50.0	8	2	C39690	neural cell adhesi
40	2	50.0	8	2	A35180	neutral proteinase
41	2	50.0	8	2	A25836	L-serine ammonia-1
42	2	50.0	9	2	S30494	cat gene leader pe
43	2	50.0	9	2	B24362	chloramphenicol O-
44	2	50.0	9	2	S55696	phosphoenolpyruvat
45	2	50.0	9	2	A61820	locustamyotropin I
46	2	50.0	9	2	A37027	macrophage chemota
47	2	50.0	9	2	PH0942	T-cell receptor be
48	2	50.0	9	2	PH0935	T-cell receptor be
49	2	50.0	9	2	PH0917	T-cell receptor be
50	2	50.0	9	2	PH0921	T-cell receptor be
51	2	50.0	10	1	RHAQ1	gonadoliberin I -
52	2	50.0	10	2	S39392	calpain (EC 3.4.22
53	2	50.0	10	2	A24196	acetylcholinestera
54	2	50.0	10	2	S26506	collagen alpha 1(V
55	2	50.0	10	2	S10785	enamelin, 22K - bo
56	2	50.0	10	2	PT0215	T-cell receptor be
57	2	50.0	10	2	PH0900	T-cell receptor be
58	2	50.0	10	2	PH0927	T-cell receptor be
59	2	50.0	10	2	PH0925	T-cell receptor be
60	2	50.0	10	2	PH0926	T-cell receptor be
61	2	50.0	10	2	PH0895	T-cell receptor be
62	2	50.0	10	2	PH0948	T-cell receptor be
63	2	50.0	10	2	B61218	alpha-gliadin 6Ha
64	2	50.0	11	1	EOOCC	eledoisin - curled
65	2	50.0	11	1	EOOCC	eledoisin - musky
66	2	50.0	11	1	GMROL	leucosulfakinin -
67	2	50.0	11	2	B49164	chromogranin-B - r
68	2	50.0	11	2	D60409	kassinin-like pept
69	2	50.0	11	2	P60409	substance P-like p
70	2	50.0	11	2	E60409	substance P-like p
71	2	50.0	11	2	YHRT	morphogenetic neur
72	2	50.0	11	2	YHHU	morphogenetic neur
73	2	50.0	11	2	YHBO	morphogenetic neur
74	2	50.0	11	2	YHXAE	morphogenetic neur
75	2	50.0	11	2	YHJFHY	morphogenetic neur
76	2	50.0	11	2	B60409	kassinin-like pept
77	2	50.0	11	2	C60409	kassinin-like pept
78	2	50.0	11	2	S07203	uperolein - frog (
79	2	50.0	11	2	S04875	nifs protein - Bra
80	2	50.0	11	2	S21127	precortin methyltr
81	2	50.0	11	2	B43689	hypothetical prote
82	2	50.0	11	2	PC2372	58K heat shock pro
83	2	50.0	11	2	PU0029	33K protein 3218 -
84	2	50.0	11	2	P80259	39K protein 3225 -
85	2	50.0	11	2	A60656	perisulfakinin - A
86	2	50.0	11	2	D56979	collagen alpha 1(I)
87	2	50.0	11	2	S23926	major glycoprotein
88	2	50.0	11	2	PT0044	protein kinase C 1
89	2	50.0	11	2	PT0214	T-cell receptor be
90	2	50.0	11	2	PH0941	T-cell receptor be
91	2	50.0	11	2	PH0929	T-cell receptor be
92	2	50.0	11	2	PH0947	T-cell receptor be
93	2	50.0	11	2	PH0924	T-cell receptor be
94	2	50.0	11	2	PH0914	T-cell receptor be
95	2	50.0	12	2	PN0577	tyrosine 3-monooxy
96	2	50.0	12	2	PN0578	tyrosine 3-monooxy
97	2	50.0	12	2	PN0579	tyrosine 3-monooxy
98	2	50.0	12	2	PN0580	tyrosine 3-monooxy
99	2	50.0	12	2	PN0581	tyrosine 3-monooxy
100	2	50.0	12	2	PN0576	tyrosine 3-monooxy

## ALIGNMENTS

RESULT 1  
S77984  
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa - bigeye tuna (fragment)  
C:Species: Thunnus obesus (bigeye tuna)  
C:Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998  
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
submitted to the Protein Sequence Database, June 1997  
A:Reference number: S77980  
A:Accession: S77984  
A:Molecule type: protein  
A:Residues: 1-9 <ARN>  
A:Experimental source: heart  
C:Genetics:  
A:Genome: nuclear  
C:Function:  
A:Pathway: oxidative phosphorylation; respiratory chain  
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 75.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EQP 4  
Db 2 EQP 4

RESULT 2  
E58502  
43.2K bile stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C:Accession: E58502  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: E58502  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <BIN>  
A:Experimental source: human bile with stones  
A>Note: a secondary sequence DVKIGVAGS was also found

Query Match 75.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EQP 4  
Db 7 EQP 9

RESULT 3  
S47363  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47363  
R:Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A:Reference number: S47355  
A:Accession: S47363  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <LEH>  
A:Cross-references: EMBL:Z35671; NID:G527467; PIDN:CAA84740.1; PID:G527468  
C:Keywords: T-cell receptor

Query Match 75.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEQ 3  
Db 8 SEQ 10

RESULT 4  
S29209  
avenin alpha-2 - oat (fragment)  
N:Alternate names: Cip-3; coeliac immunoreactive protein 3  
C:Species: Avena sativa (oat)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C:Accession: S29209  
R:Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.  
FEBS Lett. 310, 37-40, 1992  
A:Title: Identification of the three major coeliac immunoreactive proteins and one a  
A:Reference number: S29207; MUID:92405739; PMID:1526282  
A:Accession: S29209  
A:Molecule type: protein  
A:Residues: 1-14 <ROC>  
A:Experimental source: endosperm  
C:Superfamily: gliadin  
C:Keywords: prolamin; seed

Query Match 75.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEQ 3  
Db 9 SEQ 11

RESULT 5  
S29207  
avenin gamma-4 - oat (fragment)  
N:Alternate names: Cip-1; coeliac immunoreactive protein 1  
C:Species: Avena sativa (oat)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C:Accession: S29207  
R:Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.  
FEBS Lett. 310, 37-40, 1992  
A:Title: Identification of the three major coeliac immunoreactive proteins and one a  
A:Reference number: S29207; MUID:92405739; PMID:1526282  
A:Accession: S29207  
A:Molecule type: protein  
A:Residues: 1-15 <ROC>  
A:Experimental source: endosperm  
C:Superfamily: gliadin  
C:Keywords: prolamin; seed

Query Match 75.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEQ 3  
Db 2 SEQ 4

RESULT 6  
I52698  
hypothetical THRAl/BTR mutant fusion protein, cell line BT474 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
C:Accession: I52698  
R:Futreal, P.A.; Cochran, C.; Marks, J.R.; Iglehart, J.D.; Zimmerman, W.; Barrett, J.  
Cancer Res. 54, 1791-1794, 1994  
A:Title: Mutation analysis of the THRAl gene in breast cancer: deletion/fusion of th

A:Reference number: I52698; MUID:94185019; PMID:7511052  
 A:Accession: I52698  
 A>Status: translated from GB/EMBL/DDSU  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <FUT>  
 A:Cross-references: GB:S71020; NID:G546112; PIDN:AAB30341.1; PID:G546112  
 C:Comment: This sequence is the chimeric product of a deletion or translocation mutation  
 C:Genetics:  
 A:Gene: THRAl/BTR  
 A:Map position: 17q11.2  
 C:Keywords: fusion protein

Query Match 75.0%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 4 SEQ 6

RESULT 7  
 C54052  
 phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3.6.1.15)  
 C:Species: Klebsiella pneumoniae  
 C:Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2002  
 C:Accession: C54052  
 R:Kieder, G.; Merrick, M.J.; Castorff, H.; Kleiner, D.  
 J. Biol. Chem. 269, 14386-14390, 1994  
 A:Title: Function of hisF and hisH gene products in histidine biosynthesis.  
 A:Reference number: A54052; MUID:94237842; PMID:8182043  
 A:Accession: C54052  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-20 <RIE>  
 A:Experimental source: M5al  
 A:Note: sequence extracted from NCBI backbone (NCBIN:148607, NCBIPI:148610)  
 C:Genetics:  
 A:Gene: hisE  
 C:Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein  
 C:Keywords: histidine biosynthesis; hydrolase; multifunctional enzyme

Query Match 75.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 3 SEQ 5

RESULT 8  
 B46174  
 RNA-binding protein TIAR - human (fragment)  
 N:Alternate names: cytotoxic granule-associated RNA-binding protein; TIA-1 related protein  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 02-Jul-1998  
 C:Accession: B46174  
 R:Kawakami, A.; Tian, Q.; Duan, X.; Streuli, M.; Schlossman, S.F.; Anderson, P.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 8681-8685, 1992  
 A:Title: Identification and functional characterization of a TIA-1-related nucleolysin.  
 A:Reference number: A46174; MUID:92409580; PMID:1326761  
 A:Accession: B46174  
 A>Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-20 <KAW>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:114067, NCBIPI:114068)  
 C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein

Query Match 75.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 2 EQP 4

## RESULT 9

I57745  
 D-mannonate hydrolase (uxuA) - Escherichia coli  
 C:Species: Escherichia coli  
 C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999  
 C:Accession: I57745  
 R:Blanco, C.; Ritzenthaler, P.; Kolb, A.  
 Mol. Gen. Genet. 202, 112-119, 1986  
 A:Title: The regulatory region of the uxuA operon in Escherichia coli K12.  
 A:Reference number: I57745; MUID:86174344; PMID:3083215  
 A:Accession: I57745  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-4 <RES>  
 A:Cross-references: EMBL:X03411; NID:G43300; PIDN:CAA27147.1; PID:G581254

Query Match 50.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 |||  
 Db 2 EQ 3

## RESULT 10

B37325  
 pap fibrial regulatory protein papI - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C:Date: 11-Sep-1992 #sequence\_revision 11-Sep-1992 #text\_change 23-Mar-1993  
 C:Accession: B37325  
 R:Bratzen, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.  
 J. Bacteriol. 173, 1789-1800, 1991  
 A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus  
 A:Reference number: A37325; MUID:91154136; PMID:1671857  
 A:Accession: B37325  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <BRA>  
 A:Cross-references: GB:M63747

Query Match 50.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 |||  
 Db 2 SE 3

## RESULT 11

D60274  
 major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C:Accession: D60274  
 R:Nagai, S.; Wiker, H.O.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A:Title: Isolation and partial characterization of major protein antigens in the cult  
 A:Reference number: A60274; MUID:91099989; PMID:1898899  
 A:Accession: D60274  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <NAG>

Query Match 50.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
||  
Db 3 SE 4

## RESULT 12

B44823  
synaptosomal-associated protein SNAP-25 peptide 10A - rabbit (fragment)  
N;Alternate names: superprotein peptide 10A  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C;Accession: B44823  
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A;Reference number: A44823; MUID:92044785; PMID:1941090  
A;Accession: B44823  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <LOE>  
A;Experimental source: visual tissue  
A;Note: sequence extracted from NCBI backbone (NCBIP:64255)  
C;Keywords: membrane trafficking

Query Match 50.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3  
||  
Db 1 EQ 2

## RESULT 13

PT0610  
T-cell receptor beta chain V-D-J region (100-2E) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0610  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0610  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
||  
Db 3 SE 4

## RESULT 14

PT0535  
T-cell receptor beta chain V-D-J region (126-1AE) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0535  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0535  
A;Status: translation not shown  
A;Molecule type: mRNA

A;Residues: 1-5 <FEE>  
A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
||  
Db 3 SE 4

## RESULT 15

PT0684  
T-cell receptor beta chain V-D-J region (140-1BK) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0684  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N region:  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0684  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: day 18 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
||  
Db 3 SE 4

## RESULT 16

A61419  
sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)  
C;Species: Pseudomonas sp.  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C;Accession: A61419  
R;Pinto, J.T.; Frisell, W.R.  
Arch. Biochem. Biophys. 169, 483-491, 1975  
A;Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehy:  
A;Reference number: A61419; MUID:76038634; PMID:241294  
A;Accession: A61419  
A;Molecule type: protein  
A;Residues: 1-6 <FIN>  
C;Keywords: FAD; flavoprotein; oxidoreductase; phosphoprotein  
F:6/Modified site: 3'-FAD-histidine (His) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
||  
Db 3 SE 4

## RESULT 17

T11779  
phosphoglycerate transport regulatory protein pgTA - Salmonella typhimurium (fragmen:  
C;Species: Salmonella typhimurium  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: T11779  
R;Yang, Y.L.; Goldrick, D.; Hong, J.S.  
J. Bacteriol. 170, 4299-4303, 1988  
A;Title: Identification of the products and nucleotide sequences of two regulatory g:

A:Reference number: Z17339; MUID:88314933; PMID:2842311  
 A:Accession: T11779  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-6 <YAN>  
 A:Cross-references: EMBL:M21279; NID:g858752; PID:g154260  
 A:Experimental source: strain LT2

Query Match 50.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 ||  
 Db 3 EQ 4

RESULT 18  
 S29637  
 jacalin beta-II chain - Artocarpus champedon (fragment)  
 C:Species: Artocarpus champedon  
 C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
 C:Accession: S29637  
 R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
 Biochim. Biophys. Acta 1156, 219-222, 1993  
 A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD  
 A:Reference number: S29635; MUID:93152601; PMID:8427879  
 A:Accession: S29637  
 A:Molecule type: protein  
 A:Residues: 1-6 <NGO>  
 A:Experimental source: seed  
 C:Complex: heterotetramer; two alpha and two beta chains  
 C:Function:

A:Description: seed storage protein  
 A:Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine  
 C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 50.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 ||  
 Db 2 EQ 3

RESULT 19  
 PT0648  
 T-cell receptor beta chain V-D-J region (121-3BK) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0648  
 R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0648  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <FEE>  
 A:Experimental source: day 4 postnatal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 3 SE 4

RESULT 20

B39127  
 phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C:Date: 27-Nov-1991 #sequence\_revision 27-Nov-1991 #text\_change 08-Oct-1999  
 C:Accession: B39127  
 R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.  
 J. Bacteriol. 173, 449-456, 1991  
 A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of  
 rin.  
 A:Reference number: A39127; MUID:91100329; PMID:1846143  
 A:Accession: B39127  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-7 <HAR>  
 A:Cross-references: GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:g155144  
 C:Keywords: phosphotransferase

Query Match 50.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 ||  
 Db 4 EQ 5

RESULT 21  
 A44428  
 platelet aggregation-associated protein - Streptococcus sanguis (fragment)  
 C:Species: Streptococcus sanguis  
 C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 11-Nov-1994  
 C:Accession: A44428  
 R:Rickson, P.R.; Herzberg, M.C.  
 J. Biol. Chem. 269, 1646-1649, 1993  
 A:Title: The Streptococcus sanguis platelet aggregation-associated protein. Identific.  
 A:Reference number: A44428; MUID:93131902; PMID:8420939  
 A:Accession: A44428  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <ERI>  
 C:Keywords: cell wall

Query Match 50.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 ||  
 Db 3 EQ 4

RESULT 22  
 S71299  
 ICL2 protein - Paramecium tetraurelia (fragment)  
 C:Species: Paramecium tetraurelia  
 C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
 C:Accession: S71299  
 R:Madaddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
 Eur. J. Biochem. 238, 121-128, 1996  
 A:Title: Characterization of centrin genes in Paramecium.  
 A:Reference number: S71298; MUID:96248429; PMID:8665928  
 A:Accession: S71299  
 A:Molecule type: protein  
 A:Residues: 1-7 <MAD>  
 A:Experimental source: strain d4-2  
 C:Genetics:

A:Genetic code: SGC5

Query Match 50.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4



Db 2 QP 3  
||

## RESULT 23

PC1316  
large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)  
C;Species: Tachyplesus tridentatus  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: PC1316  
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa  
J. Biochem. 114, 307-316, 1993  
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)  
A;Reference number: PC1309; MUID:94110249; PMID:8282718  
A;Accession: PC1316  
A;Molecule type: protein  
A;Residues: 1-7 <SH1>  
C;Comment: This protein participates in immobilization of invading microbes.

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
Db 3 QP 4

## RESULT 24

PT0283  
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0283  
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0283  
A;Molecule type: DNA  
A;Residues: 1-7 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
||  
Db 3 EQ 4

## RESULT 25

PT0529  
T-cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0529  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0529  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 3 SE 4

## RESULT 26

PT0667  
T-cell receptor beta chain V-D-J region (121-2I) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0667  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0667  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 3 SE 4

## RESULT 27

PT0702  
T-cell receptor beta chain V-D-J region (161-2AA) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0702  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0702  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 3 SE 4

## RESULT 28

A39690  
neural cell adhesion molecule, cardiac splice form -, -, -, - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1993  
C;Accession: A39690  
R;Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule  
A;Reference number: A39690; MUID:91141516; PMID:1996115  
A;Accession: A39690  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-7 <REY>  
A;Cross-references: GB:M63970

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
1 QP 2

RESULT 29  
A58718  
carnocin U149 - Carnobacterium sp. (fragment)  
C;Species: Carnobacterium sp.  
C;Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C;Accession: A58718  
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.  
Appl. Environ. Microbiol. 58, 1417-1422, 1992  
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnobac-  
A;Reference number: A58718; PMID:92321768; PMID:1622206  
A;Accession: A58718  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <STO>  
C;Keywords: antibiotic; lanthionine

Query Match 50.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
2 SE 3

RESULT 30  
A32523  
peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)  
N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 11-May-2000  
C;Accession: A32523  
R;Harris, R.B.  
Adv. Exp. Med. Biol. 198, 513-521, 1986  
A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-converting  
A;Reference number: A32523; PMID:87123961; PMID:3028071  
A;Accession: A32523  
A;Molecule type: protein  
A;Residues: 1-8 <HAR>  
C;Superfamily: mammalian peptidyl-dipeptidase A  
C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase; z

Query Match 50.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
7 SE 8

RESULT 31  
B24749  
neuropeptide B - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000  
C;Accession: B24749  
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.  
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985  
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b  
A;Reference number: A94074; PMID:86067985; PMID:3865193  
A;Accession: B24749

A;Molecule type: protein  
A;Residues: 1-8 <YAN>  
C;Superfamily: unassigned animal peptides  
C;Keywords: neuropeptide

Query Match 50.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
4 QP 5

RESULT 32  
S43971  
tumor-associated antigen MUT1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
C;Accession: S43971  
R;Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
Nature 369, 67-71, 1994  
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murin  
A;Reference number: S43971; PMID:94217811; PMID:8164742  
A;Accession: S43971  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <MAN>  
C;Superfamily: unassigned animal peptides

Query Match 50.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
||  
2 EQ 3

RESULT 33  
S43972  
tumor-associated antigen MUT2 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
R;Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
Nature 369, 67-71, 1994  
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murin  
A;Reference number: S43971; PMID:94217811; PMID:8164742  
A;Accession: S43972  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <MAN>  
C;Superfamily: unassigned animal peptides

Query Match 50.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
||  
2 EQ 3

RESULT 34  
PT0030  
inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)  
N;Alternate names: inulase  
C;Species: Aspergillus ficuum  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
C;Accession: PT0030  
R;Etalibi, M.; Barattii, J.C.  
Agric. Biol. Chem. 54, 61-68, 1990

A;Title: Molecular and kinetic properties of Aspergillus ficum inulinases.  
 A;Reference number: PT0030; MUID:90344234; PMID:1368526  
 A;Accession: PT0030  
 A;Molecule type: protein  
 A;Residues: 1-8 <ETT>  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 50.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4  
 ||  
 Db 5 QP 6

## RESULT 35

B27867 homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)  
 C;Species: Drosophila melanogaster  
 C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 23-Feb-1997  
 C;Accession: B27867

R;Saari, G.; Bienz, M.  
 EMBO J. 6, 1775-1779, 1987

A;Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.  
 A;Reference number: A91072

A;Accession: B27867  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <SAA>  
 C;Genetics:

A;Gene: FlyBase:Ubx

A;Cross-references: FlyBase:FBgn0003944  
 C;Keywords: DNA binding; nucleus; transcription regulation

Query Match 50.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3  
 ||  
 Db 6 EQ 7

## RESULT 36

Al4683 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragment)  
 N;Alternate names: aspartate aminotransferase, mitochondrial  
 C;Species: Gallus gallus (Chicken)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000

C;Accession: Al4683

R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.  
 FEBS Lett. 108, 98-102, 1979

A;Title: Microsequence analysis. IV. Automatic liquid-phase sequencing using DABITC.  
 A;Reference number: Al4683; MUID:80092116; PMID:520566

A;Accession: Al4683

A;Molecule type: protein

A;Residues: 1-8 <ML>

C;Keywords: aminotransferase; mitochondrion

Query Match 50.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
 ||  
 Db 1 SE 2

## RESULT 37

PN0043 phosphatidylethanol amine-binding protein - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C;Accession: PN0043

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne

A;Reference number: PN0041

A;Accession: PN0043

A;Molecule type: protein

A;Residues: 1-8 <KAR>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is bloc

C;Keywords: brain

Query Match 50.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3  
 ||  
 Db 3 EQ 4

## RESULT 38

PT0595 T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0595

R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0595

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-8 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
 ||  
 Db 3 SE 4

## RESULT 39

C39690 neural cell adhesion molecule, cardiac splice form -, -, -, + - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: C39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: C39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A;Molecule type: mRNA

A;Residues: 1-8 <KEY>

A;Cross-references: GB:M63970

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4  
 ||  
 Db 1 QP 2

```

RESULT 40
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C:Accession: A35180
R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Sato, M.
J. Biol. Chem. 265, 5809-5815, 1990
A:Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A:Reference number: A35180; MUID:90202830; PMID:2318836
A:Accession: A35180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Keywords: hydrolase

Query Match          50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 4 SE 5

RESULT 41
A25836
L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change 21-Jun-2002
C:Accession: A25836
R:Heinacz, M.C.; McFall, E.
J. Bacteriol. 123, 1163-1169, 1975
A:Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operator
A:Reference number: A25836; MUID:76005414; PMID:1099073
A:Contents: K12
A:Accession: A25836
A:Molecule type: protein
A:Residues: 1-8 <HEI>
C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; seri

Query Match          50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 2 SE 3

RESULT 42
S30494
cat gene leader peptide - Streptococcus agalactiae plasmid pIP501
C:Species: Streptococcus agalactiae
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 24-Sep-1999
C:Accession: S30494
R:Trieu-Cuot, P.; de Cespedes, G.; Haraud, T.
Plasmid 28, 272-276, 1992
A:Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Strept
A:Reference number: JQ1950; MUID:93096867; PMID:1461942
A:Accession: S30494
A:Molecule type: DNA
A:Residues: 1-9 <TRI>
A:Cross-references: EMBL:X65462; NID:g49071; PIDN:CAA46454.1; PID:g581554
C:Genetics:
A:Genome: plasmid pIP501
C:Superfamily: unassigned leader peptides

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 1 SE 2

```

```

Db 4 SE 5
    ||

RESULT 43
B24362
chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pU1
C:Species: Staphylococcus aureus
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 11-May-2000
C:Accession: B24362
R:Bruckner, R.; Matzura, H.
EMBO J. 4, 2295-2300, 1985
A:Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the St.
A:Reference number: A24362; MUID:86081739; PMID:3865770
A:Accession: B24362
A:Molecule type: DNA
A:Residues: 1-9 <BRU>
A:Cross-references: GB:X02872; NID:g46536; PIDN:CAA26630.1; PID:g581555
C:Comment: Ribosome stalling in the translation of this leader peptide, caused by the
relation of the chloramphenicol O-acetyltransferase from a ribosome binding site local
C:Genetics:
A:Genome: plasmid
C:Superfamily: unassigned leader peptides

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 4 SE 5

RESULT 44
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C:Species: Trypanosoma brucei
C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55696
R:Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from
A:Reference number: S55696; MUID:95284106; PMID:7766679
A:Accession: S55696
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <HUN>

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
    ||
Db 1 QP 2

RESULT 45
A61620
locustamyotropin III - migratory locust
C:Species: Locusta migratoria (migratory locust)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61620
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamyotropin III and IV, two
A:Reference number: A61620
A:Accession: A61620
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <SCH>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Leu) #status experimental

```

Query Match 50.0%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 ||  
 Db 3 QP 4

RESULT 46  
 A37027  
 macrophage chemotactic factor - human (fragment)  
 N;Alternate names: T-cell hybridoma D6-18 protein  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 23-Feb-1997  
 C;Accession: A37027  
 R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.  
 Cell. Immunol. 123, 212-225, 1989  
 A;Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.  
 A;Reference number: A37027; MUID:89376581; PMID:2505934  
 A;Accession: A37027  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <YOS>

Query Match 50.0%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 8 SE 9

RESULT 47  
 PH0942  
 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0942  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0942  
 A;Molecule type: mRNA  
 A;Residues: 1-9 <GOL>  
 A;Experimental source: complete Freund's adjuvant-immunized lymph node  
 A;Note: the authors translated the codon TGC for residue 2 as Ala  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 ||  
 Db 8 EQ 9

RESULT 48  
 PH0935  
 T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0935  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0935  
 A;Molecule type: mRNA

A;Residues: 1-9 <GOL>  
 A;Experimental source: complete Freund's adjuvant-immunized lymph node  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 4 SE 5

RESULT 49  
 PH0917  
 T-cell receptor beta chain V-D-J region (isolate 3) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0917  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0917  
 A;Molecule type: mRNA  
 A;Residues: 1-9 <GOL>  
 A;Experimental source: concanavalin A-activated lymphoblast  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 4 SE 5

RESULT 50  
 PH0921  
 T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0921  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0921  
 A;Molecule type: mRNA  
 A;Residues: 1-9 <GOL>  
 A;Experimental source: concanavalin A-activated lymphoblast  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 4 SE 5

RESULT 51  
 PHA01  
 gonadoliberin I - American alligator  
 N;Alternate names: gonadotropin-releasing hormone I  
 C;Species: Alligator mississippiensis (American alligator)  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C;Accession: A60066  
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swar  
 Regul. Pept. 33, 105-116, 1991  
 A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains

A;Reference number: A60066; MUID:91352338; PMID:1882082

A;Accession: A60066

A;Molecule type: protein

A;Residues: 1-10 <LOV>

C;Superfamily: gonadoliberin

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

||

8 QP 9

Db

RESULT 52

S39392

calpain (EC 3.4.22.17) II light chain - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 18-Feb-1994 #sequence\_revision 24-Jul-1998 #text\_change 29-Sep-1999

C;Accession: S39392

R;Crawford, C.; Brown, N.R.; Willis, A.C.

Biochem. J. 296, 135-142, 1993

A;Title: Studies of the active site of m-calpain and the interaction with calpastatin.

A;Reference number: S39391; MUID:94071815; PMID:8250833

A;Accession: S39392

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CRA>

C;Superfamily: calpain small chain; calmodulin repeat homology

C;Keywords: cysteine proteinase; EF hand; hydrolase

Query Match

Best Local Similarity 50.0%; Score 2; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

||

4 SE 5

Db

RESULT 53

A24196

acetylcholinesterase (EC 3.1.1.7) - electric eel (fragment)

C;Species: Electrophorus electricus (electric eel)

C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 28-Apr-1993

C;Accession: A24196

R;Kieffer, B.; Goeldner, M.; Hirth, C.; Abersold, R.; Chang, J.Y.

FEBS Lett. 202, 91-96, 1986

A;Title: Sequence determination of a peptide fragment from electric eel acetylcholinesterase

A;Reference number: A24196

A;Accession: A24196

A;Molecule type: protein

A;Residues: 1-10 <KIE>

C;Keywords: carboxylic ester hydrolase

Query Match

Best Local Similarity 50.0%; Score 2; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

||

5 SE 6

Db

RESULT 54

S26506

collagen alpha 1(VI) chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Dec-1998

C;Accession: S26506

R;Jander, R.; Rautenberg, J.; Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and human

A;Reference number: S26506; MUID:83209648; PMID:6852033

A;Accession: S26506

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <JAN>

C;Keywords: hydroxyproline

F;9/Modified site: hydroxyproline (Pro) #status experimental

Query Match

Best Local Similarity 50.0%; Score 2; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

||

3 QP 4

Db

RESULT 55

S10785

enamelin, 22K - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998

C;Accession: S10785

R;Strawich, E.; Gilmcher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Accession: S10785

A;Molecule type: protein

A;Residues: 1-10 <STR>

C;Keywords: enamel; phosphoprotein

Query Match

Best Local Similarity 50.0%; Score 2; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

||

3 QP 4

Db

RESULT 56

PT0215

T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0215

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0215

A;Molecule type: mRNA

A;Residues: 1-10 <NAK>

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 50.0%; Score 2; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3

||

7 EQ 8

Db

RESULT 57

PH0900

T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

```

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0900
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0900
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 58
PH0927
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0927
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0927
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 59
PH0925
T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0925
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0925
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 60
PH0926
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0926
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0926
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon AGA for residue 4 as Thr
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 61
PH0895
T-cell receptor beta chain V-D-J region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0895; PH0896
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0895
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell; clones 15 and 16
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SE 2
      |||
Db      7 SE 8

RESULT 62
PH0948
T-cell receptor beta chain V-D-J region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 19-Oct-1995 #text_change 30-May-1997
C;Accession: PH0948; PH0897; PH0909; PH0899
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0948
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from
A;Accession: PH0897
A;Molecule type: mRNA
A;Residues: 1-10 <GO3>
A;Experimental source: myelin basic protein-immunized T-cell, clones 3, 6-2, 14, hyb;
A;Accession: PH0909
A;Molecule type: mRNA
A;Residues: 1-10 <GO3>
A;Accession: PH0899
A;Status: preliminary
A;Molecule type: mRNA

```

A;Residues: 1-10 <G04>  
A;Experimental source: clone 14  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
||  
Db 9 EQ 10

## RESULT 63

Be1218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C;Species: Haynaldia villosa, Dasyphyrum villosum  
C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
C;Accession: B61218  
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa  
A;Reference number: A61218; MUID:91315394; PMID:1859356  
A;Accession: B61218  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <SHE>  
C;Keywords: seed; storage protein

Query Match 50.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
Db 9 QP 10

## RESULT 64

EOCC  
eledoisin - curled octopus  
C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998  
C;Accession: B01561; A01561  
R;Anastasi, A.; Erspaner, V.  
Arch. Biochem. Biophys. 101, 56-65, 1963  
A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of eledoisin  
A;Reference number: A01561  
A;Accession: B01561  
A;Molecule type: protein  
A;Residues: 1-11 <ANA>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagog  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
Db 1 QP 2

## RESULT 65

EOCC  
eledoisin - musky octopus  
C;Species: Eledone moschata, Ozaena moschata (musky octopus)  
C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998  
C;Accession: A01561  
R;Anastasi, A.; Erspaner, V.  
Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide  
A;Reference number: A01561  
A;Accession: A01561  
A;Molecule type: protein  
A;Residues: 1-11 <ANA>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagog  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
Db 1 QP 2

## RESULT 66

GMROL  
leucosulfakinin - Madeira cockroach  
N;Alternate names: LSK  
C;Species: Leucophaea madeira (Madeira cockroach)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996  
C;Accession: A01622  
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.  
Science 234, 71-73, 1986  
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and leucosulfakinin  
A;Reference number: A01622; MUID:86315858; PMID:3749893  
A;Accession: A01622  
A;Molecule type: protein  
A;Residues: 1-11 <NAC>  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; hormone; sulfoprotein  
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
||  
Db 1 EQ 2

## RESULT 67

B49164  
chromogranin-B - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
C;Accession: B49164  
R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides  
A;Reference number: A49164; MUID:92063871; PMID:1954895  
A;Accession: B49164  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <NIE>  
A;Note: sequence extracted from NCBI backbone (NCBI:66370)  
C;Superfamily: chromogranin B precursor

Query Match 50.0%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 3 SE 4



```

RESULT 68
D60409
kassinin-like peptide X-III - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: D60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: D60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 50.0%; Score 2; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
  ||
Db 1 QP 2

RESULT 69
F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: F60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: F60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 50.0%; Score 2; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
  ||
Db 1 QP 2

RESULT 70
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: E60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: E60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 50.0%; Score 2; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
  ||
Db 1 QP 2

```

```

Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
  ||
Db 1 QP 2

RESULT 71
YHRT
morphogenetic neuropeptide - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru-
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h-
een found in mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutam
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity 50.0%; Score 2; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
  ||
Db 1 QP 2

RESULT 72
YHHT
morphogenetic neuropeptide - human
C:Species: Homo sapiens (man)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: B01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru-
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h-
malian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuro
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #st

Query Match
Best Local Similarity 50.0%; Score 2; DB 2; Length 11;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
  ||

```

Db 1 QP 2

## RESULT 73

YHBO

morphogenetic neuropeptide - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C:Accession: Col427; A01427  
 R:Bodenmuller, H.; Schaller, H.C.  
 Nature 293, 579-580, 1981  
 A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis  
 A:Reference number: A93266; MUID:82035850; PMID:7290191  
 A:Accession: Col427

A:Molecule type: protein  
 A:Residues: 1-11 <SCH>  
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4

||

Db 1 QP 2

## RESULT 74

YHAE

morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)  
 N:Alternate names: head activator  
 C:Species: Anthopleura elegantissima  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C:Accession: A93900; A01427  
 R:Schaller, H.C.; Bodenmuller, H.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A:Reference number: A93900

A:Accession: A93900  
 A:Molecule type: protein  
 A:Residues: 1-11 <SCH>  
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4

||

Db 1 QP 2

## RESULT 75

YHJFHY

morphogenetic neuropeptide - Hydra attenuata  
 N:Alternate names: head activator  
 C:Species: Hydra attenuata  
 C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C:Accession: B93900; A01427  
 R:Schaller, H.C.; Bodenmuller, H.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A:Reference number: A93900

A:Accession: B93900  
 A:Molecule type: protein  
 A:Residues: 1-11 <SCH>  
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A:Reference number: A91296; MUID:82050803; PMID:7297679  
 A:Contents: annotation; synthesis  
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure  
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4

||

Db 1 QP 2

Search completed: November 25, 2003, 18:28:20

Job time : 3.68085 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 1.93617 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	100.0	9	1	RT33_BOVIN
2	3	75.0	4	1	COXE_THUOB
3	2	50.0	4	1	BOSI_HUMAN
4	2	50.0	7	1	LANC_CARUI
5	2	50.0	7	1	UH11_RAT
6	2	50.0	8	1	NPB_BOVIN
7	2	50.0	8	1	UF06_MOUSE
8	2	50.0	9	1	AL10_CARMA
9	2	50.0	9	1	D1_NEPNO
10	2	50.0	9	1	FAR3_PENNO
11	2	50.0	9	1	FAR4_PENNO
12	2	50.0	9	1	FRF1_SARBU
13	2	50.0	9	1	LMT3_LOCOMI
14	2	50.0	9	1	LPCA_STAAU
15	2	50.0	10	1	CATB_SHEEP
16	2	50.0	10	1	FAR6_PANRE
17	2	50.0	10	1	GONI_ALLMI
18	2	50.0	10	1	PORB_METTM
19	2	50.0	10	1	SVK_CAMUP
20	2	50.0	10	1	UPA4_HUMAN
21	2	50.0	10	1	UPA5_HUMAN
22	2	50.0	10	1	URA6_HUMAN
23	2	50.0	10	1	LSK1_LEUMA
24	2	50.0	11	1	LSKP_PERAM
25	2	50.0	11	1	MORN_HUMAN
26	2	50.0	11	1	TKN1_PSEGU
27	2	50.0	11	1	TKN1_UPERU
28	2	50.0	11	1	TKN2_PSEGU
29	2	50.0	11	1	TKN3_PSEGU
30	2	50.0	11	1	TKN4_PSEGU
31	2	50.0	11	1	TKN5_PSEGU
32	2	50.0	11	1	TKN5_ELENO
33	2	50.0	12	1	CALM_TETTH

Q05055 tetrahymena

34	2	50.0	12	1	FARI_CALVO
35	2	50.0	12	1	FIFI_SARBU
36	2	50.0	12	1	H59A_RAT
37	2	50.0	12	1	UR2_POLSP
38	2	50.0	13	1	ACT7_SOYBN
39	2	50.0	13	1	CPI_APLCA
40	2	50.0	13	1	CRTC_BOVIN
41	2	50.0	13	1	ECDE_LYMDI
42	2	50.0	13	1	ET22_LITRU
43	2	50.0	13	1	EP65_HUMAN
44	2	50.0	13	1	FARB_ASCSU
45	2	50.0	13	1	PEDI_HYDAT
46	2	50.0	13	1	PSAE_PEA
47	2	50.0	13	1	UHA3_CANPA
48	2	50.0	14	1	ATP6_SPIOL
49	2	50.0	14	1	MARI_ALTSP
50	2	50.0	14	1	NSK2_SARBU
51	2	50.0	14	1	PPK6_PERAM
52	2	50.0	14	1	TAT_HV1W2
53	2	50.0	14	1	TAT_HV1Z8
54	2	50.0	15	1	APF3_MALPA
55	2	50.0	15	1	ARCA_STRP5
56	2	50.0	15	1	CHI1_PEA
57	2	50.0	15	1	IRBP_CRISP
58	2	50.0	15	1	LEC2_PSOSC
59	2	50.0	15	1	MMO1_RAT
60	2	50.0	15	1	PGKH_PHYPA
61	2	50.0	15	1	PGTS_PELAC
62	2	50.0	15	1	RBS_PHYPA
63	2	50.0	15	1	RS20_BACST
64	2	50.0	15	1	RT32_BOVIN
65	2	50.0	15	1	UC13_WAIZE
66	2	50.0	15	1	UC27_WAIZE
67	2	50.0	15	1	UNO1_PINPS
68	2	50.0	15	1	URE2_MORMO
69	2	50.0	16	1	BRB_BASAL
70	2	50.0	16	1	FIBA_EQUAS
71	2	50.0	16	1	FIBA_MELME
72	2	50.0	16	1	FIBA_MUSVI
73	2	50.0	16	1	HTPG_ACICA
74	2	50.0	16	1	IBP4_PIG
75	2	50.0	16	1	LPX1_LOCOMI
76	2	50.0	17	1	ACT6_SOYBN
77	2	50.0	17	1	PH4_PERAM
78	2	50.0	17	1	PSBL_SINUV
79	2	50.0	17	1	RM35_YEAST
80	2	50.0	17	1	TPIS_PINPS
81	2	50.0	17	1	UN15_CLOPA
82	2	50.0	18	1	A2M_OCTVU
83	2	50.0	18	1	AGI_EUPCH
84	2	50.0	18	1	ALL2_CVDPO
85	2	50.0	18	1	D7AL_ACASC
86	2	50.0	18	1	DRPH_UCAPU
87	2	50.0	18	1	LCTN_LAMGL
88	2	50.0	18	1	LUXB_KRYAS
89	2	50.0	18	1	RL24_SERMA
90	2	50.0	19	1	ADC_CLOPA
91	2	50.0	19	1	AL22_HORSE
92	2	50.0	19	1	ETFA_CLOPA
93	2	50.0	19	1	FIBA_CERNI
94	2	50.0	19	1	IRBP_CAVPO
95	2	50.0	19	1	LPRM_STAAU
96	2	50.0	19	1	RL10_CITFR
97	2	50.0	20	1	TPIS_CLOPA
98	2	50.0	20	1	ALBG_EQUAS
99	2	50.0	20	1	COGC_PARCM
100	2	50.0	20	1	COXE_THUOB

## ALIGNMENTS

RESULT 1

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RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome: identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4
Db 3 SEQ 6

RESULT 2
COXE_THUOB
ID COXE_THUOB STANDARD; PRT; 9 AA.
DT P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferriocytochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Cytochrome oxidase; Inner membrane; Mitochondrion.
FT NON_TER 1 1

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FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 75.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 2 EQP 4

RESULT 3
EOSI_HUMAN
ID EOSI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilic toxic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic toxic peptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS (ANAPHYLAXIS). THEIR ACTIVITIES, PREPARENTIALLY AFFECTING EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR GO; GO:0030105; P:anaphylaxis; IDA.
DR GO; GO:0006935; P:chemotaxis; IDA.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 3 SE 4

RESULT 4
LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).

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CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;  
 Query Match 50.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 Db 2 SE 3

RESULT 5  
 UH11 RAT STANDARD; PRT; 7 AA.  
 ID UH11 RAT  
 AC P56576;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Weistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 8.5, ITS MW IS: 42 kDa.  
 FT UNSURE 2 2 OR A.  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 Db 5 EQ 6

RESULT 6  
 NPB\_BOVIN STANDARD; PRT; 8 AA.  
 ID NPB\_BOVIN  
 AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropeptide B.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=86067985; PubMed=3865193;  
 RA Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;  
 RT "Isolation, sequencing, synthesis, and pharmacological  
 RT characterization, of two brain neuropeptides that modulate the action  
 RT of morphine.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).  
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
 DR PIR: B24749; B24749.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;  
 Query Match 50.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 Db 4 QP 5

RESULT 7  
 UF06\_MOUSE STANDARD; PRT; 8 AA.  
 ID UF06\_MOUSE  
 AC P38644;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 Db 2 SE 3

RESULT 8  
 AL10\_CARMA STANDARD; PRT; 9 AA.  
 ID AL10\_CARMA  
 AC P81813;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 10.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 ||  
 Db 3 QP 4

RESULT 9  
 DI\_NEPNO  
 ID -DI\_NEPNO STANDARD; PRT; 9 AA.  
 AC P24816;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Gastrin/cholecystokinin-like peptide DI.  
 OS Nephrops norvegicus (Norway lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Nephrops.  
 OC NCBI\_TaxID=6929;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Stomach;  
 RX MEDLINE=92082847; PubMed=1747388;  
 RA Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;  
 RT "Structure and biological activity of crustacean gastrointestinal  
 peptides identified with antibodies to gastrin/cholecystokinin";  
 RL Biochimie 73:1233-1239(1991).  
 CC -!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR; S47432; S47432.  
 KW Hormone.  
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 1 SE 2

RESULT 10  
 FAR3\_PENMO  
 ID -FAR3\_PENMO STANDARD; PRT; 9 AA.  
 AC P83318;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OC NCBI\_TaxID=6687;  
 RN [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,  
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;  
 Query Match 50.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 ||  
 Db 2 QP 3

RESULT 11  
 FAR4\_PENMO  
 ID -FAR4\_PENMO STANDARD; PRT; 9 AA.  
 AC P83319;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OC NCBI\_TaxID=6687;  
 RN [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,  
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 ||  
 Db 2 QP 3

RESULT 12  
 FRF1\_SARBU  
 ID -FRF1\_SARBU STANDARD; PRT; 9 AA.  
 AC P83350;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neb-FMRFamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OC NCBI\_TaxID=7385;  
 RN [1]  
 RN SEQUENCE, AMIDATION, AND FUNCTION.  
 RP TISSUE=CNS;  
 RX MEDLINE=23342733; PubMed=12438685;  
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
 RT "Identification in Drosophila melanogaster of the invertebrate G  
 protein-coupled FMRFamide receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular

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CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRP/AMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2DB10699CAB6C5A7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 13
LMT3_LOGMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytotropin peptide family.";
RT Locustamytotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY)
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 14
LPCA_STAAU STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus agalactiae.
OG Plasmid pSCS6, Plasmid pSCS7, Plasmid PUB112, and Plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]

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RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSCS7;
RX MEDLINE=92021652; PubMed=1929326;
RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus.";
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pSCS6;
RX MEDLINE=92388047; PubMed=1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus.";
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pUB112;
RX MEDLINE=86081739; PubMed=3865770;
RA Brueckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid PUB112.";
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.agalactiae; PLASMID=pIP501;
RX MEDLINE=93096867; PubMed=1461942;
RA Trieu-Cuot P., de Cespedes G., Haraud T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501.";
RL Plasmid 28:272-276(1992).
CC -----
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CC -----
CC EMBL; M58515; AAA26612.1; -
CC EMBL; M58516; AAA16528.1; -
CC EMBL; X02872; CAA26630.1; -
CC EMBL; X60827; CAA43217.1; -
CC EMBL; X65462; CAA46454.1; -
CC PIR; B24362; B24362.
CC PIR; S30494; S30494.
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA; 1074 MW; 5D9CAB5AAB05B333 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 4 SE 5

RESULT 15
CATB_SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CTSB.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

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Wed Nov 26 09:06:32 2003

OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]\_SEQUENCE.  
 RP TISSUE=Placenta;  
 RX MEDLINE=22394055; PubMed=12506352;  
 RC El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,  
 RA Mboko H.B., Beckers J.-F.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated  
 RT glycoproteins from the ewe placenta."  
 RL Mol. Reprod. Dev. 64:199-206(2003).  
 CC -!- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins. Has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin L). In  
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
 CC by a disulfide bond (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro: IPR00169; Shprot\_acctse.  
 DR PROSITE; PS00640; THIOLEPROTEASE ASN; PARTIAL.  
 DR PROSITE; PS00139; THIOLEPROTEASE CYS; PARTIAL.  
 DR PROSITE; PS00639; THIOLEPROTEASE HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3  
 ||  
 Db 9 EQ 10

RESULT 16  
 FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82660;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]\_SEQUENCE, FUNCTION, AND AMIDATION.  
 RP Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of RMRamide-related  
 RT peptides (FaRs) from free-living nematode, Panagrellus redivivus";  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;  
 Query Match 50.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4  
 ||  
 Db 5 QP 6

RESULT 17  
 GONI\_ALLMI STANDARD; PRT; 10 AA.  
 ID GONI\_17  
 AC P37041; P20407;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)  
 DE (Luliberin I).  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]\_SEQUENCE.  
 RP TISSUE=Brain;  
 RX MEDLINE=91352338; PubMed=1882082;  
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
 Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure of two forms of gonadotropin-releasing hormone  
 RT from brains of the American alligator (Alligator mississippiensis).";  
 RL Regul. Pept. 33:105-116(1991).  
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE GnRH family.  
 DR InterPro: IPR002012; GnRH.  
 DR PIR; A60066; RHAQ1.  
 DR PROSITE; PS00473; GnRH; 1.  
 DR Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.  
 KW MOD\_RES 10 10  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4  
 ||  
 Db 8 QP 9

RESULT 18  
 PORB\_METTM STANDARD; PRT; 10 AA.  
 ID PORB\_METTM  
 AC P80901;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase  
 DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)  
 DE (Fragment).  
 GN PORB  
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter.  
 OX NCBI\_TaxID=79929;  
 RN [1]\_SEQUENCE  
 RP MEDLINE=97261844; PubMed=9108258;  
 RX Tersteegen A., Linder D., Thauer R.K., Hedderich R.;  
 RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases  
 RT in Methanobacterium thermoautotrophicum.";  
 RL Eur. J. Biochem. 244:862-868(1997).  
 CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
 CC CoA + CO(2) + reduced ferredoxin.  
 CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
 CC GAMMA CHAIN.  
 CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature  
 CC of 80 degrees Celsius.



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KW Oxidoreductase.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 5 EQ 6

RESULT 19
SYK CAMUP
ID SYK CAMUP STANDARD; PRT; 10 AA.
AC Q46464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE (Fragment).
GN LYSS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=28080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43954;
RX MEDLINE=97149302; PubMed=8996110;
RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RT "Characterization of Campylobacter upsaliensis fur and its
RT localization in a highly conserved region of the Campylobacter
RT genome.";
RL Gene 183;219-224(1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to Class-II aminoacyl-tRNA synthetase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; L77076; AAB41342.1; -.
CC DR HAMAP; MF_00252; -.
CC DR InterPro; IPR006195; tRNA ligase II.
CC DR PROSITE; PS50862; AA tRNA_LIGASE II, PARTIAL.
CC KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Metal-binding; Magnesium.
CC FT NON_TER 1
CC FT NON_TER 1
SQ SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 3 SE 4

RESULT 20
UPA4 HUMAN
ID UPA4 HUMAN STANDARD; PRT; 10 AA.
AC P30090;

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DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 40.5 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
CC DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1
FT UNSURE 4
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 6 SE 7

RESULT 21
UPA5 HUMAN
ID UPA5 HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
CC DR SWISS-2DPAGE; P30091; HUMAN.
FT NON_TER 1
FT VARIANT 9
FT VARIANT 9
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 50.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 Db 1 EQ 2

## RESULT 24

LSKP PERAM STANDARD; PRT; 11 AA.  
 AC P3685;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Perisulfakinin (Pea-SK-I).  
 DB Perisulfakinin (Pea-SK-I).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90137190; PubMed=2615921;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of two gastrin/CKK-like neuropeptides from  
 the American cockroach homologous to the leucosulfakinins.";  
 RL Neuropeptides 14:145-149(1989).  
 CC -!- FUNCTION: STIMULATES HINDGUT CONTRACTIONS.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR; A60656; A60656.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Hormone; Amidation; Sulfation.  
 FT MOD\_RES 6 6 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 Db 1 EQ 2

## RESULT 25

MORN HUMAN STANDARD; PRT; 11 AA.  
 ID MORN\_HUMAN  
 AC P01163;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Morphogenetic neuropeptide (Head activator) (HA).  
 OS Homo sapiens (Human).  
 OS Rattus norvegicus (Rat).  
 OS Bos taurus (Bovine).  
 OS Anthopleura elegantissima (Sea anemone), and  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Human, Rat, and Bovine;  
 RX MEDLINE=82035850; PubMed=7290191;  
 RA Bodenmuller H., Schaller H.C.;  
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
 from coelenterates to humans.";  
 RL Nature 293:579-580(1981).

QY 3 QP 4  
 Db 3 QP 4

RESULT 22  
 URA6 HUMAN STANDARD; PRT; 10 AA.  
 ID URA6\_HUMAN  
 AC P32080;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of red blood cells (Spot 17) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Erythrocyte;  
 RX MEDLINE=94147970; PubMed=8313871;  
 RA Golaz O., Hughes G.J., Fruiger S., Paquet N., Bairoch A.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
 RA Balant L., Hochstrasser D.F.;  
 RT "Plasma and red blood cell protein maps: update 1993.";  
 RL Electrophoresis 14:1223-1231(1993).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.4, ITS MW IS: 65 kDa.  
 DR SWISS-2DPAGE; P32080; HUMAN.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 965 MW; 63DDC8D8GAE1EDDB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 Db 2 SE 3

## RESULT 23

LSK1 LEUMA STANDARD; PRT; 11 AA.  
 ID LSK1\_LEUMA  
 AC P04428;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Leucosulfakinin-I (LSK-I).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86315858; PubMed=3749893;  
 RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;  
 RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to  
 gastrin and cholecystokinin.";  
 RL Science 234:71-73(1986).  
 CC -!- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF  
 THE COCKROACH HINDGUT. INHIBITS MUSCLE CONTRACTION OF HINDGUT.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR; A01622; GMR0L.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Hormone; Amidation; Sulfation.  
 FT MOD\_RES 6 6 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;



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AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; C60409; C60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 29
TKN3_PSEGU ID TKN3_PSEGU STANDARD; PRT; 11 AA.
AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; D60409; D60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; E60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DEA7C37C9CB1457 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 30
TKN4_PSEGU ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SP1).
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; E60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
OS Pseudophryne guntheri (Gunther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

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RESULT 31
TKN5_PSEGU STANDARD; PRT; 11 AA.
ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.",
RL Peptides 11:299-304 (1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; F60409; F60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 32
TKN_ELEMO STANDARD; PRT; 11 AA.
ID TKN_ELEMO STANDARD; PRT; 11 AA.
AC F01293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eledoisin.
OS Eledone moschata (Musk octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrhosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eledoisin, the active
RT endopeptide of the posterior salivary glands of Eledone.",
RL Arch. Biochem. Biophys. 101:56-65 (1963).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
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CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B01561; EOCC.
DR PIR; B01561; EOCC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 33
CALM_TETTH STANDARD; PRT; 12 AA.
ID CALM_TETTH STANDARD; PRT; 12 AA.
AC Q05055;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calmodulin (Fragment).
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymena; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93281388; PubMed=8506136;
RA Katoh M., Hirono M., Takemasa T., Kimura M., Watanabe Y.;
RT "A microtubule-specific sequence exists in the 5'-upstream region of
RT calmodulin gene in Tetrahymena thermophila.",
RL Nucleic Acids Res. 21:2409-2414 (1993).
CC -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC PHOSPHATASES.
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D12774; BAA02239.1; -.
CC InterPro; IPR002048; EF-hand.
CC PROSITE; PS00018; EF_HAND; PARTIAL.
CC Calcium-binding; Repeat; Acetylation.
KW INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1393 MW; 83F31CD443DB1B01 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
```

Db 7 EQ 8

Query Match 50.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
DB 4 QP 5

RESULT 34  
FARI-CALVO STANDARD; PRT; 12 AA.  
ID FARI-CALVO STANDARD; PRT; 12 AA.  
AC P41869;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Callimyrinamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Jonsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callimyrinamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: BELONGS TO THE FARI (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; E44787;  
KW Neuropeptide; Amidation.  
FT MOD RES 12 12  
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
DB 4 QP 5

RESULT 35  
FIFI-SARBU STANDARD; PRT; 12 AA.  
ID FIFI-SARBU STANDARD; PRT; 12 AA.  
AC P83349;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neb-FIRFamide 1.  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, AMIDATION, AND FUNCTION.  
RC TISSUE=CNS;  
RX MEDLINE=22342733; PubMed=12438685;  
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
RT "Identification in Drosophila melanogaster of the invertebrate G  
RT protein-coupled FMRFamide receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
CC junctions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE FARI (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 12 12  
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
DB 9 QP 10

RESULT 37  
UR2-POLSP STANDARD; PRT; 12 AA.  
ID UR2-POLSP STANDARD; PRT; 12 AA.  
AC P81022;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urotensin II (U-II) (U-II).  
OS Polyodon spathula (North American paddlefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;  
OC Polyodon.  
OX NCBI\_TaxID=7913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spinal cord;  
RX MEDLINE=96051494; PubMed=8536944;  
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;

Query Match 50.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
DB 9 QP 10

RESULT 38  
UR2-POLSP STANDARD; PRT; 12 AA.  
ID UR2-POLSP STANDARD; PRT; 12 AA.  
AC P81022;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urotensin II (U-II) (U-II).  
OS Polyodon spathula (North American paddlefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;  
OC Polyodon.  
OX NCBI\_TaxID=7913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spinal cord;  
RX MEDLINE=96051494; PubMed=8536944;  
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;

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RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT spathula).";
RL Gen. Comp. Endocrinol. 99:323-332(1995).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11 BY SIMILARITY.
SQ SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 4 SE 5

RESULT 38
ACT7 SOYBN STANDARD; PRT; 13 AA.
ID ACT7 SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SACT7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17120; CAA34980.1; --
CC F01; S15755; S15755.
CC InterPro; IPR004001; Actin.
CC DR InterPro; IPR004000; Actin like.
CC DR PROSITE; PS00406; ACTINS 1; PARTIAL.
CC DR PROSITE; PS00432; ACTINS 2; PARTIAL.
CC DR PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.
KW Structural protein; Multigene family.

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FT NON TER 13 13
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 8 QP 9

RESULT 39
CPI_APLCA STANDARD; PRT; 13 AA.
ID CPI_APLCA STANDARD; PRT; 13 AA.
AC Q10598;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Cerebral peptide 1 (CPI).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=97001771; PubMed=8844763;
RA Phares G.A., Lloyd P.E.;
RT "Purification, primary structure, and neuronal localization of
RT cerebral peptide 1 from Aplysia.";
RL Peptides 17:753-761(1996).
CC -!- FUNCTION: MAY FUNCTION AS A PEPTIDE TRANSMITTER.
CC -!- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN THE CEREBRAL AND PEDAL
CC GLANDLIA.
SQ SEQUENCE 13 AA; 1314 MW; 9DBC3CE82C667B05 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 6 SE 7

RESULT 40
CRTC_BOVIN STANDARD; PRT; 13 AA.
ID CRTC_BOVIN STANDARD; PRT; 13 AA.
AC P28489;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin (CRP55) (Calregulin) (HACBP) (ERP60) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Bakesh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: Monomer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR PIR; A33208; A33208.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON TER 13
SQ SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 8 EQ 9

RESULT 41
ECDE LYMDI STANDARD; PRT; 13 AA.
AC P80941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide E (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 12 SE 13

RESULT 42
EI22 LITRU STANDARD; PRT; 13 AA.
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
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RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1598 MW; C1808EF3B357322 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 9 QP 10

RESULT 43
EP65 HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=9004678; PubMed=2507249;
RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
DR GO; GO:0005737; Cytoplasm; NAS.
KW Glycoprotein.
FT NON TER 1 1
FT CARBOHYD 2 2 O-LINKED (GLCNAC).
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 6 QP 7

RESULT 44
FARB ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 6 SE 7

RESULT 45
PEDI_HYDAT
ID PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroidea; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris."
RL Development 122:1941-1948 (1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 12 SE 13

RESULT 46
PSAE_PEA
ID PSAE_PEA STANDARD; PRT; 13 AA.
AC P20118;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 13 kDa
DE protein) (Fragment).
DN PSAE.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE.
RX MEDLINE=88137587; PubMed=3277857;
RA Dunn P.P.J., Packman L.C., Pappin D., Gray J.C.;
RT "N-terminal amino acid sequence analysis of the subunits of pea
RT photosystem I."
RL FEBS Lett. 228:157-161 (1988).
CC -!- FUNCTION: Stabilizes the interaction between psaC and the PSI
CC core, assists the docking of the ferredoxin to PSI and interacts
CC with ferredoxin-NADP oxidoreductase (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.

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CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.
DR PIR, S00316; S00316.
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1190 MW; D895A63A52D8DB1D CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 47
UHA3_CANFA
ID UHA3_CANFA STANDARD; PRT; 13 AA.
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart;
CC MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802 (1997).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9, ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 12 SE 13

RESULT 48
ATP6_SPIOL
ID ATP6_SPIOL STANDARD; PRT; 14 AA.
AC P80086;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase A chain (BC 3.6.3.14) (protein 6) (Fragment).
DN ATP6.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX STRAIN=cv. Medania; TISSUE=Leaf mesophyll;
RA Hamasur B., Glaser E.;
RT "Plant mitochondrial FoF1 ATP synthase. Identification of the
RT individual subunits and properties of the purified spinach leaf
RT mitochondrial ATP synthase."

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RL Eur. J. Biochem. 205:409-416(1992).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
DR PIR; S21247; S21247.
DR InterPro; IPR000568; ATPsynt_Asub.
DR PROSITE; PS00449; APPASE_A; PARTIAL.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT NON TER 14
FT SEQUENCE 14 AA; 1619 MW; 9F1D60181FC1PF45 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 4 EQ 5

RESULT 49
MARI ALTSP
ID MARI ALTSP STANDARD; PRT; 14 AA.
AC P2939;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinostatin C-2 [Marinostatin C-1; Marinostatin D].
OS Alteromonas sp. (strain B-10-31).
CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
CC Alteromonadales; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamei K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31."
RL J. Biochem. 110:856-858(1991).
CC -1- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14
FT PEPTIDE 3 14 MARINOSTATIN C-2.
FT PEPTIDE 4 14 MARINOSTATIN C-1.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT SITE 6 7 REACTIVE BOND.
FT SEQUENCE 14 AA; 1644 MW; 6E7CEE92EF32E44 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 13 SE 14

RESULT 50
NSK2_SARBU
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-FEB-1996 (Rel. 33, Last annotation update)
DE Neosulfakinin-II (NEB-SK-II).

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OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OC NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata."
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: MYOTROPIC PEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A56632; A56632.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Neuropeptide; Amidation; Sulfation.
FT MOD RES 9 9 SULFATION (POTENTIAL).
FT MOD RES 14 14 AMIDATION (POTENTIAL).
FT SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 4 EQ 5

RESULT 51
PPK6 PERAM
ID PPK6 PERAM STANDARD; PRT; 14 AA.
AC P82693;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-6 (Pea-PK-6) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC -1- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN
CC ABDOMINAL PERISYPHATHETIC ORGANS.
CC -1- MASS SPECTROMETRY: MW=1590.8; METHOD=WALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinnin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Amidation; Pyrokinnin.
FT MOD RES 14 14 AMIDATION.
FT SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 1 SE 2

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RESULT 52
TAT_HV1W2      STANDARD;      PRT;      14 AA.
ID   P12509;
AC
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   TAT protein (Transactivating regulatory protein) (Fragment).
GN   TAT.
OS   Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC   Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11705;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86235450; PubMed=3012778;
RA   Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA   Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT   "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT   at risk for AIDS.";
RL   Science 232:1548-1553(1986).
CC   -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC   TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC   ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC   PROMOTER.
CC   -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC   -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC   BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC   WAS PERINATALLY INFECTED BY HER MOTHER.
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EMBL; M12507; AAB12991.1; -.
DR   HIV; M12507; TAT$WMJ2
KW   Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW   AIDS.
FT   NON TER      1
SQ   SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AA8 CRC64;
Query Match      50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      3 QP 4
Db      4 QP 5

RESULT 53
TAT_HV1W2      STANDARD;      PRT;      14 AA.
ID   P12511;
AC
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   TAT protein (Transactivating regulatory protein) (Fragment).
GN   TAT.
OS   Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC   Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11681;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86281278; PubMed=3395517;
RA   Younso J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA   Gallo R.C.;
RT   "Nucleotide sequence analysis of the env gene of a new Zairian
RT   isolate of HIV-1.";

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RL   AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC   -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC   TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
CC   ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC   PROMOTER.
CC   -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC   -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC   ZAIREAN MALE.
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EMBL; J03653; AAA44685.1; -.
DR   HIV; J03653; TAT$JVI1
KW   Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW   AIDS.
FT   NON TER      1
SQ   SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;
Query Match      50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      3 QP 4
Db      4 QP 5

RESULT 54
APP3_MALPA     STANDARD;      PRT;      15 AA.
ID   P83137;
AC
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Antifungal protein 3 (CW-3) (Fragment).
OS   Malva parviflora (little mallow) (Cheeseweed).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX   NCBI_TaxID=145753;
RN   [1]
RP   SEQUENCE AND FUNCTION.
RC   TISSUE=Seed.
RX   MEDLINE=21199399; PubMed=11302747;
RA   Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT   "Purification and characterization of three antifungal proteins from
RT   Cheeseweed (Malva parviflora).";
RL   Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
CC   -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC   not F.graminearum.
CC   -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC   concentration.
CC   GO: GO:0003799; F:antifungal peptide activity; IDA.
CC   GO: GO:0007275; P:development; NAS.
KW   Fungicide; Antibiotic.
FT   NON TER      15
SQ   SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;
Query Match      50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 EQ 3
Db      11 EQ 12

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RESULT 55
ARCA_STRPS
ID ARCA_STRP5 STANDARD; PRT; 15 AA.
AC P58827;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)
DE (Streptococcus acid glycoprotein) (Fragment).
GN ARCA OR SAGP.
OS Streptococcus pyogenes (serotype M5).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=160491;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RC STRAIN=Manfredo / Serotype M5.
RX MEDLINE=98298018; PubMed=9632565;
RA Degan B.A., Palmer J.M., Robson T., Jones C.E.D., Fischer M.,
RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;
RT "Inhibition of human peripheral blood mononuclear cell proliferation
RT by Streptococcus pyogenes cell extract is associated with arginine
RT deiminase activity.";
RL Infect. Immun. 66:3050-3058(1998).
CC -!- FUNCTION: Antitumor protein. Has a powerful and dose-dependent
CC inhibitory effect on antigen, superantigen, or mitogen-stimulated
CC human peripheral blood mononuclear cell (PBMC) proliferation. It
CC may inhibit cell proliferation by arresting cell cycle and
CC inducing apoptosis.
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the arginine deiminase family.
DR HAMAP: MF_00242; -; 1.
KW Hydrolase; Arginine metabolism; Glycoprotein.
FT INIT MET 0
FT NON TER 15
SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EE46 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 10 SE 11

RESULT 56
CHIL_PEA
ID CHIL_PEA STANDARD; PRT; 15 AA.
AC P21225;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endochitinase A1 (EC 3.2.1.14) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Birte; TISSUE=Leaf;
RA Vad K., Mikkelsen J.D., Collinge D.B.;
RT "Induction, purification and characterization of chitinase isolated
RT from pea leaves inoculated with Ascochyta pisi.";
RL Planta 184:24-29(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-

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CC acetyl-D-glucosamine polymers of chitin.
CC -!- INDUCTION: By infection with the fungal pathogen Ascochyta pisi.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CC CHITIN IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC InterPro: IPR001002; Chitin_binding_1.
DR InterPro; IPR000726; Glyco_Hydro_19.
DR PROSITE; PS00026; CHITIN BINDING; PARTIAL.
DR PROSITE; PS00773; CHITINASE 19.1; PARTIAL.
DR PROSITE; PS00774; CHITINASE 19.2; PARTIAL.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;
KW Multigene family.
FT NON TER 15
SQ SEQUENCE 15 AA; 1438 MW; 23355ED6B811E869 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 1 EQ 2

RESULT 57
IRBP_CRISP
ID IRBP_CRISP STANDARD; PRT; 15 AA.
AC P12665;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
DE retinol-binding protein) (Fragment).
OS RBP3.
OS Cricetidae sp. (Hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
OX NCBI_TaxID=36483;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
RA Bridges C.D.B.;
RT "N-terminal sequence homologies in interstitial retinol-binding
RT proteins from 10 vertebrate species.";
RL FEBS Lett. 205:309-312(1986).
CC -!- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -!- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
CC EPITHELIUM CELLS.
DR PIR; G24417; G24417.
KW Vitamin A; Transport.
FT NON TER 15
SQ SEQUENCE 15 AA; 1752 MW; C51A8780C85DEC1E CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 8 QP 9

RESULT 58
LEC2_PSOSC
ID LEC2_PSOSC STANDARD; PRT; 15 AA.
AC P22585;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)

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DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Basic lectin B2 (Fragment).  
 OC Psophocarpus scandens.  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eusoids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OX NCBI\_TaxID=3890;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Seed;  
 RA Kortt A.A.;  
 RT "Isolation and characterization of the lectins from the seeds of  
 RT Psophocarpus scandens.";  
 RL Phytochemistry 27:2847-2855(1988).  
 CC -!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF  
 CC -!- ABOUT 32000 APPARENT MW.  
 CC -!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE  
 CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.  
 CC -!- SIMILARITY: WITH P.TETRAONOLOBUS BASIC LECTINS IN N-TERMINAL  
 CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.  
 DR PIR: PA0008; PA0008.  
 KW Lectin; Glycoprotein.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1847 MW; D194CE400C832796 CRC64;  
  
 Query Match 50.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 EQ 3  
 Db 12 EQ 13  
  
 RESULT 59  
 ID MW01 RAT STANDARD; PRT; 15 AA.  
 AC P81563;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)  
 DE (MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (Fragment).  
 GN MMP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=96201136; PubMed=8605638;  
 RA Tyagi S.C.; Cleutjens J.P.M.;  
 RT "Myocardial collagenase: purification and structural  
 RT characterization.";  
 RL Can. J. Cardiol. 12:165-171(1996).  
 CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN  
 CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY  
 CC PLAY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR  
 CC MATRIX PROTEINS DURING THE ONSET OF DILATED CARDIOMYOPATHY.  
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
 CC collagen. Cleavage of the triple helix of collagen at about three-  
 CC quarters of the length of the molecule from the N-terminus, at  
 CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 CC substrates and alpha-macroglobulins at bonds where P1' is a  
 CC hydrophobic residue.  
 CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.  
 CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE  
 CC ACTIVATION PEPTIDE.  
 CC -!- PTM: THE N-TERMINAL IS BLOCKED.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.  
 KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;

KW Extracellular matrix.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;  
  
 Query Match 50.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 SE 2  
 Db 5 SE 6  
  
 RESULT 60  
 ID PGKH PHYPA STANDARD; PRT; 15 AA.  
 AC P80659;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoglycerate kinase, chloroplast (EC 2.7.2.3) (Fragment).  
 OS Physcomitrella patens (Moss).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrellia.  
 OX NCBI\_TaxID=3218;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Protonema;  
 RX MEDLINE=97275459; PubMed=9129336;  
 RA Kasten B., Buck F., Nuske J., Reski R.;  
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting  
 RT plastid enzymes.";  
 RL Planta 201:261-272(1997).  
 CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-  
 CC phospho-D-glyceroyl phosphate.  
 CC -!- PATHWAY: Calvin cycle.  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Chloroplast.  
 CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.  
 DR InterPro; IPR001576; PGK.  
 DR PROSITE; PS00111; PGLYCERATE KINASE; PARTIAL.  
 KW Transferase; Kinase; Multigene family; Calvin cycle; Chloroplast.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1531 MW; 56A5ECC1F677EEC6 CRC64;  
  
 Query Match 50.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 EQ 3  
 Db 4 EQ 5  
  
 RESULT 61  
 ID PGTS PELAC STANDARD; PRT; 15 AA.  
 AC P80564;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE Pyrogallol hydroxyltransferase small subunit (EC 1.9.7.1.2)  
 DE (Transhydroxylase) (Fragment).  
 OS Pelobacter acidgallii.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
 OC Pelobacteraceae; Pelobacter.  
 OX NCBI\_TaxID=35816;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 2377 / Braunschweig;  
 RX MEDLINE=96215436; PubMed=8647079;  
 RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;

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RT "One molecule of molybdopterin guanine dinucleotide is associated
RT with each subunit of the heterodimeric Mo-Fe-S protein
RT transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE
RT and mass spectrometry."
RL Eur. J. Biochem. 237:406-413(1996).
CC -!- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3,5-
CC trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
CC tetrahydroxybenzene.
CC -!- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
DR PIR, S65429; S65429.
KW Oxidoreductase; Molybdenum; Iron-sulfur.
FT NON_TER 15
FT SEQUENCE 15 AA; 1843 MW; 0567BDD004C28499 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 2 EQ 3

RESULT 62
RBS PHYPA
ID - RBS PHYPA STANDARD; PRT; 15 AA.
AC P80657;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO
DE small subunit) (Fragment).
GN RBCs.
OS Physcomitrella patens (Moss).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
CC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes."
RL Planta 201:261-272(1997).
CC -!- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
CC carbon dioxide fixation, as well as the oxidative fragmentation of
CC the pentose substrate in the photorespiration process. Both
CC reactions occur simultaneously and in competition at the same
CC active site.
CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 3-
CC phospho-D-glycerate.
CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =
CC 3-phospho-D-glycerate + 2-phosphoglycolate.
CC -!- SUBUNIT: 8 large chains + 8 small chains.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
KW Photosynthesis; Carbon dioxide fixation; Photorespiration;
KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.
FT NON_TER 15
FT SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6CE0 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 9 QP 10

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RESULT 63
RS20_BACST
ID RS20_BACST STANDARD; PRT; 15 AA.
AC P59681;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE 30S ribosomal protein S20 (BS20) (Fragment).
GN RPST.
OS Bacillus stearothermophilus.
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RC STRAIN=10;
RX PubMed=4607606;
RA Yaguchi M., Matheson A.T., Visentin L.P.;
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and
RT structural correspondence of 30 S ribosomal proteins from Escherichia
RT coli and Bacillus stearothermophilus."
RL FEBS Lett. 46:296-300(1974).
CC -!- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity).
CC -!- SIMILARITY: BELONGS TO THE S20P FAMILY OF RIBOSOMAL PROTEINS.
DR HAMAP; MF 00500; -; 1.
KW Ribosomal protein; rRNA-binding.
FT INIT_MET 0
FT NON_TER 15
FT SEQUENCE 15 AA; 1645 MW; 4E4646265E4C6206 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 13 SE 14

RESULT 64
RT32_BOVIN
ID RT32_BOVIN STANDARD; PRT; 15 AA.
AC P82927;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Mitochondrial 28S ribosomal protein S32 (S32mt) (MRP-S32) (Fragment).
GN MRPS32.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Xoc E.C.; Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present."
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrion.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 15
FT SEQUENCE 15 AA; 1725 MW; 34E58A79E31DB758 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3

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Db      11 EQ 12

RESULT 65
UC13 MAIZE
ID UC13 MAIZE          STANDARD;          PRT;          15 AA.
AC P80619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 243)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 56.9 kDa.
CC -!- SIMILARITY: TO GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASES.
DR Maize-2DPAGE; P80619; COLEOPTILE.
DR MaizeDB; 123946; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1739 MW; 02038EE7471AE038 CRC64;

Query Match      50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 13 SE 14

RESULT 66
UC27 MAIZE
ID UC27 MAIZE          STANDARD;          PRT;          15 AA.
AC P80633;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 688)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.4, ITS MW IS: 48.4 kDa.
CC -!- SIMILARITY: TO XENOPUS HISTONE-BINDING PROTEIN N1/N2 AND RABBIT
CC AND HUMAN NUCLEAR AUTOANTIGENIC SPERM PROTEIN.
DR Maize-2DPAGE; P80633; COLEOPTILE.
DR MaizeDB; 123958; -.
FT NON_TER 1 1
FT NON_TER 15 15

us-09-641-801-10.oligo.rsp

FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1853 MW; CA0E12A5DAED8DC7 CRC64;

Query Match      50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
   ||
Db 3 EQ 4

RESULT 67
UN01_PINPS
ID UN01_PINPS          STANDARD;          PRT;          15 AA.
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)
DE (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map.";
RL Silvae Genet. 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match      50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
   ||
Db 3 EQ 4

RESULT 68
URE2_MORMO
ID URE2_MORMO          STANDARD;          PRT;          15 AA.
AC P17338;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREB.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
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RX MEDLINE=90264298; PubMed=23451135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
  isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER UREASES BETA SUBUNITS.
DR PIR; B35389; B35389.
KW Hydrolase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2P20C7E8 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 5 QP 6

RESULT 69
BRB_BASAL STANDARD; PRT; 16 AA.
ID BRB_BASAL
AC P83187;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-basurubin (Fragment)
OS Basella alba (Malabar spinach) (Ceylon spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Basellaceae; Basella.
ON NCBI_TaxID=3589;
RN [1];
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21547763; PubMed=11688973;
RA Wang H., Ng T.B.;
RT "Novel antifungal peptides from ceylon spinach seeds.";
RL Biochem. Biophys. Res. Commun. 288:765-770(2001).
CC -!- FUNCTION: Possesses antifungal activity against B.cinerea,
CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.
CC Inhibits HIV-1 reverse transcriptase and cell-free translation.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IDA.
KW Fungicide.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1952 MW; 28F9FE4FC181682C CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 11 EQ 12

RESULT 70
FIBA_EQUAS STANDARD; PRT; 16 AA.
ID FIBA_EQUAS
AC P14449;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
ON NCBI_TaxID=9793;

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RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
  POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
  AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
  (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
  THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
  CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
  RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 10 SE 11

RESULT 71
FIBA_MELME STANDARD; PRT; 16 AA.
ID FIBA_MELME
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
ON NCBI_TaxID=9662;
RN [1];
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
  POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
  AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
  (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
  THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
  CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
  RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 6 SE 7

RESULT 72
FIBA_MUSVI STANDARD; PRT; 16 AA.
ID FIBA_MUSVI

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AC P14458;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 6 SE 7

RESULT 73
HTPG ACICA STANDARD; PRT; 16 AA.
AC P81876;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein htpg (Heat shock protein htpg) (High temperature
DE protein G) (Fragment).
GN HTPG.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE.
RC STRAIN=69-V;
RX MEDLINE=99274045; PubMed=10344248;
RA Benndorf D., Loffhagen N., Babel W.;
RT "Induction of heat shock proteins in response to primary alcohols in
RT Acinetobacter calcoaceticus.";
RL Electrophoresis 20:781-789(1999).
CC -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: BY HEAT SHOCK AND PRIMARY ALCOHOLS.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR HAMAP; MF_00505; -; 1.
DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1769 MW; 316C70D8928CB482 CRC64;

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Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 1 SE 2

RESULT 74
IBP4_PIG STANDARD; PRT; 16 AA.
ID IBP4_PIG
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Ethernon T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 IGFBP domain.
CC PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac.pr.
DR InterPro; IPR000716; Thyroglobulin_1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 10 SE 11

RESULT 75
LPK1_LOCMI STANDARD; PRT; 16 AA.
ID LPK1_LOCMI
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrrolin 1 (LOM-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=91224474; PubMed=2026322;

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RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a  
RL myotropic peptide of Locusta migratoria.";  
RL Gen. Comp. Endocrinol. 81:97-104(1991).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR FIR; A49761; A49761.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 16 16 AMIDATION.  
SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;  
  
Query Match 50.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred.No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 QP 4  
|  
|  
Db 10 QP 11

Search completed: November 25, 2003, 18:17:30  
Job time : 2.93617 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 9.6383 Seconds  
(without alignment)  
107.095 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	100.0	18	4	Q9UCF4
2	3	75.0	9	8	Q8WFT4
3	3	75.0	10	8	Q8WFT6
4	3	75.0	10	8	Q8WFT5
5	3	75.0	14	10	P82332
6	3	75.0	16	2	P82597
7	3	75.0	17	4	Q9UCT3
8	3	75.0	17	5	Q9TWI6
9	3	75.0	18	6	Q9TOR0
10	3	75.0	18	11	Q99MD5
11	3	75.0	18	12	Q9DS59
12	3	75.0	20	10	Q9SM31
13	3	75.0	20	12	Q8UXT4
14	3	75.0	20	12	Q8UXS4
15	3	75.0	20	12	Q8UXT3
16	3	75.0	20	12	Q8UXS2
17	3	75.0	20	12	Q8UXS2
18	3	75.0	20	12	Q8UXS2
19	3	75.0	20	12	Q8UXS2
20	3	75.0	20	12	Q8UXS2
21	3	75.0	20	12	Q8UXS2
22	3	75.0	20	12	Q8UXS2
23	3	75.0	20	12	Q8UXS2
24	3	75.0	20	12	Q8UXS2
25	3	75.0	20	12	Q8UXS2
26	3	75.0	20	12	Q8UXS2
27	3	75.0	20	12	Q8UXS2
28	3	75.0	20	12	Q8UXS2
29	3	75.0	20	12	Q8UXS2
30	3	75.0	20	12	Q8UXS2
31	3	75.0	20	12	Q8UXS2
32	3	75.0	20	12	Q8UXS2
33	3	75.0	20	12	Q8UXS2
34	3	75.0	20	12	Q8UXS2
35	3	75.0	20	12	Q8UXS2
36	3	75.0	20	12	Q8UXS2
37	3	75.0	20	12	Q8UXS2
38	3	75.0	20	12	Q8UXS2
39	3	75.0	20	12	Q8UXS2
40	3	75.0	20	12	Q8UXS2
41	3	75.0	20	12	Q8UXS2
42	3	75.0	20	12	Q8UXS2
43	3	75.0	20	12	Q8UXS2
44	3	75.0	20	12	Q8UXS2
45	3	75.0	20	12	Q8UXS2
46	3	75.0	20	12	Q8UXS2
47	3	75.0	20	12	Q8UXS2
48	3	75.0	20	12	Q8UXS2
49	3	75.0	20	12	Q8UXS2
50	3	75.0	20	12	Q8UXS2
51	3	75.0	20	12	Q8UXS2
52	3	75.0	20	12	Q8UXS2
53	3	75.0	20	12	Q8UXS2
54	3	75.0	20	12	Q8UXS2
55	3	75.0	20	12	Q8UXS2
56	3	75.0	20	12	Q8UXS2
57	3	75.0	20	12	Q8UXS2
58	3	75.0	20	12	Q8UXS2
59	3	75.0	20	12	Q8UXS2
60	3	75.0	20	12	Q8UXS2
61	3	75.0	20	12	Q8UXS2
62	3	75.0	20	12	Q8UXS2
63	3	75.0	20	12	Q8UXS2
64	3	75.0	20	12	Q8UXS2
65	3	75.0	20	12	Q8UXS2
66	3	75.0	20	12	Q8UXS2
67	3	75.0	20	12	Q8UXS2
68	3	75.0	20	12	Q8UXS2
69	3	75.0	20	12	Q8UXS2
70	3	75.0	20	12	Q8UXS2
71	3	75.0	20	12	Q8UXS2
72	3	75.0	20	12	Q8UXS2
73	3	75.0	20	12	Q8UXS2
74	3	75.0	20	12	Q8UXS2
75	3	75.0	20	12	Q8UXS2
76	3	75.0	20	12	Q8UXS2
77	3	75.0	20	12	Q8UXS2
78	3	75.0	20	12	Q8UXS2
79	3	75.0	20	12	Q8UXS2
80	3	75.0	20	12	Q8UXS2
81	3	75.0	20	12	Q8UXS2
82	3	75.0	20	12	Q8UXS2
83	3	75.0	20	12	Q8UXS2
84	3	75.0	20	12	Q8UXS2
85	3	75.0	20	12	Q8UXS2
86	3	75.0	20	12	Q8UXS2
87	3	75.0	20	12	Q8UXS2
88	3	75.0	20	12	Q8UXS2
89	3	75.0	20	12	Q8UXS2

Q8UXT0 hepatitis c  
Q8UXS5 hepatitis c  
Q8UXT1 hepatitis c  
Q8UXS6 hepatitis c  
Q8UXS9 hepatitis c  
Q8UXS3 hepatitis c  
Q8UXT2 hepatitis c  
Q8UXS1 hepatitis c  
Q8RSR3 lactobacilli  
Q47273 escherichia  
Q16428 homo sapien  
Q9P285 homo sapien  
Q8MUN6 heliconius  
Q9MYL5 pongo pygma  
Q99NX9 hydrochoeru  
Q62721 rattus norv  
Q9WJ33 pseudorabie  
P72345 pseudomonas  
Q53914 streptomyce  
Q47063 escherichia  
Q9XS10 capra hircu  
Q9TRSO oryctolagus  
Q8W875 bostriychia  
Q8H921 cyanophaga  
P82429 nicotiana t  
P82440 nicotiana t  
Q9QW2 mus musculu  
Q08979 mus musculu  
Q82622 avian infec  
Q83622 murray vall  
Q8AYL5 carassius a  
Q8AUM7 carassius a  
Q8AEM8 human immun  
Q93591 salmonella  
Q92181 clostridium  
P82588 streptococc  
Q8NEO0 homo sapien  
Q00493 homo sapien  
Q96Q99 homo sapien  
Q8MUP1 heliconius  
Q8WPL6 kikopleura  
Q8MUN7 heliconius  
P82217 bombyx mori  
Q8MJ52 equus cabal  
P83205 ovis aries  
Q8WBR7 chaitophoru  
Q96041 oenothera b  
Q8SHA8 rhampholeon  
Q8LLJ0 cryza sativ  
Q8GU66 capsella ru  
Q91WZ3 rattus sp.  
Q9QVE8 mus sp. pro  
Q9QVF0 mus sp. pro  
Q9QVF1 mus sp. pro  
Q9QVE7 mus sp. pro  
Q8CJE0 rattus norv  
P90391 tomato yell  
Q86580 simian para  
Q86324 rous sarcom  
Q86325 rous sarcom  
Q86326 rous sarcom  
Q52526 rhizobium s  
Q9HFN8 candida rug  
Q16427 homo sapien  
Q9UBM2 homo sapien  
Q9UCR1 homo sapien  
Q16217 homo sapien  
Q55916 plasmodium  
Q8MM58 heliconius  
Q9XSP7 pygathrix n  
Q9XSP2 hyllobates s  
Q9XSP5 pan troglod  
Q9XSP8 presbytis j

90 Q9XSP6 2 50.0 11 6 Q9XSP6  
91 Q9XSQ4 2 50.0 11 6 Q9XSQ4  
92 Q77885 2 50.0 11 7 Q77885  
93 Q77884 2 50.0 11 7 Q77884  
94 O19718 2 50.0 11 7 O19718  
95 Q77913 2 50.0 11 7 Q77913  
96 Q32704 2 50.0 11 8 Q32704  
97 Q8RV30 2 50.0 11 10 Q8RV30  
98 P82336 2 50.0 11 10 P82336  
99 Q9QVH3 2 50.0 11 11 Q9QVH3  
100 Q9R0K9 2 50.0 11 11 Q9R0K9

Q9XSP6 pongo pygma  
Q9XSQ4 gorilla gor  
Q77885 oreochromis  
Q77884 oreochromis  
O19718 homo sapien  
Q77913 oreochromis  
Q32704 nicotiana t  
Q8RV30 zea mays (m  
P82336 pisum sativ  
Q9QVH3 rattus sp.  
Q9R0K9 mus musculu

## ALIGNMENTS

## RESULT 1

Q9UCF4 ID Q9UCF4 PRELIMINARY; PRT; 18 AA.  
AC Q9UCF4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Chymotrypsinogen homolog (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Diarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_  
RP SEQUENCE.  
RX MEDLINE=93285747; PubMed=8509158;  
RA Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D.,  
RA Warfel K.A., Vandagriff J., Davis J.K., Kwon B.S.;  
RT "IDDM patients' sera recognize a novel 30-kD pancreatic autoantigen  
RT related to chymotrypsinogen".  
RL Immunol. Invest. 22:219-227(1993).  
SQ SEQUENCE 18 AA; 1826 MW; 38105D1037CA6837 CRC64;

Query Match 100.0%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEQ 4  
Db 14 SEQ 17

## RESULT 2

Q8WFT4 ID Q8WFT4 PRELIMINARY; PRT; 9 AA.  
AC Q8WFT4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN COII.  
OS Diadema antillarum.  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Diademataceae; Diadematoidea; Diadematiidae;  
OC Diadema.  
OX NCBI\_TaxID=105358;  
RN [1]\_  
RP SEQUENCE FROM N.A.  
RX STRAIN=DCA3;  
RX MEDLINE=21323357; PubMed=11430656;  
RA Lessios H.A., Kessing B.D., Pearse J.S.;  
RT "Population structure and speciation in tropical seas: global  
RT phylogeography of the sea urchin Diadema";  
RL Evolution 55:955-975(2001).  
RN [2]\_  
RP SEQUENCE FROM N.A.  
RX STRAIN=DCA3;

RX MEDLINE=21561594; PubMed=11703875;  
RA Lessios H.A., Garrido M.J., Kessing B.D.;  
RT "Demographic history of Diadema antillarum, a keystone herbivore on  
RT Caribbean reefs";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
DR EMBL; AY012858; AAL33832.2; -.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;  
Query Match 75.0%; Score 3; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EQP 4  
Db 7 EQP 9

## RESULT 3

Q8WFT6 ID Q8WFT6 PRELIMINARY; PRT; 10 AA.  
AC Q8WFT6;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN COII.  
OS Diadema antillarum.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Diademataceae; Diadematoidea; Diadematiidae;  
OC Diadema.  
OX NCBI\_TaxID=105358;  
RN [1]\_  
RP SEQUENCE FROM N.A.  
RX STRAIN=DCA1;  
RX MEDLINE=21323357; PubMed=11430656;  
RA Lessios H.A., Kessing B.D., Pearse J.S.;  
RT "Population structure and speciation in tropical seas: global  
RT phylogeography of the sea urchin Diadema";  
RL Evolution 55:955-975(2001).  
RN [2]\_  
RP SEQUENCE FROM N.A.  
RX STRAIN=DCA1;  
RX MEDLINE=21561594; PubMed=11703875;  
RA Lessios H.A., Garrido M.J., Kessing B.D.;  
RT "Demographic history of Diadema antillarum, a keystone herbivore on  
RT Caribbean reefs";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
DR EMBL; AY012856; AAL33830.2; -.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1301 MW; EDEB101B173B46CA CRC64;

OY 2 EQP 4  
Db 8 EQP 10

## RESULT 4

Q8WFT5 ID Q8WFT5 PRELIMINARY; PRT; 10 AA.  
AC Q8WFT5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Cytochrome oxidase subunit II (Fragment).  
GN COII.

Query Match 75.0%; Score 3; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EQP 4  
Db 8 EQP 10

		Qy	2 EQP 4     4 EQP 6	
		Dd		
RESULT 6		P82597		
ID	PD2597	PRELIMINARY;	PRT;   16 AA.	
AC	P82597;			
DT	01-OCT-2000 (TrEMBLrel_15, Created)			
DI	01-OCT-2000 (TrEMBLrel_15, Last sequence update)			
DE	01-JUN-2001 (TrEMBLrel_17, Last annotation update)			
DE	Thermotable monoacylglycerol lipase [MGLP] (24 kDa) (EC 3.1.1.23)			
DE	(Fragment).			
OS	Bacillus sp.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBJ_TaxID=1409;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=H-257;			
RK	MEDLINE=20198254; PubMed=10731713;			
RA	Inamura S., Kitaoura S.;			
RT	"Purification and characterization of a monoacylglycerol lipase from the moderately thermophilic Bacillus sp. H-257.";			
RL	J. Biochem. 127:419-425(2000).			
CC	-I- FUNCTION: HYDROLYZES MONOACYLGYCEROLS, WITH THE HIGHEST ACTIVITY OCCURRING WITH 1-MONOLAORYLGYCEROL.			
CC	-I- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.			
CC	-I- SUBUNIT: MONOMER.			
CC	-I- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8			
CC	-I- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS OTHER BACTERIAL LIPASES.			
KW	Hydrolase.			
PT	NON_TER	16		
SQ	SEQUENCE	16 AA; 1787 MW; 900CF59289521D8F CRC64;		
Query Match	75.0%; Score 3; DB 2; Length 16;			
Best Local Similarity	100.0% ; Pred.No. 1.7e+03;			
Matches	3; Conservative     0; Mismatches     0; Indels       0; Gaps			
Qy	1 SEQ 3			
Dd	1 SEQ 3			
RESULT 7				
Q9UCT3				
ID	Q9UCT3	PRELIMINARY;	PRT;   17 AA.	
AC	Q9UCT3;			
DT	01-MAY-2000 (TrEMBLrel_13, Created)			
DI	01-MAY-2000 (TrEMBLrel_13, Last sequence update)			
DE	01-JUN-2002 (TrEMBLrel_21, Last annotation update)			
DE	ALZHEIMER'S beta-amylloid precursor protein, kunitz-type protease inhibitor, neutrophil elastase inhibitor, P1-VAL-APP-KD (fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RK	MEDLINE=32041969; PubMed=1939150;			
RA	Sinha S.; Knops J., Esch F., Moyer E.D., Oltersdorf T.;			
RT	"Conversion of the Alzheimer's beta-amylloid precursor protein (APP) Kunitz domain into a potent human neutrophil elastase inhibitor."			
RL	J. Biol. Chem. 266:21011-21013(1991).			
FT	NON TER	1		
FT	NON_TER	17		
SQ	SEQUENCE	17 AA; 1778 MW; FOCCDC28D6712BA CRC64;		
Query Match	75.0%; Score 3; DB 4; Length 17;			

Best Local Similarity 100.0%; Pred. No. 1.8e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Q99MD5 PRELIMINARY; PRT; 18 AA.	
QY 1 SEQ 3 		AC Q99MD5; 17, Created)	
Db 5 SEQ 7		DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)	
		DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)	
		DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)	
		DE Killer cell lectin-like receptor 7 (Fragment).	
		GN KLR47.	
		OS Mus musculus (Mouse).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		OX NCBI_TaxID=10090;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RC STRAIN=CS7BL/6;	
		RX MEDLINE=21291699; PubMed=11398966;	
		RA Wilhelm B.T., McQueen K.L., Freeman J.D., Takei F., Mager D.L.;	
		RT "Comparative analysis of the promoter regions and transcriptional	
		RT start sites of mouse Ly49 genes.";	
		RL Immunogenetics 53:215-224(2001).	
		DR EMBL; AF349732; AAK19750.1; -.	
		KW Lectin; Receptor.	
		FT NON_TER 18	
		SQ SEQUENCE 18 AA; 2173 MW; A99F15B657328112 CRC64;	
Query Match 75.0%; Score 3; DB 11; Length 18; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		QY 1 SEQ 3 	
		Db 2 SEQ 4 	
RESULT 11			
Q9DSS9 PRELIMINARY; PRT; 18 AA.		ID Q9DSS9	
		AC Q9DSS9;	
		DT 01-MAR-2001 (TREMBlrel. 16, Created)	
		DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)	
		DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)	
		DE P23 protease (Fragment).	
		GN P23.	
		OS Human adenovirus type 4.	
		OC Viruses; GSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.	
		OX NCBI_TaxID=28280;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RC STRAIN=Z-G T95-873;	
		RX MEDLINE=99175282; PubMed=10074533;	
		RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;	
		RT "Strain variation in adenovirus serotypes 4 and 7a causing acute	
		RT respiratory disease.";	
		RL J. Clin. Microbiol. 37:1107-1112(1999).	
		RN [2]	
		RP SEQUENCE FROM N.A.	
		RC STRAIN=Z-G T95-873;	
		RA Crawford-Miksza L.K.;	
		RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
		DR EMBL; AF065064; AAD03661.3; -.	
		DR HSSP; P03252; IAVP.	
		KW Protease.	
		FT NON_TER 18	
		SQ SEQUENCE 18 AA; 1917 MW; 12FCE2715E7FB445 CRC64;	
Query Match 75.0%; Score 3; DB 12; Length 18; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		QY 1 SEQ 3 	
		Db 3 SEQ 5 	
RESULT 10			
Q99MD5 PRELIMINARY; PRT; 17 AA.		ID Q9TWI6	
		AC Q9TWI6;	
		DT 01-MAY-2000 (TREMBlrel. 13, Created)	
		DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)	
		DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)	
		DE Major cuticular protein (Fragment).	
		OS Ceratitis capitata (Mediterranean fruit fly).	
		OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
		OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
		OC Tephritidae; Tephritidae; Ceratitis.	
		OX NCBI_TaxID=7213;	
		RN [1]	
		RP SEQUENCE.	
		RX MEDLINE=95279142; PubMed=7759285;	
		RA Tsiliras A., Koromantou E., Allen G., Dimitriadis G.;	
		RT "Partial N-terminal sequences of larval cuticular proteins from the	
		RT dipteran Ceratitis capitata.";	
		RL Hereditas 122:79-83(1995).	
		SQ SEQUENCE 17 AA; 1900 MW; 1731BE55C2FB97DA CRC64;	
Query Match 75.0%; Score 3; DB 5; Length 17; Best Local Similarity 100.0%; Pred. No. 1.8e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		QY 1 SEQ 3 	
		Db 9 SEQ 11 	
RESULT 9			
Q9TOR0 PRELIMINARY; PRT; 18 AA.		ID Q9TOR0	
		AC Q9TOR0;	
		DT 01-MAY-2000 (TREMBlrel. 13, Created)	
		DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)	
		DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)	
		DE CAMP-dependent protein kinase subunit CB (Fragment).	
		OS Sus scrofa (Pig).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.	
		OX NCBI_TaxID=9823;	
		RN [1]	
		RP SEQUENCE.	
		RX MEDLINE=93094224; PubMed=1460017;	
		RA Toner-Webb J., van Patten S.M., Walsh D.A., Taylor S.S.;	
		RT "Autophosphorylation of the catalytic subunit of CAMP-dependent	
		RT protein kinase.";	
		RL J. Biol. Chem. 267:25174-25180(1992).	
		FT NON_TER 1	
		FT NON_TER 18	
		SQ SEQUENCE 18 AA; 2155 MW; 2A709A3F639968D7 CRC64;	
Query Match 75.0%; Score 3; DB 6; Length 18; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		QY 1 SEQ 3 	
		Db 2 SEQ 4 	

## RESULT 12

Q9SM31 ID Q9SM31 PRELIMINARY; PRT; 20 AA.  
 AC Q9SM31;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Putative sucrose synthase (Fragment).  
 GN SSI.  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Chinese spring;  
 RA Helguera M., Khan I.A., Dubcovsky J.;  
 RT "Development of PCR markers for wheat leaf rust resistance gene  
 Lr47.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ249623; CAB61261.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 20 AA; 2298 MW; CC4FE0F3877CCDC CRC64;

Query Match 75.0%; Score 3; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
 Db 15 EQP 17

## RESULT 13

Q8UXT4 ID Q8UXT4 PRELIMINARY; PRT; 20 AA.  
 AC Q8UXT4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Genome polyprotein (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,  
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;  
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of  
 RT hepatitis C virus after a second course of alpha interferon.";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF466512; AAL70092.1; -.  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 Db 7 SEQ 9

## RESULT 14

Q8UXS4 ID Q8UXS4 PRELIMINARY; PRT; 20 AA.  
 AC Q8UXS4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Genome polyprotein (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,  
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;  
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of  
 RT hepatitis C virus after a second course of alpha interferon.";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF466522; AAL70102.1; -.  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 Db 7 SEQ 9

## RESULT 15

Q8UXT3 ID Q8UXT3 PRELIMINARY; PRT; 20 AA.  
 AC Q8UXT3;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Genome polyprotein (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,  
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;  
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of  
 RT hepatitis C virus after a second course of alpha interferon.";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF466513; AAL70093.1; -.  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 Db 7 SEQ 9

## RESULT 16

Q8UXT3 ID Q8UXT3 PRELIMINARY; PRT; 20 AA.  
 AC Q8UXT3;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Genome polyprotein (Fragment).  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,  
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;  
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of  
 RT hepatitis C virus after a second course of alpha interferon.";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF466522; AAL70102.1; -.  
 DR InterPro; IPR002531; HCV\_NSI.  
 DR Pfam; PF01560; HCV\_NSI; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;  
 KW Polyprotein; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 Db 7 SEQ 9

```
Q8UXS2
ID Q8UXS2; PRELIMINARY; PRT; 20 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466524; AAL70104.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB |||
7 SEQ 9

RESULT 17
Q8UXT0
ID Q8UXT0; PRELIMINARY; PRT; 20 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466516; AAL70096.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB |||
7 SEQ 9

RESULT 18
Q8UXS5
ID Q8UXS5; PRELIMINARY; PRT; 20 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466521; AAL70101.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB |||
7 SEQ 9

RESULT 19
Q8UXT1
ID Q8UXT1; PRELIMINARY; PRT; 20 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466515; AAL70095.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB |||
7 SEQ 9
```



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RESULT 20
Q8UXS6
ID Q8UXS6 PRELIMINARY; PRT; 20 AA.
AC Q8UXS6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466520; AAL70100.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db |||
7 SEQ 9

RESULT 21
Q8UXS9
ID Q8UXS9 PRELIMINARY; PRT; 20 AA.
AC Q8UXS9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466517; AAL70097.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db |||
7 SEQ 9

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RESULT 22
Q8UXS3
ID Q8UXS3 PRELIMINARY; PRT; 20 AA.
AC Q8UXS3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466523; AAL70103.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db |||
7 SEQ 9

RESULT 23
Q8UXT2
ID Q8UXT2 PRELIMINARY; PRT; 20 AA.
AC Q8UXT2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466514; AAL70094.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db |||
7 SEQ 9

```

```
Db 7 SEQ 9

RESULT 24
Q8UXS1
ID Q8UXS1 PRELIMINARY; PRT; 20 AA.
AC Q8UXS1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulesin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Fael J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466525; AAL70105.1; -.
DR InterPro: IPR002531; HCV NS1.
DR Pfam: PF01560; HCV NS1; I.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 7 SEQ 9

RESULT 25
Q8RSR3
ID Q8RSR3 PRELIMINARY; PRT; 8 AA.
AC Q8RSR3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PduG protein (Fragment).
GN PDUg.
OS Lactobacillus collinoides.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33960;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMG 18050;
RA Sauvageot N., Gouffi K., Laplace J.M., Auffray Y.;
RT "Characterisation of the diol dehydratase pdu operon of Lactobacillus
RT collinoides.";
RL FEMS Microbiol. Lett. 0:0-0(0).
DR EMBL; AJ297723; CAD01093.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 882 MW; ECA40B05B85BDD6 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 5 SE 6
```

```
RESULT 26
Q47273
ID Q47273 PRELIMINARY; PRT; 8 AA.
AC Q47273;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf33, orf151, orf56, orf96, rus, orf45, orf127, and nmpC
DE genes.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=96196428; PubMed=8648624;
RA Mandi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.;
RT "Holliday Junction Resolvases encoded by homologous rusa genes in
RT Escherichia coli K-12 and Phage 32.";
RL J. Mol. Biol. 257:561-573(1996).
DR EMBL; X92587; CAA63323.1; -.
SQ SEQUENCE 8 AA; 935 MW; FD4041A05B05B336 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 3 SE 4

RESULT 27
Q16428
ID Q16428 PRELIMINARY; PRT; 8 AA.
AC Q16428;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163501; PubMed=8566960;
RA Holder E., Maeda M., Bies R.D.;
RT "Expression and regulation of the dystrophin Purkinje promoter in
RT human skeletal muscle, heart, and brain.";
RL Hum. Genet. 97:232-239(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; S81419; AAD14363.1; -.
DR EMBL; AB037493; BAA90413.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 28
```

Q9P285  
 ID Q9P285 PRELIMINARY; PRT; 8 AA.  
 AC Q9P285;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE Clotting factor VIII (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shibata M., Shima M., Morichika S., Yoshiola A.;  
 RT "Human clotting factor VIII gene, junction regions of the deletion of  
 exon 4 through 7.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB040872; BAA94312.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 866 MW; 1C15987AAB05BDD3 CRC64;  
 Query Match 50.0%; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SE 2  
 Db ||  
 3 SE 4  
 RESULT 29  
 Q8MUN6  
 ID Q8MUN6 PRELIMINARY; PRT; 8 AA.  
 AC Q8MUN6;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN MPI.  
 OS Heliconius melpomene melpomene.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.  
 OX NCBI\_TaxID=171917;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
 RA Mallet J.;  
 RT "Molecular evidence for gene flow between species of Heliconius.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF516247; AAM61933.1; -.  
 KW isomerase.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 977 MW; 16E736DB1DD1EAA3 CRC64;  
 Query Match 50.0%; Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EQ 3  
 Db ||  
 5 EQ 6  
 RESULT 30  
 Q9MYL5  
 ID Q9MYL5 PRELIMINARY; PRT; 8 AA.  
 AC Q9MYL5;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE Dystrophin.  
 OS Pongo pygmaeus (Orangutan),  
 OS Pan troglodytes (Chimpanzee), and  
 OS Gorilla gorilla (Gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 OX NCBI\_TaxID=9600, 9598, 9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.pygmaeus, P.troglodytes, and G.gorilla;  
 RA Kitano T., Kobayakawa H., Saitou N.;  
 RT "Silver Project";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB037496; BAA90419.1; -.  
 DR EMBL; AB037494; BAA90415.1; -.  
 DR EMBL; AB037495; BAA90417.1; -.  
 SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;  
 Query Match 50.0%; Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SE 2  
 Db ||  
 2 SE 3  
 RESULT 31  
 Q99NX9  
 ID Q99NX9 PRELIMINARY; PRT; 8 AA.  
 AC Q99NX9;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Amyloid beta protein (Fragment).  
 GN APP.  
 OS Eukaryotes hydrochaeris (Capybara) (Carpincho).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;  
 OC Hydrochaeris.  
 OX NCBI\_TaxID=10149;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL; AY011342; AAG47377.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1071 MW; 1356D686DB19C9C3 CRC64;  
 Query Match 50.0%; Score 2; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EQ 3  
 Db ||  
 4 EQ 5  
 RESULT 32  
 Q62721  
 ID Q62721 PRELIMINARY; PRT; 8 AA.  
 AC Q62721;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE Prohibitin (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17178; AAA86692.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 50.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 4 SE 5

RESULT 33
Q9WJ33
ID Q9WJ33 PRELIMINARY; PRT; 8 AA.
AC Q9WJ33;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Suid herpesvirus 1 putative UL47 and UL46 genes and partial gb
DE (Fragment).
GN GB.
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=33703;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kaplan;
RX MEDLINE=99239778; PubMed=10225272;
RA Bras F., Dezelee S., Simonet B., Nguyen X., Vende P., Flamand A.,
RA Masse M.J.;
RT "The left border of the genomic inversion of pseudorabies virus
RT contains genes homologous to the UL46 and UL47 genes of Herpes Simplex
RT virus type 1, but no UL45 gene.";
RL Virus Res. 60:29-40(1999).
DR EMBL; AJ010303; CAA09075.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 875 MW; 262DDAB76AAB05BB CRC64;

Query Match 50.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 34
P72345
ID P72345 PRELIMINARY; PRT; 9 AA.
AC P72345;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TABA (Fragment).
GN TABA.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.

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OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR2R;
RX MEDLINE=93167809; PubMed=7679566;
RA Barta T.M., Kinscherf T.G., Uchytel T.F., Willis D.K.;
RT "DNA sequence and transcriptional analysis of the tbla gene required
RT for tabtoxin biosynthesis by Pseudomonas syringae.";
RL Appl. Environ. Microbiol. 59:458-466(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BR2R;
RA Kinscherf T.G., Willis D.K.;
RT "sequence analysis of the tabtoxin biosynthetic region.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1037 MW; 2B34D9D5BB05B047 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 4 SE 5

RESULT 35
Q53914
ID Q53914 PRELIMINARY; PRT; 9 AA.
AC Q53914;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Curd protein (Fragment).
OS Streptomyces cyaneus (Streptomyces curacoi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1904;
RN [1]
RP SEQUENCE FROM N.A.
RA Bergh S.T., Uhlen M.;
RT "Cloning, analysis and heterologous expression of the polyketides
RT synthesis genes of Streptomyces curacoi.";
RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; M33704; AAA26724.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1027 MW; 995BDDDDC4140AB1 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 8 QP 9

RESULT 36
Q47063
ID Q47063 PRELIMINARY; PRT; 9 AA.
AC Q47063;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE URF 1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=W;
RX MEDLINE=85215599; PubMed=2987841;
RA Takagi J.S., Ida N., Tokushige M., Sakamoto H., Shimura Y.;
RT "Cloning and nucleotide sequence of the aspartase gene of Escherichia
RT coli W.";
RL Nucleic Acids Res. 13:2063-2074 (1985).
DR EMBL: X02307; CAA26175.1; -.
SQ SEQUENCE 9 AA; 1061 MW; 9DE21EASB9C72EA1 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 8 EQ 9

RESULT 37
Q9XSLO PRELIMINARY; PRT; 9 AA.
ID Q9XSLO
AC Q9XSLO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha s2-casein (Fragment).
GN CSNIS2.
OS Capra hircus (Goat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=21313038; PubMed=11419340;
RX Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
RA Cosenza G., Mariani P., Pastore N., Masina P.;
RT "An allele associated with a non detectable amount of as2 casein in
RT goat milk.";
RL Anim. Genet. 32:19-26(2001).
DR EMBL: AJ238475; CAB44298.1; -.
FT NON_TER 1 1 I -> V.
FT VARIANT 5 5
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5ASB051EB16 CRC64;

Query Match 50.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 8 SE 9

RESULT 38
Q9TRSO PRELIMINARY; PRT; 9 AA.
ID Q9TRSO
AC Q9TRSO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein
DE L-7 fragment (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;

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RT "A calcyclin-associated protein is a newly identified member of the
RT CA2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924 (1992).
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;

Query Match 50.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 1 SE 2

RESULT 39
Q8W875 PRELIMINARY; PRT; 9 AA.
ID Q8W875
AC Q8W875;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ribulose-1,5-bisphosphate large subunit (Fragment).
GN RECL.
OS Bostrychia calliptera.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
OC Bostrychia.
OX NCBI_TaxID=161377;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.E350.PA, and P3999.NT;
RA Zuccarello G.C., West J.A.;
RT "Phylogeography of the Bostrychia calliptera/B. pinnata complex
RT (Rhodomelaceae, Rhodophyta) and divergence rates based on nuclear,
RT mitochondrial and plastid DNA markers.";
DR EMBL: AF382914; AAL67249.1; -.
DR EMBL: AF382916; AAL67253.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 981 MW; 93B94DC1B771AB05 CRC64;

Query Match 50.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 2 SE 3

RESULT 40
Q8H9Z1 PRELIMINARY; PRT; 9 AA.
ID Q8H9Z1
AC Q8H9Z1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Capsid protein.
GN G20.
OS Cyanophage S-KM1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=187678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S-KM1;
RA Okunishi S., Maeda H.;
RT "Cyanophage in Kagoshima Bay.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB080247; BAC54112.1; -.
SQ SEQUENCE 9 AA; 1167 MW; DB9205AB59DB42D6 CRC64;

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Query Match          50.0%; Score 2; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 7 SE 8

RESULT 41
P82429 ID P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 44 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 9 AA; 986 MW; C22CCADC6C77776 CRC64;

Query Match          50.0%; Score 2; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
   ||
Db 2 QP 3

RESULT 42
P82440 ID P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 42 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;

Query Match          50.0%; Score 2; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 7 SE 8

RESULT 43
P82429 ID P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Protein G beta-2 subunit (Fragment).
GN GNB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98030528; PubMed=9365246;
RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
RA Lacombe C.;
RT "Abnormal erythropoietin (Epo) gene expression in the murine
RT erythroleukemia IW32 cells is issued from a rearrangement between the
RT G-protein b2 gene subunit and the Epo genes.";
RL Oncogene 15:1995-1999(1997).
DR EMBL; Y11970; CAA72706.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1133 MW; 86FD0736DB172B05 CRC64;

Query Match          50.0%; Score 2; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 2 SE 3

RESULT 44
P82440 ID P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AML1 protein (Fragment).
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Tumor;
RX MEDLINE=97332339; PubMed=9188573;
RA Antoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match          50.0%; Score 2; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||

Db 3 QP 4

#### RESULT 45

Q82622 Q82622 PRELIMINARY; PRT; 9 AA.  
AC Q82622; 99  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ORF A (Fragment).  
OS Avian infectious bronchitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
CN NCBI\_TaxID=11120;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8610264; PubMed=2995560;  
RA Bourns M.E., Binns M.M., Brown T.D.K.;  
RT "Sequencing of coronavirus IBV genomic RNA: Three open reading frames  
in the 5' 'unique' region of mRNA D.";  
RL J. Gen. Virol. 66:2253-2258(1985).  
DR EMBL; M29338; AAA46234.1; -.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1134 MW; D2C4B3327741B46 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
||

Db 1 EQ 2

#### RESULT 46

Q83622 Q83622 PRELIMINARY; PRT; 9 AA.  
AC Q83622;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical 1.1 kDa protein (Fragment).  
OS Murray valley encephalitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Flavivirus.  
CN NCBI\_TaxID=11079;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88118912; PubMed=2828633;  
RA Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,  
RA Strauss J.H.;  
RT "Conserved elements in the 3' untranslated region of flavivirus RNAs  
and potential cyclization sequences.";  
RL J. Mol. Biol. 198:33-41(1987).  
DR EMBL; M35172; AAA66627.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1055 MW; FF36D40AAB05A2C1 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||

Db 4 SE 5

#### RESULT 47

Q8AYL5 Q8AYL5 PRELIMINARY; PRT; 9 AA.  
AC Q8AYL5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome P450 aromatase (Fragment).  
GN CYP19A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
RT "Promoter characteristics of two CYP19 genes differentially expressed  
in the brain and ovary of teleost fish.";  
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
DR EMBL; AF324897; AAN32618.1; -.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;

Query Match 50.0%; Score 2; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||

Db 7 QP 8

#### RESULT 48

Q8AUM7 Q8AUM7 PRELIMINARY; PRT; 9 AA.  
AC Q8AUM7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome P450 aromatase (Fragment).  
GN CYP19A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
RT "Promoter characteristics of two CYP19 genes differentially expressed  
in the brain and ovary of teleost fish.";  
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
DR EMBL; AF324895; AAN32616.1; -.  
DR EMBL; AF324896; AAN32617.1; -.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match 50.0%; Score 2; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||

Db 7 QP 8

#### RESULT 49

Q8AEW8 Q8AEW8 PRELIMINARY; PRT; 9 AA.  
AC Q8AEW8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (Fragment).
GN Human immunodeficiency virus 1.
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAART patient 26;
RA Saurya S.;
RT "Characterization of HIV-1 genes from AIDS patients on combination
RT therapy with discordance between viral load and CD4+ T cell counts.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ496724; CAD43154.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1020 MW; 9D2A4411ADC1AB05 CRC64;

Query Match 50.0%; Score 2; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 50
Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCW1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churchill J., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FDC77776D86767 CRC64;

Query Match 50.0%; Score 2; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 5 QP 6

RESULT 51
Q9Z1B1 PRELIMINARY; PRT; 10 AA.
ID Q9Z1B1
AC Q9Z1B1;
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DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Toxin B (Fragment).
GN TOXB.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8864;
RA Dogson A.F., Borriello S.P.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035716; AAD02038.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1120 MW; 913DA042C736DDC1 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 9 SE 10

RESULT 52
P82588 PRELIMINARY; PRT; 10 AA.
ID P82588
AC P82588;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -1- MASS SPECTROMETRY: MW=23573.25; METHOD=ELECTROSPRAY.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1134 MW; 4D5A1DCB105685B7 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 1 SE 2

RESULT 53
Q8NER0 PRELIMINARY; PRT; 10 AA.
ID Q8NER0
AC Q8NER0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ahi-1 isoform I (fragment).
GN AHI-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12186888;
RA Jiang X., Hanna Z., Kaouas M., Girard L., Jolicoeur P.;
RT "Ahi-1, a Novel Gene Encoding a Modular Protein with WD40-Repeat and
RT SH3 Domains, Is Targeted by the Ahi-1 and Mis-2 Provirus
RT Integrations.";
RL J. Virol. 76:9046-9059(2002).
DR EMBL; AY133243; ANM94177.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1062 MW; 838C04DB05BB1DC1 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 6 SE 7

RESULT 54
O00493 PRELIMINARY; PRT; 10 AA.
ID O00493
AC O00493;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MJD1 alt MS (Fragment).
GN MJD1 INC 45.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Leukocyte;
RA Sugawara M., Toyoshima I., Takeda S., Imota T., Kato K., Wada C.,
RT "Genomic DNA containing the insertion that is seen in the alternative
RT transcript of MJD1.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003802; BAA20388.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1161 MW; 9A6E507B1AB2CB05 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 3 SE 4

RESULT 55
Q96QT9 PRELIMINARY; PRT; 10 AA.
ID Q96QT9
AC Q96QT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein tyrosine phosphatase 1B (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21326081; PubMed=11316810;
RA Fukada T., Tonks N.K.;
RT "The Reciprocal Role of Egr-1 and Sp Family Proteins in Regulation of

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RT the PTP1B Promoter in Response to the p210 Bcr-Abl Oncoprotein-
RT tyrosine Kinase";
RL J. Biol. Chem. 276:25512-25519(2001).
DR EMBL; AY029236; AAK31734.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1314 MW; AC08E219CB133B16 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 8 EQ 9

RESULT 56
Q8MUP1 PRELIMINARY; PRT; 10 AA.
ID Q8MUP1
AC Q8MUP1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius cydno chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171915;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-STRI-B-569-Mpi-1;
RA Bull V., Beltran M., Birmingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516213; AAM61899.1; -.
KW Isomerase.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1175 MW; 56A626DB1DD1EAA3 CRC64;

Query Match 50.0%; Score 2; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 7 EQ 8

RESULT 57
Q8WPL6 PRELIMINARY; PRT; 10 AA.
ID Q8WPL6
AC Q8WPL6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to wasp protein (Fragment).
GN BAC001.19.
OS Oikopleura dioica.
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC Oikopleuridae; Oikopleura.
OX NCBI_TaxID=34765;
RN [1]
RP SEQUENCE FROM N.A.
RA Seo H.C., Kube M., Edvardsen R.B., Jensen M.F., Beck A., Spriet E.,
RA Gorsky G., Thompson E.M., Lehrach H., Reinhardt R., Chourrout D.;
RT "The marine chordate Oikopleura dioica has a miniature genome.";
RL Science 0:0-0(2001).
DR EMBL; AF374376; AAL56467.1; -.
FT NON_TER 10

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SQ SEQUENCE 10 AA; 1079 MW; 7C9F8A3DDB05A40B CRC64;

Query Match 50.0%; Score 2; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 DB 5 SE 6

RESULT 58  
 Q8MUN7 PRELIMINARY; PRT; 10 AA.  
 AC Q8MUN7; (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN MPI.  
 OS Heliconius melpomene rosina.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.  
 OC NCBI\_TaxID=171916;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STRI-B-548-Mpi-1;  
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McWilliam O.,  
 RA Mallet J.;  
 RT "Molecular evidence for gene flow between species of Heliconius."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516237; AAM61923.1; -.  
 KW Isomerase.  
 FT NON\_TER 1 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1175 MW; 56A626DB1DD1EAA3 CRC64;

Query Match 50.0%; Score 2; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 DB 7 EQ 8

RESULT 59  
 P82217 PRELIMINARY; PRT; 10 AA.  
 AC P82217; (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DE Unknown protein from 2D-page (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OC NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;  
 RA MDLINE=211177481; PubMed=11280994;  
 RA Zhong B.X.;  
 RT "Protein database for several tissues derived from five instar of  
 RT silkworm."  
 RL I Chuan Hsueh Pao 28:217-224 (2001).  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1148 MW; DC779AB32AE451A9 CRC64;

Query Match 50.0%; Score 2; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 DB 1 SE 2

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 DB 1 SE 2

RESULT 60  
 Q8MJ52 PRELIMINARY; PRT; 10 AA.  
 AC Q8MJ52; (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DE Ganglioside-induced differentiation-associated protein 1  
 DE (Fragment).  
 GN GDAP1.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OC NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Blechhynden L.M., Hilbert B.J., Laing N.G.;  
 RT "Four type I equine microsatellites associated with the MITF, KIT,  
 RT ATP2A1 and GDAP1 genes."  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF521637; AAN03945.1; -.  
 FT NON\_TER 1 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1256 MW; 13A904D1B6DB173B CRC64;

Query Match 50.0%; Score 2; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
 DB 5 EQ 6

RESULT 61  
 P83205 PRELIMINARY; PRT; 10 AA.  
 AC P83205; (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 23, Last sequence update)  
 DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Placenta;  
 RA El Amir B., Remy B., Sousa N.M., Beckers J.-F.M.P.;  
 RT "Isolation and characterization of pregnancy-associated glycoproteins  
 RT extracted from sheep (Ovis aries) placentas."  
 RL Mol. Reprod. Dev. 0:0-0(2002).  
 CC -!- FUNCTION: THIOLESTERASE WHICH IS BELIEVED TO PARTICIPATE IN  
 CC INTRACELLULAR DEGRADATION AND TURNOVER OF PROTEINS. HAS ALSO BEEN  
 CC IMPLICATED IN TUMOR INVASION AND METASTASIS (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: HYDROLYZES PROTEINS, WITH A SPECIFICITY  
 CC RESEMBLING THAT OF PAPAIN.  
 CC -!- SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN CROSS-LINKED BY  
 CC A DISULFIDE BOND (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro; IPR000169; SHprot acsite.  
 DR PROSITE; PS00640; THIOLESTERASE ASN; PARTIAL.  
 DR PROSITE; PS00139; THIOLESTERASE\_CYS; PARTIAL.

DR PROSITE; PS00639; THIOLE PROTEASE HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysozyme.  
 FT CHAIN 1 >10 CATHEPSIN B LIGHT CHAIN.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;  
 Query Match 50.0%; Score 2; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 EQ 3  
 Db 9 EQ 10  
 RESULT 62  
 Q8WB7 ID Q8WB7 PRELIMINARY; PRT; 10 AA.  
 AC Q8WB7;  
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit I (Fragment).  
 GN COI.  
 OS Chaitophorus leucomelas.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
 OC Aphidoidea; Drepanosiphidae; Chaitophorus.  
 OX NCBI\_TaxID=136351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shingleton A.W., Stern D.L.;  
 RT "Molecular phylogenetic evidence for multiple origins of ant mutualism within the aphid genus Chaitophorus."  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF444288; AAL38565.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;  
 Query Match 50.0%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SE 2  
 Db 2 SE 3  
 RESULT 63  
 Q96041 ID Q96041 PRELIMINARY; PRT; 10 AA.  
 AC Q96041;  
 DT 01-FEB-1997 (T-EMBLrel. 02, Created)  
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase subunit 3 (Fragment).  
 GN NAD3.  
 OS Oenothera bertiana (Bertero's evening primrose).  
 OG Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Myrtales; Onagraceae; Oenothera.  
 OX NCBI\_TaxID=3950;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schuster W.;  
 RT "Ribosomal protein gene rpl5 is cotranscribed with the nad3 gene in Oenothera mitochondria."  
 RL Mol. Gen. Genet. 240:445-449 (1993).  
 DR EMBL; X69553; CAA49285.1; -.

KW Mitochondrion; Ubiquinone.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1097 MW; 723067B0476DD9CB CRC64;  
 Query Match 50.0%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SE 2  
 Db 2 SE 3  
 RESULT 64  
 Q8SHA8 ID Q8SHA8 PRELIMINARY; PRT; 10 AA.  
 AC Q8SHA8;  
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE Cytochrome c oxidase subunit I (fragment).  
 GN COI.  
 OS Rhampholeon spectrum.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;  
 OC Rhampholeon.  
 OX NCBI\_TaxID=179929;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Townsend T.M., Larson A.L.;  
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata)."  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF448772; AAL90598.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1279 MW; 35BF8E27336409D7 CRC64;  
 Query Match 50.0%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 OP 4  
 Db 2 QP 3  
 RESULT 65  
 Q8LLJ0 ID Q8LLJ0 PRELIMINARY; PRT; 10 AA.  
 AC Q8LLJ0;  
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE Cytochrome C (Fragment).  
 GN CCI.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoidae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22167279; PubMed=12177461;  
 RA Jang I.-C., Choi W.-B., Lee K.-H., Song S.-I., Nahm B.H., Kim J.-K.;  
 RT "High-Level and Ubiquitous Expression of the Rice Cytochrome c Gene Oscc1 and Its Promoter Activity in Transgenic Plants Provides a Useful Plant Physiol. 129:1473-1481 (2002)."  
 RL Promoter for Transgenesis of Monocots."  
 DR EMBL; AF399666; AAM95337.1; -.  
 DR Gramene; Q8LLJ0; -.  
 FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 993 MW; 973D4B6DD805B9D5 CRC64;

Query Match  
Best Local Similarity 50.0%; Score 2; DB 10; Length 10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 5 SE 6

RESULT 66

Q8GUV6 PRELIMINARY; PRT; 10 AA.

AC Q8GUV6;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Putative receptor-like kinase (Fragment).  
GN RLK1.  
OS Capsella rubella.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eurosid II; Brassicales; Brassicaceae; Capsella.  
OX NCBI\_TaxID=81985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wanke D., Gielkowski I., Spitzer C., Mukhtar M.S., Bollenbach L.,  
RA Bruemmer J., Deslandes L., Seki H., Turck F., Zhou A., Uelker B.,  
RA Somssich I.;  
RT "Structure and evolution of stress related proteins."  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY167750; AA012512.1; --  
KW Receptor; Kinase.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1010 MW; 6C9C7DC455A1ADDB CRC64;

Query Match  
Best Local Similarity 50.0%; Score 2; DB 10; Length 10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 2 SE 3

RESULT 67

Q91WZ3 PRELIMINARY; PRT; 10 AA.

AC Q91WZ3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Lutetizing hormone/chorionic gonadotropin receptor homolog  
(Fragment).  
DE Rattus sp.  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=96147985; PubMed=8571710;  
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;  
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in  
insect cells].";  
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).  
DR EMBL; S80660; AAB50710.1; --  
KW Chorion; Receptor.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1129 MW; 09A5F22DC4177760 CRC64;

Query Match  
Best Local Similarity 50.0%; Score 2; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
DB 1 QP 2

RESULT 68

Q9QVE8 PRELIMINARY; PRT; 10 AA.

AC Q9QVE8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Protamine MP2 intermediate protein PMP2/16 (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92174934; PubMed=1541289;  
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;  
RT "Molecular characterization of six intermediate proteins in the  
RT processing of mouse protamine P2 precursor."  
RL Eur. J. Biochem. 204:759-765(1992).  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1224 MW; D4050B040B1EAB6 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 2; DB 11; Length 10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3  
DB 9 EQ 10

RESULT 69

Q9QVF0 PRELIMINARY; PRT; 10 AA.

AC Q9QVF0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Protamine MP2 intermediate protein PMP2/5 (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92174934; PubMed=1541289;  
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;  
RT "Molecular characterization of six intermediate proteins in the  
RT processing of mouse protamine P2 precursor."  
RL Eur. J. Biochem. 204:759-765(1992).  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1125 MW; 9E14CE687B05A775 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 2; DB 11; Length 10;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 5 SE 6

RESULT 70

Q9QVF1

```

ID Q9QVF1 PRELIMINARY; PRT; 10 AA.
AC Q9QVF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarie M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1280 MW; 01DD2975A406841B CRC64;

Query Match 50.0%; Score 2; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 9 SE 10

RESULT 71
Q9QVE7 PRELIMINARY; PRT; 10 AA.
ID Q9QVE7;
AC Q9QVE7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMF2/20 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarie M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1197 MW; 79920ED86DB1B04 CRC64;

Query Match 50.0%; Score 2; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 5 EQ 6

RESULT 72
Q8CJEO PRELIMINARY; PRT; 10 AA.
ID Q8CJEO;
AC Q8CJEO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Resistin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Nohira T., Hisatomi H.;
RT "Rattus norvegicus resistin DNA, intron2.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB093559; BAC21195.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1079 MW; 34EA46D326DDC777 CRC64;

Query Match 50.0%; Score 2; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 9 QP 10

RESULT 73
P90391 PRELIMINARY; PRT; 10 AA.
ID P90391;
AC P90391;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C2 protein (Fragment).
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYLCV-Is;
RA Wernecke M.E., Roye M.E., McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
RT "Identification of tomato yellow leaf curl geminivirus (TYLCV-Is) in
RT tomatoes and peppers in Jamaica.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84397; AAB47965.1; -.
FT NON_TER 10
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SQ SEQUENCE 10 AA; 1058 MW; 25FF98B5A775A5A7 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 2 QP 3

RESULT 74
Q86580 PRELIMINARY; PRT; 10 AA.
ID Q86580;
AC Q86580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Large protein (Fragment).
OS Simian parainfluenza virus 5.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11207;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93224905; PubMed=8385701;
RA Higuchi Y., Miyahara Y., Kawano M., Tsurudome M., Matsumura H.,
RA Kusagawa S., Komada H., Nishio M., Ito Y.;
RT "Sequence analysis of the large (L) protein of simian virus 5.";
RL J. Gen. Virol. 74:789-789(1993).
DR EMBL; S57860; AAB26118.1; -.
FT NON_TER 1
FT NON_TER 1

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SQ SEQUENCE 10 AA; 1144 MW; 0C25A0D9C86776D4 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
Db - 4 QP 5

RESULT 75

Q86324 ID Q86324 PRELIMINARY; PET; 10 AA.

AC Q86324;  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE Gp37 (Fragment).

GN ENV.

OS Rous sarcoma virus.

OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

OX NCBI\_TaxID=11886;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Schmidt-Ruppin subgroup A;

RX MEDLINE=98083689; PubMed=9421881;

RA Hara H., Kaji A.;

RT "The U3 region of the long terminal repeat of a subgroup A transformation-defective Rous sarcoma virus (tdpH2010) converts a noncytopathic virus to a cytopathic virus.";

RL Virus Genes 15:171-180(1997).

DR EMBL; U41726; AAB60580.1; -.

FT NON TER 1

SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 50.0%; Score 2; DB 15; Length 10;  
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
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Db - 4 QP 5

Search completed: November 25, 2003, 18:25:30  
Job time : 11.6883 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 12.9574 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4	100.0	4	22	Colostrin derive
2	4	100.0	4	22	Colostrin peptid
3	4	100.0	4	22	Colostrin peptid
4	4	100.0	4	22	Ewe colostrin
5	4	100.0	4	23	Colostrin consti
6	4	100.0	4	23	Colostrin consti
7	4	100.0	4	23	Neural cell regula
8	4	100.0	8	22	Ewe colostrin pe
9	4	100.0	10	22	Human peptide #165

10	4	100.0	13	18	AAW38008	WW domain binding
11	4	100.0	15	19	AAW21371	Human HUPF-I mutan
12	4	100.0	17	20	AAW81031	Melanoma associate
13	4	100.0	18	21	AAW23520	Human negative elo
14	4	100.0	20	21	AAW03800	ppe III activity i
15	3	75.0	3	22	AAW91032	Thyrotropin releas
16	3	75.0	5	21	AAW29539	Alpha-helical link
17	3	75.0	5	22	AAW07152	Substituted phenan
18	3	75.0	6	16	AAW83516	Peptide mimetic of
19	3	75.0	6	19	AAW61750	Peptide mimetic of
20	3	75.0	6	20	AAW97058	Peptidomimetic cap
21	3	75.0	6	20	AAW94750	Mutant H protein a
22	3	75.0	6	20	AAW84413	HIV-1 nucleic acid
23	3	75.0	6	22	AAW86473	Human gliadin pept
24	3	75.0	6	22	AAW86474	Human gliadin pept
25	3	75.0	6	22	AAW86481	Human gliadin pept
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27	3	75.0	6	22	AAW86487	Human gliadin pept
28	3	75.0	6	22	AAW86494	Human gliadin pept
29	3	75.0	6	22	AAW86497	Human gliadin pept
30	3	75.0	6	22	AAE05001	Synthetic peptide
31	3	75.0	6	22	AAW60618	Stp100 thrombospon
32	3	75.0	6	24	ABP70731	Phosphorylation si
33	3	75.0	7	20	AAW50012	Thermus thermophil
34	3	75.0	7	20	AAW48764	Membrane dipeptid
35	3	75.0	7	22	AAW44117	H11 binding site c
36	3	75.0	7	22	AAW44119	H11 binding site c
37	3	75.0	7	22	AAW44154	H11 binding site c
38	3	75.0	7	22	AAW44232	H11 binding site c
39	3	75.0	7	22	AAW44237	H11 binding site c
40	3	75.0	7	22	AAW44242	H11 binding site c
41	3	75.0	7	22	AAW44247	H11 binding site c
42	3	75.0	7	22	AAW44252	H11 binding site c
43	3	75.0	7	22	AAW44257	H11 binding site c
44	3	75.0	7	22	AAW46757	H11 binding site c
45	3	75.0	7	22	AAW68700	Cleavage signal pe
46	3	75.0	8	5	AAW0108	Hexapeptide coded
47	3	75.0	8	7	AAW60137	Sequence of prefer
48	3	75.0	8	14	AAW35925	Hepatitis C virus
49	3	75.0	8	15	AAW59433	Gp2b(896-903) pept
50	3	75.0	8	15	AAW48371	Peptide fragment w
51	3	75.0	8	15	AAW58622	G2b residues 96-
52	3	75.0	8	15	AAW56119	Peptide derived fr
53	3	75.0	8	18	AAW33664	Polliovirus type 3
54	3	75.0	8	19	AAW79269	Bovine glucuronyl
55	3	75.0	8	19	AAW45999	Peptide #24 based
56	3	75.0	8	19	AAW46001	Peptide #27 based
57	3	75.0	8	22	ABP21164	HIV A03 motif pol
58	3	75.0	8	22	ABP21201	HIV A03 motif pol
59	3	75.0	8	22	ABP23175	HIV A11 motif pol
60	3	75.0	8	22	ABW52109	Human API-73 trypt
61	3	75.0	8	23	AAO15739	Haemophilus influe
62	3	75.0	8	23	ABG31180	Rat delta PKC regi
63	3	75.0	8	23	ABG60428	Selective targetin
64	3	75.0	8	24	ABJ38203	Human cytomagalovi
65	3	75.0	9	13	AAW26441	N-terminal auxilia
66	3	75.0	9	16	AAW87291	Plasmodium falcipa
67	3	75.0	9	17	AAW49287	Human leucocyte an
68	3	75.0	9	17	AAW07112	Synthetic peptide
69	3	75.0	9	18	AAW29260	Soybean hydrolysat
70	3	75.0	9	20	AAW53335	Bcr-Abl epitope (a
71	3	75.0	9	20	AAW40157	Amino acid sequenc
72	3	75.0	9	20	AAW26673	BCR-ABL-derived li
73	3	75.0	9	20	AAW74273	HJ loop peptide K1
74	3	75.0	9	20	AAW74285	HJ loop peptide K0
75	3	75.0	9	20	AAW96177	YKK-alpha polypept
76	3	75.0	9	21	AAW56091	LCMW nucleoprotein
77	3	75.0	9	21	AAW44419	HLA-A1 binding orn
78	3	75.0	9	22	ABP21125	HIV A03 motif pol
79	3	75.0	9	22	AAU23816	Human MHC class I
80	3	75.0	9	22	AAU23945	Human MHC class I
81	3	75.0	9	22	AAW07143	N-terminal sequenc
82	3	75.0	9	22	AAW22208	HIV peptide SEQ ID

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 86 3 75.0 9 22 AAU06901 Human MHC molecule  
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 88 3 75.0 9 22 AAB76046 Trypanosoma cruzi  
 89 3 75.0 9 22 AAB37962 Anthithrombin III m  
 90 3 75.0 9 23 ABG79105 Human ELF2 class I  
 91 3 75.0 9 23 ABG79105 Hepatitis B virus  
 92 3 75.0 9 23 ABG32314 HLA-A2 associated  
 93 3 75.0 9 23 ABB51670 Human 34P3D7 HLA A  
 94 3 75.0 9 23 ABB51848 Human 34P3D7 HLA B  
 95 3 75.0 9 23 ABB51967 Human 34P3D7 HLA B  
 96 3 75.0 9 24 ABJ38202 Human cytomagalovi  
 97 3 75.0 9 24 ABJ38205 Human cytomagalovi  
 98 3 75.0 9 24 ABR16023 Human cancer-relat  
 99 3 75.0 9 24 ABR16177 Human cancer-relat  
 100 3 75.0 9 24 ABR16202 Human cancer-relat

## ALIGNMENTS

RESULT 1  
 AAB72255  
 ID AAB72255 standard; peptide; 4 AA.

AC AAB72255;  
 DT 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 10.

KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.

OS Synthetic.

PN WO200111937-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

PR 17-AUG-1999; 99US-0149311.

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (REGS-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI WPI; 2001-202804/20.

PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

PS Claim 1; Page 34; 50pp; English.

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4  
 Db ||||  
 1 SEQP 4

## RESULT 2

AAB72509  
 ID AAB72509 standard; Peptide; 4 AA.

XX AAB72509;

AC AAB72509;

DT 09-MAY-2001 (first entry)

DE Colostrinin peptide #10.

XX Dermatological; oxidative stress regulator; colostrinin.

OS Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22665.

PR 17-AUG-1999; 99US-0149310.

PA (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4  
 Db ||||  
 1 SEQP 4

## RESULT 3

AAB72541  
 ID AAB72541 standard; Peptide; 4 AA.

XX AAB72541;

DT 09-MAY-2001 (first entry)

XX



DE Colostrinin peptide #10.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 XX  
 PI WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 PT  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 XX differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 Db |||||  
 1 SEQP 4

RESULT 4  
 AAB59314  
 ID AAB59314 standard; Peptide; 4 AA.  
 XX  
 AC AAB59314;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment A-5.  
 XX  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 KW  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 PN  
 XX 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 Db |||||  
 1 SEQP 4

RESULT 5  
 AAE20237  
 ID AAE20237 standard; peptide; 4 AA.  
 XX  
 AC AAE20237;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 XX Colostrinin constituent peptide #10.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "Optionally C-terminal amide"  
 XX  
 XX WO200213850-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boidogh I;  
 PI WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 FT constituent peptide and/or analog -  
 XX  
 XX Claim 6; Page 25; 51pp; English.  
 PS  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 4 AA;

Query Match 100.0%; Score 4; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4  
 ||||  
 Db 1 SEQP 4

#### RESULT 6

AAWS1045  
 ID AAMS1045 standard; Peptide; 4 AA.

AC AAMS1045;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 4  
 FT /note= "optional C-terminal amidation"

PN WO200213849-A1.

XX 21-FEB-2002.

PD 17-AUG-2000; 2000WO-US22775.

PF 17-AUG-2000; 2000WO-US22775.

PR 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REG- ) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI WPI; 2002-269150/31.

DR Modulation of blood cell proliferation in a patient involves use of

XX Blood cell regulator selected from colostrinin, its constituent peptide

PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. Methods are  
 CC claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX Sequence 4 AA;

Query Match 100.0%; Score 4; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4  
 ||||  
 Db 1 SEQP 4

#### RESULT 7

AAO14586  
 ID AAO14586 standard; peptide; 4 AA.

AC AAO14586;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 10.

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 4  
 FT /note= "Optional C-terminal amide"

PN WO200213851-A1.

XX 21-FEB-2002.

PD 17-AUG-2000; 2000WO-US22777.

PF 17-AUG-2000; 2000WO-US22777.

PR 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA Boldogh I, Stanton JG, Hughes TK;

PI WPI; 2002-269152/31.

DR Promoting cell differentiation in a patient involves use of blood cell

XX regulator selected from colostrinin, its constituent peptide and/or

PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

XX Sequence 4 AA;  
SQ Query Match 100.0%; Score 4; DB 23; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SEQP 4  
Db 1 SEQP 4  
|||||  
  
RESULT 8  
AAB59345  
ID AAB59345 standard; Peptide; 8 AA.  
AC AAB59345;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Ewe colostrinin peptide fragment derived sequence #5.  
XX  
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX  
OS Ovis sp.  
XX  
PN WO200075173-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-GB02128.  
XX  
PR 02-JUN-1999; 99GB-0012852.  
XX  
PA (REGG-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA;  
XX  
DR WPI; 2001-071058/08.  
XX  
PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
PS Claim 8; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
SQ Sequence 8 AA;  
  
Query Match 100.0%; Score 4; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SEQP 4  
Db 1 SEQP 4  
|||||  
  
RESULT 9  
AAM98380  
ID AAM98380 standard; Peptide; 10 AA.  
XX  
AC AAM98380;

XX 24-JAN-2002 (first entry)  
XX  
DE Human peptide #1655 encoded by a SNP oligonucleotide.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesis; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
PR 27-DEC-2000; 2000US-0173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI; 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
PS Disclosure; Page 4031; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesis, cytokines, thioesterases.  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptides encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms.  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SEQP 4  
Db 3 SEQP 6  
|||||  
  
RESULT 10  
AAW38008  
ID AAW38008 standard; Peptide; 13 AA.  
XX  
AC AAW38008;  
XX  
DT 23-APR-1998 (first entry)  
XX

DE WW domain binding clone 4 obtained from a pp library.  
 XX  
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;  
 KW cytoskeleton organisation; targeted drug screening; modulator;  
 KW WW domain interaction.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 6..9  
 FT /note= "PPPTV motif"  
 XX  
 PN WO9737223-A1.  
 XX  
 PD 09-OCT-1997.  
 XX  
 PF 03-APR-1997; 97WO-US05547.  
 XX  
 PR 03-APR-1996; 96US-0630916.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Fowlkes DM, Kay BK, Pirozzi G;  
 XX  
 DR WPI; 1997-503234/46.  
 XX  
 XX Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are  
 PT useful in targetted drug selection  
 XX  
 PS Claim 92; Fig 27; 220pp; English.  
 XX  
 CC Peptides AAW38005-08 are the sequences of WW domain binding clones  
 CC obtained by screening random or biased libraries with the WW domains of  
 CC the novel WWP proteins. The present peptide was obtained after screening  
 CC with WW domain 1 of WWP1 (WWP1.1). The peptides are peptide recognition  
 CC units ("ligands"), and are used for analysing specificities of the WW  
 CC domains. The WW domain is a small functional domain. Its name is derived  
 CC from the observation that two tryptophan residues, one in the amino  
 CC terminal portion of the WW domain and one in the carboxyl terminal  
 CC portion, are conserved. Most proteins containing WW domains have a  
 CC function involving cell signalling and growth regulation or the  
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain  
 CC are identified by treating a multivalent recognition unit complex that  
 CC has selective binding affinity for a WW domain, with many polypeptides  
 CC and identifying those with selective affinity for the complex. Proteins  
 CC containing WW domains are used for targeted drug screening, i.e. to  
 CC identify potential modulators of specific WW domain interactions.  
 CC note: sequence in SEQ ID listing differs from sequence given in figure.  
 CC The SEQ ID sequence is as follows: GPSEQPPPEYTVK.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 100.0%; Score 4; DB 18; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 Db 3 SEQP 6  
 RESULT 11  
 AAY21371  
 ID AAY21371 standard; Protein; 15 AA.  
 XX  
 AC AAY21371;  
 XX  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human HUPF-I mutant protein fragment 23.  
 XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9845322-A2.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PF 02-APR-1998; 98WO-IB00705.  
 XX  
 PR 10-APR-1997; 97US-0043163.  
 XX  
 PA (UYUT-) RIJKSUNIV UTRECHT.  
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 PA (UYKO-) UNIV ROTTERDAM ERASMUS.  
 XX  
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;  
 XX  
 DR WPI; 1998-609901/51.  
 DR N-PSDB; AAX75768.  
 XX  
 XX Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also  
 PT for treatment and prevention with specific ribozymes or wild-type  
 PT RNA  
 XX  
 PS Disclosure; Figure 17; 258pp; English.  
 XX  
 CC This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 4; DB 19; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 Db 1 SEQP 4  
 RESULT 12  
 AAW81031  
 ID AAW81031 standard; Peptide; 17 AA.  
 XX

AC AAW81031;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Melanoma associated antigen MG50 helper T cell epitope pep-50.  
 XX  
 KW MG50; melanoma gene-50; melanoma associated antigen; human;  
 KW T cell epitope, cancer; lung cancer; rhabdomyosarcoma; diagnosis;  
 KW therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO985133-A1.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 04-JUN-1998; 98MO-US11533.  
 XX  
 PR 06-JUN-1997; 97US-0870941.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Deans RJ, Kan-Mitchell J, Minev BR, Mitchell MS;  
 XX WPI; 1999-080820/07.  
 DR  
 XX  
 PT New MG50 melanoma associated antigen fragments - used to develop  
 PT products for the detection, treatment and prevention of  
 PT MG50-expressing cancers, e.g. melanoma, lung cancer or  
 PT rhabdomyosarcoma  
 XX  
 PS Disclosure; Page 35; 79pp; English.  
 XX  
 CC This peptide, termed pep-50, is encoded by a cryptic coding sequence  
 CC of the melanoma associated antigen gene MG50 that is thought to be  
 CC located downstream of, and in a different reading frame from, the  
 CC MG50 coding region (see AAV99922). Pep-50 is a helper T cell epitope  
 CC that stimulates the proliferation of melanoma specific T cells.  
 CC The invention provides T cell epitopes (see AAW81031-45) from MG50,  
 CC including cytotoxic and helper T cell epitopes, antibodies that  
 CC specifically bind to MG50 or an MG50 T cell epitope, recombinant  
 CC vectors, and antigen presenting cells that can express an MG50 T  
 CC cell epitope (not pep-50) complexed with an MHC molecule on their  
 CC surfaces, and which are used to stimulate T lymphocytes to react  
 CC specifically against cancer cells expressing an MG50 melanoma  
 CC associated antigen. The antigen presenting cells can be  
 CC administered to a patient having a cancer that contains cells  
 CC expressing MG50 in order to stimulate an active immune response.  
 CC An MG50 vaccine comprising an MG50 polypeptide, T cell epitope,  
 CC anti-idiotypic antibody or nucleic acid molecule encoding MG50  
 CC polypeptide or T cell epitope can be administered for preventative  
 CC or therapeutic purposes. The products and methods can be used for  
 CC the detection, treatment and prevention of MG50-expressing cancers,  
 CC e.g. melanoma, lung cancer or rhabdomyosarcoma.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 4; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 |||||  
 Db 2 SEQP 5  
 RESULT 13  
 AAB23520  
 ID AAB23520 standard; Peptide; 18 AA.  
 XX  
 AC AAB23520;  
 XX  
 XX

DT 05-JAN-2001 (first entry)  
 XX  
 DE Human negative elongation factor (NELF) peptide SEQ ID 24.  
 XX  
 KW Negative elongation factor; NELF; RNA polymerase II; pol II; human;  
 KW cytosolic; cancer; transcription elongation inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 13 /label= Unknown  
 FT Misc-difference 15 /label= Unknown  
 FT  
 XX JP2000189168-A.  
 PN  
 PD 11-JUL-2000.  
 XX  
 PF 28-DEC-1998; 98JP-0373999.  
 XX  
 PR 28-DEC-1998; 98JP-0373999.  
 XX  
 PA (HAND/) HANDA H.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 DR WPI; 2000-545765/50.  
 XX  
 PT A new transcription elongation inhibiting factor -  
 PS Disclosure; Page 39; 45pp; Japanese.  
 XX  
 CC This sequence represents a human negative elongation factor (NELF)  
 CC peptide. NELF inhibits the elongation reaction of RNA polymerase II, pol  
 CC II, in the presence of 5,6-dichloro-beta-D-ribofuranosylbenzimidazole  
 CC (DRB) a sensitivity inducing factor. Sequences AAB03800, AAB03805 and  
 CC AAB23501-B23505 represent NELF DNA and protein sequences, while  
 CC AAB23506-B23519 represent NELF peptides. The invention includes  
 CC recombinant NELF DNA, a transformant carrying the recombinant DNA,  
 CC antibodies recognising the NELF protein, and a method for detecting the  
 CC protein using the antibodies. NELF exhibits cytosolic activity, and the  
 CC proteins, polynucleotides and peptides can be used in the treatment of  
 CC cancers.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 4; DB 21; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 |||||  
 Db 4 SEQP 7  
 RESULT 14  
 AAB03800  
 ID AAB03800 standard; peptide; 20 AA.  
 XX  
 AC AAB03800;  
 XX  
 DT 13-OCT-2000 (first entry)  
 XX  
 DE PDE III activity inhibitory peptide C18.  
 XX  
 KW Cyclic nucleotide phosphodiesterase III; PDEIII; inhibitor; cardiotonic;  
 KW antithrombotic agent; C18.  
 XX  
 OS Unidentified.  
 OS  
 PN JP2000125870-A.  
 XX  
 PD 09-MAY-2000.  
 XX

XX 05-AUG-1998; 98JP-0232394.  
 XX  
 XX 05-AUG-1998; 98JP-0232394.  
 XX  
 XX (SANE-) SANEI TOKA KK.  
 XX  
 XX WPI; 2000-402976/35.  
 XX  
 XX Inhibitory peptides of cyclic nucleotide phosphodiesterase III  
 PT activity. -  
 PT  
 PS Claim 1; Page 2; 5pp; Japanese.  
 XX  
 XX This invention relates to 10 peptide (see AAB03795-B03804) which have  
 CC inhibitory action against cyclic nucleotide phosphodiesterase III  
 CC (PDEIII) activity. The peptides have use as cardiotoxic and  
 CC antithrombotic agents. The present sequence represents peptide C18.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 100.0%; Score 4; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQP 4  
 DB 8 SEQP 11  
 |||||  
 RESULT 15  
 AAB91032  
 ID AAB91032 standard; Peptide; 3 AA.  
 XX  
 AC AAB91032;  
 XX  
 XX 22-JUN-2001 (first entry)  
 DT  
 XX  
 XX Thyrotropin releasing hormone (THR) related peptide SEQ ID NO:206.  
 DE  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200069900-A2.  
 PN  
 XX  
 XX 23-NOV-2000.  
 PD  
 XX  
 XX 17-MAY-2000; 2000WO-US13576.  
 PF  
 XX  
 XX 17-MAY-1999; 99US-0134406.  
 PR  
 XX 10-SEP-1999; 99US-0153406.  
 PR  
 XX 15-OCT-1999; 99US-0159783.  
 PR  
 XX  
 XX (CONJ-) CONJUCHEM INC.  
 PA  
 XX  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 PI  
 XX  
 XX WPI; 2001-112059/12.  
 DR  
 XX  
 XX Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT  
 PT  
 XX  
 XX Disclosure; Page 257; 733pp; English.  
 PS  
 XX  
 XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 XX

SQ Sequence 3 AA;

Query Match 75.0%; Score 3; DB 22; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||||  
 DB 1 EQP 3

RESULT 16  
 AAB29539  
 ID AAB29539 standard; peptide; 5 AA.  
 XX  
 AC AAB29539;

XX  
 XX 14-FEB-2001 (first entry)  
 DT  
 XX  
 XX Alpha-helical linker SEQ ID NO:7 used in IL-6R/IL-6 fusion protein.  
 DE  
 XX  
 KW Alpha-helical linker peptide; IL-6R/IL-6 fusion protein;  
 KW interleukin-6 receptor; antigenicity; stability; immunostimulant.  
 XX  
 OS Synthetic.

XX JP20000247997-A.  
 PN  
 XX  
 XX 12-SEP-2000.  
 PD  
 XX  
 XX 23-FEB-1999; 99JP-0044620.  
 PF  
 XX  
 XX 23-FEB-1999; 99JP-0044620.  
 PR  
 XX (TOXJ ) TOSOH CORP.  
 PA  
 XX  
 XX WPI; 2000-675256/66.  
 DR  
 XX

XX A fusion protein comprising interleukin-6 (IL-6) receptor and IL-6  
 PT useful as drug for stimulating immune system, comprises IL-6 coupled to  
 PT its receptor through a peptide linker of alpha helix type -  
 XX  
 PS Claim 3; Page 8; 17pp; Japanese.

XX  
 XX The invention relates to a fusion protein comprising, N to C-terminally,  
 CC an interleukin-6 receptor (IL-6R), an alpha-helical linker peptide  
 CC (AAB29535-B29541), and IL-6. The fusion protein has immunostimulant  
 CC activity, and may be useful in compositions to stimulate the immune  
 CC system. The alpha-helical linker peptides are less antigenic than  
 CC conventional linker peptides, and also increase the stability of the  
 CC fusion protein. The present sequence represents an alpha-helical  
 CC linker peptide used in the IL-6R/IL-6 fusion protein of the invention.  
 XX

SQ Sequence 5 AA;

Query Match 75.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy' 1 SEQ 3  
|||  
Db 2 SEQ 4

## RESULT 17

AAU07152  
ID AAU07152 standard; peptide; 5 AA.

XX AC AAU07152;  
XX DT 24-OCT-2001 (first entry)

XX DE Substituted Phenanthrene-9,10-dione R3 peptide group #3.

XX XX Phenanthrene-9,10-dione; T-cell mediated disorder; autoimmune disease;  
KW organ graft rejection; immunosuppressive; CD45 inhibitor; R3 peptide.  
XX OS Synthetic.

XX XX WO200146125-A2.  
PN PD 28-JUN-2001.

XX PF 18-DEC-2000; 2000WO-GB04854.  
XX PR 21-DEC-1999; 99US-0172788.

XX PA (ASTR ) ASTRAZENECA AB.  
PA (ASTR ) ASTRAZENECA UK LTD.

XX PI Chapdelaine MJ, Knappenberger K, Steelman G, Suchard S, Sygowski L;  
PI Urbanek R, Veale CA;  
XX WPI; 2001-502468/55.

XX PT Method of treating immunologically-related diseases, autoimmune  
PT disorders and organ graft rejection comprises administration of  
PT substituted phenanthrene-9,10-diones -

XX PS Claim 1; Page 37; 42pp; English.

XX CC The invention relates to a method of treating immunologically-related  
CC diseases, autoimmune disorders and organ graft rejection comprises  
CC administration of substituted phenanthrene-9,10-diones. The substituted  
CC phenanthrene-9,10-diones have been shown to inhibit the phosphatase  
CC activity of CD45 (leukocyte common antigen) which leads to  
CC proliferation of T-cells. Available treatments for autoimmune disorders  
CC and organ graft rejection have therapeutic disadvantages. For example,  
CC cyclosporin A, the drug most commonly used at present, has renal and  
CC CNS toxicity. The present sequence represents an N-linked peptide forming  
CC the R3 group of a substituted phenanthrene-9,10-dione.

XX SQ Sequence 5 AA;

Query Match 75.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 1 EQP 3

RESULT 18  
AAR83516

XX ID AAR83516 standard; Protein; 6 AA.

XX AC AAR83516;  
XX DT 23-APR-1996 (first entry)

XX DE Zif268 zinc finger 1 randomised residues with affinity for HIV-1.

XX

KW zinc finger; variant; randomised; alpha-helical region; Zif268;  
KW customised affinity; cancer; therapy; virus infection; HIV-1;  
KW human immunodeficiency virus; consensus target sequence;  
KW transcription-activator; transcription-inhibitor; plant disease.  
XX OS Synthetic.

XX PN WO9519431-A1.  
XX PD 20-JUL-1995.

XX PF 18-JAN-1995; 95WO-US00829.

XX PR 28-SEP-1994; 94US-0312604.  
XX PR 18-JAN-1994; 94US-0183119.

XX PA (SCRI ) SCRIPPS RES INST.  
XX PI Barbas CF, Gottesfeld JM, Wright PE;

XX DR WPI; 1995-263862/34.

XX PT New zinc finger-nucleotide binding polypeptide(s) - used for  
PT modulating the function of cellular nucleotide sequences, partic.  
PT for treating cell proliferative disorders  
XX Example 10; Fig 9; 135pp; English.

XX CC Regions of the alpha-helix in each of the Zif268 zinc fingers 1,  
CC 2 and 3 were randomised and selected for binding to particular  
CC conserved target sequences in HIV-1. In finger 1, the randomised  
CC residues were at positions -1,2,3,4,5 and 6 in the alpha-helical  
CC region. The present sequence has affinity for the TGT target  
CC sequence. Zinc finger proteins are useful for suppressing  
CC transcription and therefore for treating proliferative disorders.

XX SQ Sequence 6 AA;

Query Match 75.0%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
|||  
Db 1 SEQ 3

RESULT 19  
AAW61750

XX ID AAW61750 standard; peptide; 6 AA.

XX AC AAW61750;  
XX DT 09-NOV-1998 (first entry)

XX DE Peptide mimetic of cytokine receptor gamma chain 17.

XX KW Peptide mimetic; gamma-chain; cytokine receptor; signal transduction;  
KW autoimmune disease; graft vs. host disease; transplant rejection;  
KW graft rejection; interleukin; immunosuppressant; T cell; B cell.

XX OS Synthetic.  
XX PN WO9834631-A1.

XX PD 13-AUG-1998.

XX PF 06-FEB-1998; 98WO-US02339.  
XX PR 07-FEB-1997; 97US-0036941.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Korngold R, Townsend RM;  
 XX WPI; 1998-446944/38.  
 XX New peptide(s) mimicking a loop in the gamma chain of cytokine  
 PT receptors - inhibit signal transduction through these receptors,  
 PT useful as immunosuppressants for treating or preventing e.g.  
 PT leukaemia, autoimmune disease, graft rejection  
 XX  
 PS Claim 2; Page 28; 54pp; English.  
 XX  
 CC The peptide mimetics AAW61734-W61756 and AAW77001-W77014 mimic a loop on  
 CC the gamma-chain of cytokine receptors, and interacts with a cytokine or  
 CC a gamma-chain partner receptor chain of a heterodimeric cytokine  
 CC receptor. They inhibit signal transduction mediated by cytokine:receptor  
 CC binding (of cytokines that bind to receptors with a gamma-chain). They  
 CC are used to inhibit or suppress cytokine-mediated immune responses,  
 CC growth, proliferation, function and activity of cells. Particularly they  
 CC are used for treatment or prevention of lymphoma, leukaemia, allergy  
 CC (e.g. asthma), autoimmune disease (e.g. rheumatoid arthritis, lupus,  
 CC multiple sclerosis or myasthenia gravis), graft vs. host disease and  
 CC transplant or graft rejection. They inhibit function of interleukin  
 CC (II)-2, -4, -7, -9, -13 and -15 (the receptors for which include a  
 CC common gamma -chain), so function as immunosuppressants by reducing  
 CC proliferation of T and B cells.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 75.0%; Score 3; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SEQ 3  
 ||||  
 Db 3 SEQ 5  
 ||||  
 RESULT 20  
 AAW97058  
 ID AAW97058 standard; peptide; 6 AA.  
 XX  
 XX AAW97058;  
 AC  
 XX 29-APR-1999 (first entry)  
 DT  
 XX Peptidomimetic capable of inhabiting CD28 and/or CTLA-4 interactions.  
 DE  
 XX Peptidomimetic; CD28; CTLA-4; CD80; CD86; B7-1; B7-2; diabetes;  
 KW immune system disease; autoimmune disease; psoriasis; multiple sclerosis;  
 KW lupus erythematosus; rheumatoid arthritis; transplant rejection; cancer.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9856401-Al.  
 FN  
 XX 17-DEC-1998.  
 PD  
 XX 11-JUN-1998; 98WO-US12312.  
 PF  
 XX 12-JUN-1997; 97US-0049470.  
 PR  
 XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
 PA  
 XX Blechner S, El Tayar N, Jameson B, Tepper M;  
 PI WPI; 1999-080854/07.  
 XX  
 XX New peptidomimetic compounds - useful in the prophylaxis, diagnosis  
 PT and treatment of pathologies and disorders, which are improved by  
 PT inhibition of CD28 and/or CTLA-4 interaction with CD80 (B7-1) and  
 PT CD86 (B7-2)  
 XX

PS Disclosure; Page 9; 62pp; English.  
 XX  
 CC AAW97053-82 represent peptidomimetic compounds that inhibit CD28 and/or  
 CC CTLA-4 interactions with CD80 and CD86. The peptides are used in  
 CC pharmaceutical compositions for the prophylaxis, diagnosis and treatment  
 CC of pathologies and disorders, which are improved by inhibition of CD28  
 CC and/or CTLA-4 interaction with CD80 (B7-1) and CD86 (B7-2). Disorders  
 CC include immune system diseases (e.g. Autoimmune diseases such as  
 CC psoriasis, multiple sclerosis, lupus erythematosus, diabetes, rheumatoid  
 CC arthritis, and therapy against solid organ/cellular transplant  
 CC rejection) and cancer.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 75.0%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 EQP 4  
 ||||  
 Db 3 EQP 5  
 ||||  
 RESULT 21  
 AAW94750  
 ID AAW94750 standard; peptide; 6 AA.  
 XX  
 XX AAW94750;  
 AC  
 XX 20-APR-1999 (first entry)  
 DT  
 XX Mutant H protein antigen (strain CAM-70) fragment (residues 277-282).  
 DE  
 XX Measles; H protein; F protein; antigen; mutant; vaccine; detection;  
 KW diagnostic reagent; attenuated.  
 KW  
 XX Measles virus.  
 OS  
 XX WO9855627-Al.  
 FN  
 XX 10-DEC-1998.  
 PD  
 XX 04-JUN-1998; 98WO-JP02481.  
 PF  
 XX 04-JUN-1997; 97JP-0184285.  
 PR  
 XX (OSAU ) UNIV OSAKA.  
 PA  
 XX Kawanishi H, Ueda S, Watanabe M;  
 PI WPI; 1999-070272/06.  
 XX  
 PT Mutant measles virus H and F protein antigens and genes encoding  
 PT them - for production of attenuated virus or genetic vaccines and of  
 PT diagnostic reagents  
 PT  
 XX Claim 1; Page 58; 93pp; Japanese.  
 PS  
 XX Sequences AAW94746-751 represent specifically claimed peptide fragments  
 CC of a mutant measles virus H protein antigen isolated from the CAM-70  
 CC strain of measles virus. The invention provides mutant measles virus  
 CC antigenic proteins such as the H protein from the CAM-70 (attenuated) or  
 CC NA (epidemic) strain of measles virus and the F protein from the CAM-70  
 CC or NA strain and nucleic acid sequences encoding the proteins. These  
 CC antigenic proteins and their fragments are used in the production of  
 CC vaccines for measles and the production of diagnostic reagents (e.g.  
 CC measles antigens for the detection of specific antibodies in the blood  
 CC of patients). The vaccines may be recombinant or other live attenuated  
 CC measles virus strains or may be genetic vaccines (e.g. adenovirus  
 CC vectors).  
 XX  
 XX Sequence 6 AA;  
 SQ



```

Query Match      75.0%; Score 3; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
      |||
Db      1 EQP 3

RESULT 22
AAW84413
ID AAW84413 standard; Peptide; 6 AA.
XX
AC AAW84413;
XX
DT 22-MAR-1999 (first entry)
XX
DE HIV-1 nucleic acid binding protein zinc finger 1 peptide.
XX
KW zinc finger; nucleotide-binding protein; cell proliferative disorder;
KW gene therapy; cancer; psoriasis; pemphigus vulgaris; Bechet's syndrome;
KW lipid histiocytosis; human immune deficiency virus; HIV; viral infection;
KW transgenic plant.
XX
OS Synthetic.
XX
PN WC9854311-AL.
XX
PD 03-DEC-1998.
XX
PF 27-MAY-1998; 98WO-US10801.
XX
PR 27-MAY-1997; 97US-0863813.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Gottesfeld JM, Wright PE;
XX
DR WPI; 1999-059831/05.
XX
CC New zinc finger nucleotide-binding protein variant that modulates
CC selected nucleotide sequence - used for treatment of proliferative
CC PT and viral diseases by gene therapy, and can be made selective for
CC PT any target sequence
XX
PS Example 10; Fig 9; 158pp; English.
XX
CC AAW84398-421 represent the peptides obtained from randomised finger 1
CC sequences of zinc finger nucleotide-binding proteins that bind to HIV-1
CC target sequences. The peptides were produced in the course of the
CC invention. The specification describes zinc finger nucleotide-binding
CC protein variants with at least two zinc finger modules that bind to a
CC cellular nucleotide sequence and modulate its function. Zinc finger
CC proteins, and compositions containing them, are used to increase or
CC reduce transcription of a gene linked to the cellular nucleotide
CC sequence. The proteins are used specifically for treating or preventing
CC cell proliferative disorders (in humans, animals or plants, including
CC those induced by viruses), particularly where expressed from nucleic
CC acid by gene therapy (including ex vivo methods). Typical diseases that
CC can be treated are many forms of cancer, psoriasis, pemphigus vulgaris,
CC Bechet's syndrome and lipid histiocytosis, also treatment of human
CC immune deficiency virus (HIV) and other viral infections, and production
CC of transgenic plants resistant to bacterial and viral diseases. The
CC present oligonucleotide is used in the course of the invention.
XX
SQ Sequence 6 AA;

Query Match      75.0%; Score 3; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||

```

```

Db      1 SEQ 3

RESULT 23
AAB86473
ID AAB86473 standard; peptide; 6 AA.
XX
AC AAB86473;
XX
DT 29-OCT-2001 (first entry)
XX
DE Human gliadin peptide homologue SEQ ID 2.
XX
KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;
KW dermatitis herpetiformis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN DE10005932-AL.
XX
PD 23-AUG-2001.
XX
PF 10-FEB-2000; 2000DE-1005932.
XX
PR 10-FEB-2000; 2000DE-1005932.
XX
PA (UYLE ) UNIV LEIPZIG.
XX
PI Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
XX
DR WPI; 2001-503463/56.
XX
PT New tripeptide and hexapeptide compounds which are gliadin homologues
PT useful for the diagnosis of celiac disease and dermatitis herpetiformis
PT -
XX
PS Claim 1; Page 6; 10pp; German.
XX
CC This invention describes tripeptide and hexapeptide homologues of gliadin
CC which are used in a novel method for the diagnosis of celiac disease and
CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
CC washing with methanol, blocking with buffer, washing with TBS-T,
CC incubating in human serum, washing with anti-human immunoglobulin A or G,
CC conjugating with peroxide, incubating, washing, measuring the
CC luminescence and evaluating the data in a known manner; or (b)
CC biotinylating one of the tripeptides or hexapeptides, synthetically
CC produced and also containing Lys at the C-terminus, applying the
CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
CC determining the bound immunoglobulins with a second antibody carrying a
CC marker which can be evaluated. The tripeptides and hexapeptides, which
CC are cheap to produce and have long term stability in test kits, avoid the
CC use of gliadin antibodies which is expensive, subjective and
CC semi-quantitative and of enzyme immunoassays which are associated with
CC low sensitivity and low specificity. Also, the method can be automated.
CC AAB86472-AAB86501 represent the gliadin homologues described in the
CC method of the invention.
XX
SQ Sequence 6 AA;

Query Match      75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
      |||
Db      3 EQP 5

RESULT 24
AAB86474

```

ID AAB86474 standard; peptide; 6 AA.  
 XX  
 AC AAB86474;  
 XX  
 DT 29-OCT-2001 (first entry)  
 XX  
 DE Human gliadin peptide homologue SEQ ID 3.  
 XX  
 KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;  
 KW dermatitis herpetiformis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN DE10005932-A1.  
 XX  
 XX 23-AUG-2001.  
 PD  
 XX 10-FEB-2000; 2000DE-1005932.  
 PF  
 XX 10-FEB-2000; 2000DE-1005932.  
 PR  
 XX (UYLE ) UNIV LEIPZIG.  
 PA  
 XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;  
 PI  
 XX WPI; 2001-503463/56.  
 DR  
 XX  
 XX New tripeptide and hexapeptide compounds which are gliadin homologues  
 XX useful for the diagnosis of celiac disease and dermatitis herpetiformis  
 XX  
 XX Claim 1; Page 6; 10pp; German.  
 PS  
 XX This invention describes tripeptide and hexapeptide homologues of gliadin  
 XX which are used in a novel method for the diagnosis of celiac disease and  
 XX dermatitis herpetiformis comprising: (a) covalently bonding one of the  
 XX tripeptides or hexapeptides to cellulose membranes via the C-terminus,  
 XX washing with methanol, blocking with buffer, washing with TBS-T,  
 XX incubating in human serum, washing with anti-human immunoglobulin A or G,  
 XX conjugating with peroxide, incubating, washing, measuring the  
 XX luminescence and evaluating the data in a known manner; or (b)  
 XX biotinylating one of the tripeptides or hexapeptides, synthetically  
 XX produced and also containing lys at the C-terminus, applying the  
 XX biotinylated peptide to streptavidin-coated and blocked microtiter plates  
 XX in a concentration of 1 micro g/ml, washing, applying patient's serum and  
 XX determining the bound immunoglobulins with a second antibody carrying a  
 XX marker which can be evaluated. The tripeptides and hexapeptides, which  
 XX are cheap to produce and have long term stability in test kits, avoid the  
 XX use of gliadin antibodies which is expensive, subjective and  
 XX semi-quantitative and of enzyme immunoassays which are associated with  
 XX low sensitivity and low specificity. Also, the method can be automated.  
 XX AAB86472-AAB86501 represent the gliadin homologues described in the  
 XX method of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 75.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EQP 4  
 Db |||  
 3 EQP 5  
 RESULT 25  
 AAB86481  
 ID AAB86481 standard; peptide; 6 AA.  
 XX  
 AC AAB86481;  
 XX  
 DT 29-OCT-2001 (first entry)

XX Human gliadin peptide homologue SEQ ID 10.  
 DE  
 XX  
 KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;  
 KW dermatitis herpetiformis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN DE10005932-A1.  
 XX  
 XX 23-AUG-2001.  
 PD  
 XX 10-FEB-2000; 2000DE-1005932.  
 PF  
 XX 10-FEB-2000; 2000DE-1005932.  
 PR  
 XX (UYLE ) UNIV LEIPZIG.  
 PA  
 XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;  
 PI  
 XX WPI; 2001-503463/56.  
 DR  
 XX  
 XX New tripeptide and hexapeptide compounds which are gliadin homologues  
 XX useful for the diagnosis of celiac disease and dermatitis herpetiformis  
 XX  
 XX Claim 1; Page 7; 10pp; German.  
 PS  
 XX This invention describes tripeptide and hexapeptide homologues of gliadin  
 XX which are used in a novel method for the diagnosis of celiac disease and  
 XX dermatitis herpetiformis comprising: (a) covalently bonding one of the  
 XX tripeptides or hexapeptides to cellulose membranes via the C-terminus,  
 XX washing with methanol, blocking with buffer, washing with TBS-T,  
 XX incubating in human serum, washing with anti-human immunoglobulin A or G,  
 XX conjugating with peroxide, incubating, washing, measuring the  
 XX luminescence and evaluating the data in a known manner; or (b)  
 XX biotinylating one of the tripeptides or hexapeptides, synthetically  
 XX produced and also containing lys at the C-terminus, applying the  
 XX biotinylated peptide to streptavidin-coated and blocked microtiter plates  
 XX in a concentration of 1 micro g/ml, washing, applying patient's serum and  
 XX determining the bound immunoglobulins with a second antibody carrying a  
 XX marker which can be evaluated. The tripeptides and hexapeptides, which  
 XX are cheap to produce and have long term stability in test kits, avoid the  
 XX use of gliadin antibodies which is expensive, subjective and  
 XX semi-quantitative and of enzyme immunoassays which are associated with  
 XX low sensitivity and low specificity. Also, the method can be automated.  
 XX AAB86472-AAB86501 represent the gliadin homologues described in the  
 XX method of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 75.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EQP 4  
 Db |||  
 3 EQP 5  
 RESULT 26  
 AAB86486  
 ID AAB86486 standard; peptide; 6 AA.  
 XX  
 AC AAB86486;  
 XX  
 DT 29-OCT-2001 (first entry)  
 XX  
 DE Human gliadin peptide homologue SEQ ID 15.  
 KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;  
 KW dermatitis herpetiformis.

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XX OS Homo sapiens.
XX OS Synthetic.
XX PN DE10005932-A1.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 10-FEB-2000; 2000DE-1005932.
XX XX
XX PR 10-FEB-2000; 2000DE-1005932.
XX XX
XX PA (UYLE ) UNIV LEIPZIG.
XX XX
XX PI Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
XX XX
XX DR WPI; 2001-503463/56.
XX XX
XX PT New tripeptide and hexapeptide compounds which are gliadin homologues
XX PT useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX PT
XX PS Claim 2; Page 7; 10pp; German.
XX CC This invention describes tripeptide and hexapeptide homologues of gliadin
XX CC which are used in a novel method for the diagnosis of celiac disease and
XX CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX CC washing with methanol, blocking with buffer, washing with TBS-T,
XX CC incubating in human serum, washing with anti-human immunoglobulin A or G,
XX CC conjugating with peroxide, incubating, washing, measuring the
XX CC luminescence and evaluating the data in a known manner; or (b)
XX CC biotinylating one of the tripeptides or hexapeptides, synthetically
XX CC produced and also containing Lys at the C-terminus, applying the
XX CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX CC determining the bound immunoglobulins with a second antibody carrying a
XX CC marker which can be evaluated. The tripeptides and hexapeptides, which
XX CC are cheap to produce and have long term stability in test kits, avoid the
XX CC use of gliadin antibodies which is expensive, subjective and
XX CC semi-quantitative and of enzyme immunoassays which are associated with
XX CC low sensitivity and low specificity. Also, the method can be automated.
XX CC AAB86472-AAB86501 represent the gliadin homologues described in the
XX CC method of the invention.
XX SQ Sequence 6 AA;

Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db |||
2 EQP 4

RESULT 27
AAB86487
ID AAB86487 standard; peptide; 6 AA.
XX AC AAB86487;
XX XX
XX DT 29-OCT-2001 (first entry)
XX XX
XX DE Human gliadin peptide homologue SEQ ID 16.
XX KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;
XX KW dermatitis herpetiformis.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN DE10005932-A1.

```

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XX PD 23-AUG-2001.
XX XX
XX PF 10-FEB-2000; 2000DE-1005932.
XX XX
XX PR 10-FEB-2000; 2000DE-1005932.
XX XX
XX PA (UYLE ) UNIV LEIPZIG.
XX XX
XX PI Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
XX XX
XX DR WPI; 2001-503463/56.
XX XX
XX PT New tripeptide and hexapeptide compounds which are gliadin homologues
XX PT useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX PT
XX PS Claim 2; Page 7; 10pp; German.
XX CC This invention describes tripeptide and hexapeptide homologues of gliadin
XX CC which are used in a novel method for the diagnosis of celiac disease and
XX CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX CC washing with methanol, blocking with buffer, washing with TBS-T,
XX CC incubating in human serum, washing with anti-human immunoglobulin A or G,
XX CC conjugating with peroxide, incubating, washing, measuring the
XX CC luminescence and evaluating the data in a known manner; or (b)
XX CC biotinylating one of the tripeptides or hexapeptides, synthetically
XX CC produced and also containing Lys at the C-terminus, applying the
XX CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX CC determining the bound immunoglobulins with a second antibody carrying a
XX CC marker which can be evaluated. The tripeptides and hexapeptides, which
XX CC are cheap to produce and have long term stability in test kits, avoid the
XX CC use of gliadin antibodies which is expensive, subjective and
XX CC semi-quantitative and of enzyme immunoassays which are associated with
XX CC low sensitivity and low specificity. Also, the method can be automated.
XX CC AAB86472-AAB86501 represent the gliadin homologues described in the
XX CC method of the invention.
XX SQ Sequence 6 AA;

Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db |||
2 EQP 4

RESULT 28
AAB86494
ID AAB86494 standard; peptide; 6 AA.
XX AC AAB86494;
XX XX
XX DT 29-OCT-2001 (first entry)
XX XX
XX DE Human gliadin peptide homologue SEQ ID 23.
XX KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;
XX KW dermatitis herpetiformis.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN DE10005932-A1.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 10-FEB-2000; 2000DE-1005932.

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PR 10-FEB-2000; 2000DE-1005932.
XX (UYLE ) UNIV LEIPZIG.
PA Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
XX WPI; 2001-503463/56.
XX
XX New tripeptide and hexapeptide compounds which are gliadin homologues
XX useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX
XX Claim 2; Page 8; 10pp; German.
XX
XX This invention describes tripeptide and hexapeptide homologues of gliadin
XX which are used in a novel method for the diagnosis of celiac disease and
XX dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX washing with methanol, blocking with buffer, washing with TBS-T,
XX incubating in human serum, washing with anti-human immunoglobulin A or G,
XX conjugating with peroxide, incubating, washing, measuring the
XX luminescence and evaluating the data in a known manner; or (b)
XX biotinylating one of the tripeptides or hexapeptides, synthetically
XX produced and also containing Lys at the C-terminus, applying the
XX biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX determining the bound immunoglobulins with a second antibody carrying a
XX marker which can be evaluated. The tripeptides and hexapeptides, which
XX are cheap to produce and have long term stability in test kits, avoid the
XX use of gliadin antibodies which is expensive, subjective and
XX semi-quantitative and of enzyme immunoassays which are associated with
XX low sensitivity and low specificity. Also, the method can be automated.
XX AAB86472-AAB86501 represent the gliadin homologues described in the
XX method of the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 2 EQP 4

RESULT 29
AAB86497
ID AAB86497 standard; peptide; 6 AA.
XX
XX AAB86497;
XX
XX 29-OCT-2001 (first entry)
XX
XX Human gliadin peptide homologue SEQ ID 26.
XX
XX Gliadin; antibody; epitope; human; celiac disease; diagnosis;
XX dermatitis herpetiformis.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX DE10005932-A1.
XX
XX 23-AUG-2001.
XX
XX 10-FEB-2000; 2000DE-1005932.
XX
XX 10-FEB-2000; 2000DE-1005932.
XX
XX (UYLE ) UNIV LEIPZIG.
XX
XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
PI

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XX WPI; 2001-503463/56.
XX
XX New tripeptide and hexapeptide compounds which are gliadin homologues
XX useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX
XX Claim 2; Page 8; 10pp; German.
XX
XX This invention describes tripeptide and hexapeptide homologues of gliadin
XX which are used in a novel method for the diagnosis of celiac disease and
XX dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX washing with methanol, blocking with buffer, washing with TBS-T,
XX incubating in human serum, washing with anti-human immunoglobulin A or G,
XX conjugating with peroxide, incubating, washing, measuring the
XX luminescence and evaluating the data in a known manner; or (b)
XX biotinylating one of the tripeptides or hexapeptides, synthetically
XX produced and also containing Lys at the C-terminus, applying the
XX biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX determining the bound immunoglobulins with a second antibody carrying a
XX marker which can be evaluated. The tripeptides and hexapeptides, which
XX are cheap to produce and have long term stability in test kits, avoid the
XX use of gliadin antibodies which is expensive, subjective and
XX semi-quantitative and of enzyme immunoassays which are associated with
XX low sensitivity and low specificity. Also, the method can be automated.
XX AAB86472-AAB86501 represent the gliadin homologues described in the
XX method of the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 2 EQP 4

RESULT 30
AAB05001
ID AAB05001 standard; peptide; 6 AA.
XX
XX AAB05001;
XX
XX 10-SEP-2001 (first entry)
XX
XX Synthetic peptide #3 analogous to type I repeat of TSP.
XX
XX Thrombospondin; TSP; wound healing; angiogenesis; implant acceptance;
XX anti-platelet aggregation; antimetastatic; therapy; immunosuppressive;
XX sickle cell disease; cytostatic; vulnerary; anti-malaria; anti-sickling;
XX cell adhesion modulator; type I repeat.
XX
XX Synthetic.
XX
XX US6239110-B1.
XX
XX 29-MAY-2001.
XX
XX 07-JUN-1995; 95US-0476134.
XX
XX 01-MAR-1993; 93US-0024436.
XX 24-JAN-1994; 94US-0185614.
XX 22-FEB-1990; 90US-0483527.
XX 24-SEP-1990; 90US-0587197.
XX 25-MAY-1995; 95US-0450738.
XX
XX (GRAC ) GRACE & CO-CONN W R.
XX (MEDI-) MEDICAL COLLEGE PA.
XX

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PI Eyal J, Hamilton BK, Tuszynski GP;  
 DR WPI; 2001-407094/43.  
 XX  
 PT Method for promoting or inhibiting cell adhesion or thrombospondin-like  
 PT activity in a patient, comprises administering polypeptide compounds  
 PT that are synthetic analogs of thrombospondin -  
 XX  
 XX Disclosure; Column 4; 31pp; English.  
 XX  
 CC The present invention relates to peptide fragments and synthetic  
 CC analogues of thrombospondin (TSP) which retain thrombospondin-like  
 CC activity. The peptides retain and mimic the bioactivity of TSP as a  
 CC potent promoter or inhibitor of cell adhesion and attachment to  
 CC different cell lines. The polypeptide is useful for promoting or  
 CC inhibiting cellular attachment to tissue culture flasks, for promoting  
 CC wound healing, angiogenesis or implant acceptance, as agents for  
 CC anti-platelet aggregation or antineoplastic activity, as agents for  
 CC antimalarial activity, or as diagnostic reagents in different  
 CC therapeutic applications. The peptide is useful for treating sickle  
 CC cell disease. The present sequence is a synthetic peptide segment,  
 CC which is analogous to type I repeat of TSP.  
 XX  
 XX Sequence 6 AA;  
 Query Match 75.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 |||  
 DB 2 SEQ 4  
 |||  
 RESULT 31  
 AAB60618  
 ID AAB60618 standard; peptide; 6 AA.  
 XX  
 AC AAB60618;  
 XX  
 XX 27-APR-2001 (first entry)  
 XX  
 DE Etp100 thrombospondin-like hexapeptide motif #4.  
 XX  
 KW Thrombospondin-like motif; TSP; inhibitor; potentiator;  
 KW platelet aggregation; cell adhesion; cell migration;  
 KW angiogenesis; cancer metastasis; tumour growth; antitumour;  
 KW atherosclerosis; thrombosis; cardiovascular disorder;  
 KW ischaemic disorder; thrombolytic; inflammatory disorder;  
 KW rheumatoid arthritis; wound healing; vulneryary;  
 KW drug targeting moiety.  
 OS  
 XX Unidentified.  
 XX  
 PN EP1069137-A1.  
 XX  
 PD 17-JAN-2001.  
 XX  
 PF 20-SEP-1991; 2000EP-0111671.  
 XX  
 PR 24-SEP-1990; 90US-0587197.  
 PR 13-SEP-1991; 91US-0757037.  
 PR 20-SEP-1991; 91EP-0250255.  
 XX  
 XX (GRAC ) GRACE & CO-CONN W R.  
 PA (MEDI-) MEDICAL COLLEGE PENNSYLVANIA.  
 XX  
 PI Eyal J, Hamilton BK, Tuszynski GP;  
 DR WPI; 2001-212579/22.  
 XX  
 XX Use of polypeptides having thrombospondin-like activity for e.g.  
 PT treating atherosclerosis, thrombosis, angiogenesis, inflammatory

PT disorders, inhibiting tumor cell metastases and growth, reducing tumor  
 PT size and colony number -  
 XX  
 PS Disclosure; Page 4; 39pp; English.  
 XX  
 CC The invention relates to the use of a peptide with thrombospondin-  
 CC like activity for the preparation of a medicament for treating tumours.  
 CC The peptide is of the general formula: R1-X1-X2-X3-X4-X5-R2, where:  
 CC R1 is a protected or unprotected terminal amino group including  
 CC hydrogen, amino acetyl or one amino acid residue, or its desamino form;  
 CC X1 and X5 are independently Arg or Cys;  
 CC X2, X3 and X4 are independently Arg, Ser, Thr or Val;  
 CC R2 is a protected or unprotected terminal carboxyl group including  
 CC carboxyamide or its alkylamide forms.  
 CC The structure of the peptide is optionally cyclised via a bond  
 CC between X1 and X5, or via a bond between R1 and R2. Particularly  
 CC preferred is the peptide ASWTR (AAB60588). The peptides of the  
 CC invention act as potentiators or inhibitors of thrombospondin (TSP)  
 CC activity, depending on whether TSP is already present. In the presence  
 CC of endogenous TSP, the peptides act to inhibit TSP-mediated platelet  
 CC aggregation, cell adhesion, cell migration and angiogenesis, while  
 CC in its absence, the peptides potentiate these activities. The peptides  
 CC admixed with at least one carrier, are useful in the preparation of a  
 CC medicament which inhibits tumour cell metastasis, tumour growth, and  
 CC reduces tumour size and tumour colony number. The peptides may be  
 CC used to inhibit platelet aggregation for the treatment of  
 CC atherosclerosis, thrombosis, and other cardiovascular and ischaemic  
 CC disorders. They may also be used to inhibit angiogenesis for the  
 CC treatment of diabetic retinopathy, neovascular glaucoma and inflammatory  
 CC disorders such as rheumatoid arthritis. They may additionally be used  
 CC to prepare antibodies useful as diagnostic or therapeutic agents, to  
 CC promote or inhibit cellular attachment to surfaces (e.g., medical  
 CC devices), and in wound healing. The peptides may further be used to  
 CC treat or prevent conditions where thrombospondin-like activity plays a  
 CC role (e.g., cardiovascular or ischaemic disorders); as a targeting  
 CC moiety to target toxins, drugs, hormones or imaging agents to metastatic  
 CC tumour cells for diagnostic or therapeutic purposes; during surgery on  
 CC peripheral arteries, cardiovascular surgery or after angioplasty;  
 CC in dialysis applications; for preparing antisera for use in immunoassays;  
 CC and to isolate thrombospondin cell surface receptors from extracts of  
 CC cells or cell membranes. Sequences AAB60600-AAB60622 represent  
 CC thrombospondin-like peptide motifs found in a variety of proteins.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 75.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 |||  
 DB 2 SEQ 4  
 |||  
 RESULT 32  
 ABP70731  
 ID ABP70731 standard; Peptide; 6 AA.  
 XX  
 AC ABP70731;  
 XX  
 XX 22-APR-2003 (first entry)  
 DT  
 XX Phosphorylation site peptide substrate #16.  
 DE  
 XX  
 KW Glycogen synthase kinase-3 beta; protein co-ordinate data;  
 KW neurotic; neuroprotective; neuroleptic; antidiabetic; immunosuppressive;  
 KW antiinflammatory; cardiovascular; antiallergic; antisthmatic;  
 KW antiparkinsonian; anticonvulsant; dermatological; vasotropic; GSK-3;  
 KW schizophrenia; Alzheimer's disease; diabetes; autoimmune disease;  
 KW inflammatory disease; metabolic; neurological; neurodegenerative;  
 KW cardiovascular disease; allergy; asthma; Huntington's disease;  
 KW Parkinson's disease; AIDS-related dementia; Lou Gehrig's disease;

KW amyotrophic lateral sclerosis; multiple sclerosis;  
 XX cardiomyocyte hypertrophy; reperfusion; ischaemia; baldness.  
 OS Unidentified.  
 XX WC200288078-A2.  
 XX 07-NOV-2002.  
 XX 29-APR-2002; 2002WO-US13511.  
 XX 30-APR-2001; 2001US-287366P.  
 PR 08-JUN-2001; 2001US-297094P.  
 PR 27-FEB-2002; 2002US-361899P.  
 XX (VERT-) VERTEX PHARM INC.  
 XX Ter Haar E, Swenson L, Green J, Arnost MJ;  
 XX WPI; 2003-247844/24.  
 XX New pyrazolo(3,4-c)pyridazine derivatives are glucocorticoid synthase kinase  
 PT -3 inhibitors useful for treating e.g. schizophrenia, Alzheimer's  
 PT disease, diabetes, autoimmune diseases, allergy, asthma, multiple  
 PT sclerosis, and baldness -  
 XX Disclosure; Page 30; 778pp; English.  
 XX The present invention relates to novel pyrazolo(3,4-c)pyridazine  
 CC derivatives, which have glucocorticoid synthase kinase-3 (GSK-3) inhibitory  
 CC activity. The derivatives are useful for inhibiting beta-catenin  
 CC phosphorylation and hyperphosphorylated Tau protein production in a  
 CC patient and GSK-3 activity in a patient or in a biological sample. The  
 CC derivatives are also useful for treating schizophrenia, Alzheimer's  
 CC disease, diabetes, autoimmune diseases, inflammatory diseases, metabolic,  
 CC neurological and neurodegenerative diseases, cardiovascular diseases,  
 CC allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related  
 CC dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple  
 CC sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness.  
 CC The present sequence is an example of a peptide substrate comprising a  
 CC phosphorylation sequence.  
 XX Sequence 6 AA;  
 SQ Query Match 75.0%; Score 3; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SEQ 3  
 Db 2 SEQ 4  
 RESULT 33  
 AAY50012  
 ID AAY50012 standard; peptide; 7 AA.  
 XX AC AAY50012;  
 XX 19-JAN-2000 (first entry)  
 XX Thermus thermophilus dnaE inverse PCR primer #1-derived peptide.  
 DE DNA polymerase III; dnaE gene; alpha subunit; thermostable;  
 XX DNA synthesis; speed; accuracy; processivity; frameshift; holoenzyme;  
 KW assembly; exonuclease; proofreading; PCR; primer.  
 XX Synthetic.  
 OS Thermus thermophilus.  
 XX WO9953074-A1.  
 XX 21-OCT-1999.  
 PD

XX 09-APR-1998; 98WO-US07070.  
 PF 09-APR-1998; 98WO-US07070.  
 PR (UYRQ ) UNIV ROCKEFELLER.  
 XX Yurieva O, Kuriyan J, O'Donnell ME, Jeruzalmi D;  
 PI WPI; 1999-611306/52.  
 XX N-PSDB; AAZ30921.  
 DR New isolated thermostable DNA polymerase III-type enzyme, used  
 XX particularly for the amplification and sequencing of nucleic acids  
 PT Example 10; Page 78; 156pp; English.  
 PS This sequence represents a peptide encoded by the complement of Thermus  
 XX thermophilus dnaE inverse PCR primer #1. Primer #1 was used with primer  
 CC #2 (AAZ30922) to amplify a portion of the Thermus thermophilus dnaE  
 CC gene. The dnaE gene encodes the alpha subunit of a novel thermostable  
 CC DNA polymerase holoenzyme which corresponds to DNA polymerase  
 CC III (Pol III) of E. coli. Pol III-type enzymes have a high  
 CC processivity (>50 kb) and rapid rate of synthesis (750 nucleotides/s).  
 CC Pol III consists of 18 subunits of 10 different types. The DNA  
 CC polymerase core is the catalytic unit and consists of the alpha (DNA  
 CC polymerase), epsilon (3'-5' exonuclease) and theta subunits. The beta  
 CC subunit ("sliding clamp") is ring-shaped and encircles DNA and slides  
 CC along it while tethering the Pol III holoenzyme to the template. It is  
 CC the beta subunit which is responsible for the high processivity and  
 CC speed. The gamma complex (composed of gamma, delta, chi and psi  
 CC subunits) is the "clamp loader" which couples ATP hydrolysis to assembly  
 CC of beta clamps around DNA. A dimer of the tau subunit acts as a  
 CC "macromolecular organizer", holding together molecules of core  
 CC polymerase and one molecule of gamma complex, forming the Pol III\*  
 CC subassembly. Two beta dimers associate with the two cores within Pol  
 CC III\* to form the holoenzymes capable of replicating both strands of  
 CC duplex DNA simultaneously. The Thermus thermophilus Pol III-type enzyme  
 CC can be used in molecular cloning techniques such as PCR (polymerase  
 CC chain reaction). The current limitations of enzymes previously used in  
 CC PCR are that they are unable to synthesise extended lengths of  
 CC nucleotides, and in the instance of Taq (Thermus aquaticus) polymerase,  
 CC the lack of 3'-5' exonuclease activity and the subsequent inability to  
 CC excise misinserted nucleotides (proofreading).  
 XX Sequence 7 AA;  
 SQ Query Match 75.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SEQ 3  
 Db 4 SEQ 6  
 RESULT 34  
 AAY48764  
 ID AAY48764 standard; Peptide; 7 AA.  
 XX AC AAY48764;  
 XX 20-MAR-2003 (updated)  
 DT 10-DEC-1999 (first entry)  
 XX Membrane dipeptidase-binding gut homing peptide #9.  
 XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostatic; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.  
 XX Synthetic.  
 OS Homo sapiens.

XX PN WO9946284-A2.  
 XX PD 16-SEP-1999.  
 XX PF 10-MAR-1999; 99WO-US05284.  
 XX PR 13-MAR-1998; 98US-0042107.  
 XX PR 26-FEB-1999; 99US-0258754.  
 XX PA (BURN-) BURNHAM INST.  
 XX PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX DR WPI; 1999-571717/48.  
 XX PT New peptides which selectively home to organs or tissues, used for,  
 PT e.g. identifying target ligands and for therapy of pathological  
 PT conditions -  
 XX PS Example 6; Page 147; 193pp; English.  
 XX CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ  
 CC or tissue, for identifying a target molecule expressed by an organ or  
 CC tissue or for treating an organ or tissue pathology, where the organ or  
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,  
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the  
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences  
 CC which are used in the exemplification of the present invention.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX SQ Sequence 7 AA;  
 Query Match 75.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SEQ 3  
 Db 3 SEQ 5  
 RESULT 35  
 AAM44117  
 ID AAM44117 standard; Peptide; 7 AA.  
 XX AC AAM44117;  
 XX DT 25-OCT-2001 (first entry)  
 XX DE H11 binding site consensus conforming peptide (CCP) #388.  
 XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN CA2290722-A1.  
 XX PD 08-JUN-2001.  
 XX PF 08-DEC-1999; 99CA-2290722.  
 XX PR 08-DEC-1999; 99CA-2290722.  
 XX PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 XX DR Entwistle JM, MacDonald GC;  
 XX DR WPI; 2001-425937/46.

PI Entwistle JM, MacDonald GC;  
 XX DR WPI; 2001-425937/46.  
 XX PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX PS Example 4; Page 102; 154pp; English.  
 XX CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX SQ Sequence 7 AA;  
 Query Match 75.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SEQ 3  
 Db 5 SEQ 7  
 RESULT 36  
 AAM44149  
 ID AAM44149 standard; Peptide; 7 AA.  
 XX AC AAM44149;  
 XX DT 25-OCT-2001 (first entry)  
 XX DE H11 binding site consensus conforming peptide (CCP) #420.  
 XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN CA2290722-A1.  
 XX PD 08-JUN-2001.  
 XX PF 08-DEC-1999; 99CA-2290722.  
 XX PR 08-DEC-1999; 99CA-2290722.  
 XX PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 XX DR Entwistle JM, MacDonald GC;  
 XX DR WPI; 2001-425937/46.

PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 PS Example 4; Page 102; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, spindleoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 5 SEQ 7

RESULT 37  
 AAM44154  
 ID AAM44154 standard; Peptide; 7 AA.  
 XX  
 AC AAM44154;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #425.  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW spindleoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 CC Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX Example 4; Page 102; 154pp; English.  
 PS  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, spindleoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 5 SEQ 7

RESULT 38  
 AAM44232  
 ID AAM44232 standard; Peptide; 7 AA.  
 XX  
 AC AAM44232;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #503.  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW spindleoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 CC Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 PS Example 4; Page 102; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress



CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPCCs specific to target cancer (TC). (I) Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs  
 CC or a population of different SPCCs consisting of immunogenic cancer cell  
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 |||  
 Db 5 SEQ 7

RESULT 39

AAM44237  
 ID AAM44237 standard; Peptide; 7 AA.

XX AC AAM44237;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #508.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPCCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs

CC or a population of different SPCCs consisting of immunogenic cancer cell  
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 |||  
 Db 5 SEQ 7

RESULT 40

AAM44242

ID AAM44242 standard; Peptide; 7 AA.

XX AC AAM44242;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #513.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPCCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs  
 CC or a population of different SPCCs consisting of immunogenic cancer cell  
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting CC or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides CC which are used in the exemplification of the present invention.

XX  
SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 5 SEQ 7

RESULT 41  
AAM44247  
ID AAM44247 standard; Peptide; 7 AA.

XX  
AC AAM44247;

XX  
DT 25-OCT-2001 (first entry)

XX  
DE H11 binding site consensus conforming peptide (CCP) #518.

XX  
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX  
OS Homo sapiens.

OS Synthetic.

XX  
PN CA2290722-A1.

XX  
PD 08-JUN-2001.

XX  
PF 08-DEC-1999; 99CA-2290722.

XX  
PR 08-DEC-1999; 99CA-2290722.

XX  
PA (NOVO-) NOVOPHARM BIOTECH INC.

XX  
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, MacDonald GC;  
PI WPI; 2001-425937/46.

XX  
PT Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated  
PT antigen-binding fragments of an antibody that binds specifically to the  
PT complex -

XX  
PS Example 4; Page 102; 154pp; English.

XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPPCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC or a population of different SPPCs consisting of immunogenic cancer cell  
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting

CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.

XX  
SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 5 SEQ 7

RESULT 42  
AAM44252  
ID AAM44252 standard; Peptide; 7 AA.

XX  
AC AAM44252;

XX  
DT 25-OCT-2001 (first entry)

XX  
DE H11 binding site consensus conforming peptide (CCP) #523.

XX  
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX  
OS Homo sapiens.

OS Synthetic.

XX  
PN CA2290722-A1.

XX  
PD 08-JUN-2001.

XX  
PF 08-DEC-1999; 99CA-2290722.

XX  
PR 08-DEC-1999; 99CA-2290722.

XX  
PA (NOVO-) NOVOPHARM BIOTECH INC.

XX  
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, MacDonald GC;  
PI WPI; 2001-425937/46.

XX  
PT Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated  
PT antigen-binding fragments of an antibody that binds specifically to the  
PT complex -

XX  
PS Example 4; Page 102; 154pp; English.

XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPPCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC or a population of different SPPCs consisting of immunogenic cancer cell  
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.

SQ Sequence 7 AA;  
Query Match 75.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SEQ 3  
Db 5 SEQ 7  
RESULT 43  
AAM44257  
ID AAM44257 standard; Peptide; 7 AA.  
XX  
AC AAM44257;  
XX  
DT 25-OCT-2001 (first entry)  
XX  
DE H11 binding site consensus conforming peptide (CCP) #528.  
XX  
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN CA2290722-A1.  
XX  
PD 08-JUN-2001.  
XX  
PF 08-DEC-1999; 99CA-2290722.  
XX  
PR 08-DEC-1999; 99CA-2290722.  
XX  
PA (NOVO-) NOVOPHARM BIOTECH INC.  
XX  
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, MacDonald GC;  
XX  
DR WPI; 2001-425937/46.  
XX  
PT Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated  
PT antigen-binding fragments of an antibody that binds specifically to the  
PT complex -  
XX  
PS Example 4; Page 102; 154pp; English.  
XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPSCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPSCs  
CC or a population of different SPSCs consisting of immunogenic cancer cell  
CC surface-associated SPSC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 7 AA;  
Query Match 75.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SEQ 3  
Db 5 SEQ 7

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SEQ 3  
Db 5 SEQ 7  
RESULT 44  
AAM46757  
ID AAM46757 standard; Peptide; 7 AA.  
XX  
AC AAM46757;  
XX  
DT 25-OCT-2001 (first entry)  
XX  
DE H11 binding site consensus conforming peptide (CCP) #3028.  
XX  
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN CA2290722-A1.  
XX  
PD 08-JUN-2001.  
XX  
PF 08-DEC-1999; 99CA-2290722.  
XX  
PR 08-DEC-1999; 99CA-2290722.  
XX  
PA (NOVO-) NOVOPHARM BIOTECH INC.  
XX  
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, MacDonald GC;  
XX  
DR WPI; 2001-425937/46.  
XX  
PT Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated  
PT antigen-binding fragments of an antibody that binds specifically to the  
PT complex -  
XX  
PS Example 4; Page 111; 154pp; English.  
XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPSCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPSCs  
CC or a population of different SPSCs consisting of immunogenic cancer cell  
CC surface-associated SPSC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 7 AA;  
Query Match 75.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SEQ 3  
Db 5 SEQ 7

Db 5 SEQ 7

RESULT 45  
 AAB68700  
 ID AAB68700 standard; peptide; 7 AA.  
 XX  
 AC AAB68700;  
 XX  
 DT 03-MAY-2001 (first entry)  
 XX  
 DE Cleavage signal peptide.  
 XX  
 KW Cleavage signal; intein cleavage activity; protein purification.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112820-A1.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22581.  
 XX  
 PR 17-AUG-1999; 99US-0149257.  
 XX  
 PA (HEAL-) HEALTH RES INST.  
 XX  
 PI Belfort M, Belfort G, Derbyshire V, Wood D, Wu W;  
 XX  
 DR WPI; 2001-218352/22.  
 XX  
 PT Screening enhanced, reduced intein cleavage activity by expressing  
 PT randomly mutagenized intein DNA and screening cleavage activity using  
 PT varying growth medium and conditions, or by assay with chemical,  
 PT respectively -  
 XX  
 PS Disclosure; Page 6; 103pp; English.  
 XX  
 CC The present invention relates to a method for screening for enhanced or  
 CC reduced intein cleavage activity. The method involves subjecting intein  
 CC DNA to random mutagenesis, expressing the intein DNA with a reporter and  
 CC screening for elevated or reduced intein cleavage activity using varying  
 CC growth medium and conditions, or by an assay with a chemical that plays a  
 CC part in a cell metabolic and/or biochemical cycle. The method is useful  
 CC for purifying a desired protein from a fusion protein. The present  
 CC peptide is a cleavage signal peptide, which can be added to the beginning  
 CC of proteins for C-terminal cleavage.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 75.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 3 EQP 5

RESULT 46  
 AAP40188  
 ID AAP40188 standard; peptide; 8 AA.  
 XX  
 AC AAP40188;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 31-JAN-1992 (first entry)  
 XX  
 DE Hexapeptide coded for by codons 93-98 in the RNA sequence coding for  
 DE structural capsid protein VP1 of polio virus type 3 (Sabin strain)  
 DE (Leon).  
 XX  
 KW Structural capsid protein; VP1; poliovirus type 3; vaccine;

KW enterovirus; diagnosis.  
 XX  
 OS Poliovirus type 3 (Sabin strain) (Leon).  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /label= H-Glu  
 FT Modified-site 8 /label= Gln-OH  
 FT  
 XX WO8401575-A.  
 PN  
 XX 26-APR-1984.  
 PD  
 XX 11-OCT-1983; 83WO-GB00254.  
 PF  
 XX 24-JUN-1983; 83GB-0017242.  
 PR 11-OCT-1982; 82GB-0028976.  
 PR 11-OCT-1983; 83GB-0027154.  
 XX  
 XX (NABI-) NAT BIOL STAN BOARD.  
 PA (MINO/) MINOR P D.  
 PA (NATR) NAT RES DEV CORP.  
 XX  
 PI Almond J;  
 XX  
 XX WPI; 1984-113769/18.  
 DR  
 XX Antigenic poly-peptide for vaccination against Enterovirus - esp.  
 PT polio, and for diagnosis  
 PT  
 XX Disclosure; Page 7; 56pp; English.  
 PS  
 CC The inventors claim an antigenic polypeptide for vaccination against  
 CC Enterovirus. Pref. equivalents are octapeptides coded for by codons  
 CC 93-100 of poliovirus type 3 (Sabin strain) VP1 and oligopeptides  
 CC coded by a continuous run of 7-18 codons (including 93-98), starting  
 CC no lower than 86 and ending no higher than 103. A pref.  
 CC immunological carrier for the peptides is tetanus or diphtheria  
 CC toxoid. A typical dose is 0.1-1 mg, opt. given as a priming dose  
 CC before vaccination.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 75.0%; Score 3; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 1 EQP 3

RESULT 47  
 AAP60137  
 ID AAP60137 standard; peptide; 8 AA.  
 XX  
 AC AAP60137;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 07-JUL-1991 (first entry)  
 XX  
 DE Sequence of preferred type 3 poliovirus octapeptide according  
 DE to GB-A-2 128 621.  
 XX  
 XX Vaccine; diagnosis; enterovirus disease; poliovirus type 1; type 2;  
 KW type 3.  
 XX  
 XX Poliovirus.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 5

/label= T,S

FT XX EP197772-A.  
 PN 15-OCT-1986.  
 XX 03-APR-1986; 86EP-0302481.  
 PF 03-APR-1985; 85GB-0008685.  
 PR 03-APR-1986; 86GB-0008140.  
 XX (NATR ) NAT RES DEV CORP.  
 PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.  
 XX Minor PD, Evans DMA, Schild GC, Almond JW, Ferguson M;  
 DR WPI; 1986-273645/42.  
 XX Synthetic peptide for vaccination or diagnosis of enterovirus  
 PT disease - comprises fragment coded for by polio virus type 3  
 PT Sabin strain capsid protein RNA  
 XX Disclosure; Page 13; 53pp; English.  
 PS The inventors claim synthetic peptides for use in vaccination  
 CC against or diagnosis of a disease caused by an enterovirus (see  
 CC AAM60118). The peptides are coded for by codons 286-288 or 286-290 in  
 CC the RNA sequence coding for the structural capsid protein VP1 of  
 CC poliovirus type 3 Sabin strain or by equivalent codons of another  
 CC enterovirus, or antigenic equiva. Also claimed are synthetic peptides  
 CC comprising the above peptides linked to (a) a hexapeptide coded for  
 CC by codons 93-98 as above, or (b) a peptide sequence comprising AA  
 CC residues 58 and 59 of the VP3 capsid protein of an enterovirus.  
 CC Typical doses are 100mg-1mg, i.m.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 8 AA;  
 Query Match 75.0%; Score 3; DB 7; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EQP 4  
 Db ||||  
 1 EQP 3  
 RESULT 48  
 AAR35925  
 ID AAR35925 standard; protein; 8 AA.  
 XX AAR35925;  
 AC 25-MAR-2003 (updated)  
 DT 24-MAY-1993 (first entry)  
 XX Hepatitis C virus (HCV) epitope EpL.  
 DE Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 KW infection.  
 XX Hepatitis C virus type 1.  
 OS WO9300365-A2.  
 XX 07-JAN-1993.  
 PD 24-JUN-1992; 92WO-US05388.  
 XX 24-JUN-1991; 91US-0722489.  
 PR (CHIR ) CHIRON CORP.

XX Chien DY, Rutter W;  
 XX WPI; 1993-036334/04.  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 XX Example A; Page 36; 80pp; English.  
 XX This octamer was found to be immunoreactive with anti-HCV anti-sera.  
 CC In the epitope mapping experiment three different samples of anti-sera  
 CC were reacted with the peptide octamer, and then incubated with  
 CC HRP-labelled goat anti-human Ig anti-sera, to enable detection of  
 CC binding. This epitope starts from amino acid 1218 of the HCV  
 CC polyprotein.  
 CC This was found to be a particularly strong epitope.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 8 AA;  
 Query Match 75.0%; Score 3; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 Db ||||  
 5 SEQ 7  
 RESULT 49  
 AAR59433  
 ID AAR59433 standard; peptide; 8 AA.  
 XX AAR59433;  
 AC 19-JAN-1995 (first entry)  
 DT Gp2b(896-903) peptide used in anti-platelet antibody adsorbent.  
 DE Anti-platelet antibody; adsorbent; nonwoven fabric; ITP; idiopathic;  
 KW thrombocytopenic purpura; blood cleaning.  
 XX Synthetic.  
 OS JP06121834-A.  
 XX 06-MAY-1994.  
 PD 13-OCT-1992; 92JP-0274450.  
 PF 13-OCT-1992; 92JP-0274450.  
 PR (TOYM ) TOYOBO KK.  
 XX WPI; 1994-185959/23.  
 DR Adsorbent of anti-platelet antibody, permitting treatment of  
 PT serious ITP patients - comprising peptide immobilised to nonwoven  
 PT fabric  
 XX Disclosure; Page 3; 11pp; Japanese.  
 PS The invention relates to a new adsorbent for anti-platelet  
 CC antibodies consisting of a nonwoven fabric made of fibres of ave.  
 CC dia. 1-30 microns, the fibres having carboxyl groups and having  
 CC attached to them via the carboxyl groups a peptide capable of  
 CC bonding to the antibodies. The adsorbent is used for therapy of ITP  
 CC patients by cleaning their blood. The treatment is effective and  
 CC without side effects.  
 CC The present peptide is an example of a suitable peptide which can  
 CC bond the antibodies. It represents residues 896-903 of the Gp2b  
 CC protein.

```

XX SQ Sequence      8 AA;
    Query Match      75.0%; Score 3; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        3 EQP 5

RESULT 50
AAR48371
ID AAR48371 standard; peptide; 8 AA.
XX
AC AAR48371;
XX
DT 16-SEP-1994 (first entry)
XX
DE Peptide fragment which adsorbs to anti-platelet antibody.
XX
KW Peptide; fragment; anti-platelet antibody; adsorbent; ITP;
KW immune thrombocytopenia purpura.
XX
OS Synthetic.
XX
PN JP06030989-A.
XX
PD 08-FEB-1994.
XX
PF 13-JUL-1992; 92JP-0185176.
XX
PR 13-JUL-1992; 92JP-0185176.
XX
PA (TOYM ) TOYOBO KK.
XX
DR WPI; 1994-079346/10.
XX
PT New polypeptide and adsorber of anti-platelet antibody - used to
PT purify blood
XX
PS Claim 1; Page 2; 8pp; Japanese.
XX
CC The peptide is a fragment of a larger polypeptide which is used in
CC an adsorbent of anti-platelet antibody. The adsorbent is used for
CC the treatment of severe immune thrombocytopenia purpura (ITP)
CC patients.
XX
SQ Sequence      8 AA;
    Query Match      75.0%; Score 3; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        3 EQP 5

RESULT 51
AAR58622
ID AAR58622 standard; peptide; 8 AA.
XX
AC AAR58622;
XX
DT 25-APR-1995 (first entry)
XX
DE GP2b residues 896-903, anti-platelet antibody binding peptide.
XX
KW Anti-platelet; antibody; adsorbent; nonwoven; fabric; epoxy group;
KW ITP patient; external circulation; plasma.
XX

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```

OS Homo sapiens.
XX
PN JP06218050-A.
XX
PD 09-AUG-1994.
XX
PF 25-JAN-1993; 93JP-0010065.
XX
PR 25-JAN-1993; 93JP-0010065.
XX
PA (TOYM ) TOYOBO KK.
XX
DR WPI; 1994-290064/36.
XX
PT Anti-platelet antibody adsorbent, useful for external circulation
PT therapy - comprises peptide able to bind to antibodies which is
PT immobilised on nonwoven fabric having epoxy gps
XX
PS Disclosure; Page 4; 11pp; Japanese.
XX
CC The sequences given in AAR58615-23 represent peptides which have the
CC ability to bind anti-platelet antibodies. These peptides may be
CC used in an antibody adsorbent which consists of these peptides,
CC which may be opt. modified immobilised on a nonwoven fabric having
CC epoxy groups in the surface, and composed of fibre of an average of
CC 1-30 microns. The adsorbent binds effectively to anti-platelet
CC antibodies and is therefore useful for treating serious ITP patients,
CC without side effects. The use of the nonwoven fabric allows full
CC external circulation with sepn. of the plasma. Peptides are easily
CC introduced through epoxy groups.
XX
SQ Sequence      8 AA;
    Query Match      75.0%; Score 3; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        3 EQP 5

RESULT 52
AAR66119
ID AAR66119 standard; peptide; 8 AA.
XX
AC AAR66119;
XX
DT 07-JUL-1995 (first entry)
XX
DE Peptide derived from platelet GP2b receptor amino acids 896-903.
XX
KW Platelet; GP1; GP2b; GP3a; receptor; blood; factor; fibrinogen; plasma;
KW von Willebrand factor; immobilisation; adsorbent; autoimmune disease;
KW antibody; idiopathic thrombocytopenic purpura; ITP; circulation; ligand.
XX
OS Synthetic.
XX
PN JP06269498-A.
XX
PD 27-SEP-1994.
XX
PF 17-MAR-1993; 93JP-0057207.
XX
PR 17-MAR-1993; 93JP-0057207.
XX
PA (TOYM ) TOYOBO KK.
XX
DR WPI; 1994-346230/43.
XX
PT Anti-platelet-antibody adsorbent useful for external circulation
PT therapy - consisting of opt. modified peptide(s) having
PT binding-affinity and immobilised to nonwoven fabric
XX

```

XX Disclosure; Page 3; 11pp; Japanese.

PS

XX A series of peptides (AA86112-35), optionally modified, derived from

CC GPI alpha-chain, GP2b or GP3a receptors on platelets, which bind blood

CC factors such as fibrinogen and von Willebrand factor. The modified

CC peptides can be immobilised on a non-woven fabric adsorbent. The

CC adsorbent can be used to remove anti-platelet-antibodies useful in

CC treating patients with autoimmune diseases such as severe idiopathic

CC thrombocytopenic purpura (ITP). The use of the non-woven fabric

CC eliminates the need for the separation of the blood plasma and permits

CC external circulation for treatment of the entire blood. The functional

CC groups facilitate the introduction of peptides as ligands.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

DB 3 EQP 5

RESULT 53

AAW33664

ID AAW33664 standard; peptide; 8 AA.

AC AAW33664;

XX

DT 24-APR-1998 (first entry)

XX

DE Poliovirus type 3 VP1 antigenic epitope.

XX

KW Antigenic epitope; virus like particle; poliovirus type 3; VP1;

KW diagnostic reagent; antibiotic; therapy; food supplement; VLP;

XX vaccination; herbicide resistance; industrial enzyme.

OS Poliovirus.

XX

PN WO9739134-A1.

XX

PD 23-OCT-1997.

XX

PF 17-APR-1997; 97WO-GB01065.

XX

PR 17-APR-1996; 96GB-0007899.

XX

PA (SCCR-) SCOTTISH CROP RES INST.

XX

PI Chapman SN, Wilson TMA;

XX

DR WPI; 1997-526468/48.

XX

PT Production of virus like particles - using a nucleic acid sequence

PT capable of assembly with a protein having a first viral portion and

PT second non-viral portion

XX

PS Example 1; Page 9; 33pp; English.

XX

CC This is antigenic epitope from VP1 of poliovirus type 3. This was fused

CC to the 3' end of a synthetic gene coding for the tobacco mosaic virus

CC (TMV) coat protein by PCR amplification with mutagenic primers. This is

CC used in a novel method for producing a protein having a first (viral)

CC portion and a second (non-viral) portion. The method comprises

CC expressing the protein in a cell, providing a nucleic acid sequence

CC capable of assembly with the protein into a virus-like particle (VLP),

CC and permitting in vivo assembly of the protein and nucleic acid into

CC VLPs. The VLPs can be used for the production of proteins such as

CC diagnostic reagents, antibiotics, therapeutic agents or food supplements.

CC They can be used for e.g. expression of metabolic enzymes for pathway

CC engineering, nutritional supplements, anti-potato cyst nematode lectins,

CC gut protease inhibitors, anti-botrytis agents, PGIBs, anti-insect

CC Bacillus thuringiensis toxin and herbicide resistance agents, industrial

CC enzymes, pharmaceuticals, therapeutic proteins, and nucleic acids, and as

CC bioeffectors. They can also be used intact for presentation of peptide

CC epitopes for vaccination of animals, the production of therapeutic or

CC industrial proteins and polypeptides and/or the delivery of therapeutic

CC nucleic acid molecules.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 18; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

DB 1 EQP 3

RESULT 54

AAW79269

ID AAW79269 standard; Peptide; 8 AA.

XX

AC AAW79269;

XX

DT 15-FEB-1999 (first entry)

XX

DE Bovine glucuronyl C5-epimerase internal peptide.

XX

KW Glucuronyl C5-epimerase; cattle; D-glucuronic acid;

KW L-iduronic acid; heparin; heparan sulphate.

XX

OS Bos taurus.

XX

PN WO9848006-A1.

XX

PD 29-OCT-1998.

XX

PF 17-APR-1998; 98WO-SE00703.

XX

PR 18-APR-1997; 97SE-0001454.

XX

PA (LIJJ/) LI J.

PA (LIND/) LINDAHL U.

XX

PI Li J, Lindahl U;

XX

DR WPI; 1998-583655/49.

XX

PT DNA sequence coding for mammalian glucuronyl C5-epimerase and

PT functional derivatives - capable of converting D-glucuronic acid to

PT L-iduronic acid in the synthesis of heparin and heparan sulphate

XX

PS Disclosure; Page 16; 26pp; English.

XX

CC This is an internal peptide of a glucuronyl C5-epimerase purified

CC from bovine liver. It corresponds to amino acid residues 306-313.

CC of the deduced amino acid sequence (see AAW79263) of the epimerase.

CC N-terminal and internal peptides (see AAW79264-70) of the epimerase

CC were produced by digestion of the purified epimerase using a

CC lysine-specific protease. PCR primers (see AAV62689-91) based on one

CC of these peptides (see AAW79270) were used to generate a probe that

CC was utilised in the isolation of glucuronyl C5-epimerase cDNA (see

CC AAV62688) from a bovine lung cDNA library. The invention relates to

CC isolated or recombinant DNA sequences for a mammalian (including

CC human) glucuronyl C5-epimerase or its functional derivative. These

CC can be used for the recombinant production of the enzyme, which is

CC useful for converting D-glucuronic acid to L-iduronic acid in the

CC biosynthesis of heparin and heparan sulphate.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||

Db 3 SEQ 5

RESULT 55  
AAW45999  
ID AAW45999 standard; peptide; 8 AA.

AC AAW45999;

XX 03-JUL-1998 (first entry)

DT

DE Peptide #24 based on mouse SSTR 2 (residues 1-8).

DE Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;

KW insulin-like growth factor binding protein; IGFBP; SSTR; diabetes;

KW somatostatin receptor; insulin-like growth factor.

XX Synthetic.

OS Mus sp.

XX WO9744352-A1.

PN 27-NOV-1997.

XX 22-MAY-1997; 97WO-AU00312.

XX 22-MAY-1996; 96AU-0009990.

PR (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.

PA Gerraty NL, Kingston DJ, Westbrook SL;

XX WPI; 1998-018427/02.

XX New non-naturally occurring peptide(s) - which are based on portions of somatostatin, somatostatin receptors and insulin-like growth factor binding protein

PT Disclosure; Page 9; 136pp; English.

PS Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides.

XX Sequence 8 AA;

SQ

Query Match 75.0%; Score 3; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||

Db 5 SEQ 7

RESULT 56  
AAW46001  
ID AAW46001 standard; peptide; 8 AA.

AC AAW46001;

XX 03-JUL-1998 (first entry)

DT

DE Peptide #27 based on rat SSTR 2 (residues 1-8).

XX Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;

KW insulin-like growth factor binding protein; IGFBP; SSTR; diabetes;

KW somatostatin receptor; insulin-like growth factor.

XX Synthetic.

OS Rattus sp.

XX WO9744352-A1.

PN 27-NOV-1997.

XX 22-MAY-1997; 97WO-AU00312.

XX 22-MAY-1996; 96AU-0009990.

PR (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.

PA Gerraty NL, Kingston DJ, Westbrook SL;

XX WPI; 1998-018427/02.

XX New non-naturally occurring peptide(s) - which are based on portions of somatostatin, somatostatin receptors and insulin-like growth factor binding protein

PT of somatostatin, somatostatin receptors and insulin-like growth factor binding protein

PT Example 11; Page 9; 136pp; English.

XX Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides.

XX Sequence 8 AA;

SQ

Query Match 75.0%; Score 3; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||

Db 5 SEQ 7

RESULT 57  
ABP21164  
ID ABP21164 standard; Peptide; 8 AA.

XX ABP21164;

AC

XX 15-JUL-2002 (first entry)

DT

DE HIV A03 motif pol peptide #159.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

OS

XX WO200124810-A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

PF 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

PA

XX



PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 XX Claim 32; Page 303; 448pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 75.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 Db 4 SEQ 6  
 RESULT 58  
 ABP21201  
 ID ABP21201 standard; Peptide; 8 AA.  
 AC  
 AC ABP21201;  
 DT 15-JUL-2002 (first entry)  
 DE HIV A03 motif pol peptide #196.  
 XX  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO200124810-A1.  
 PN  
 PD 12-APR-2001.  
 XX  
 XX 05-OCT-2000; 2000WO-US27766.  
 PF  
 XX 05-OCT-1999; 99US-0412863.  
 PR  
 XX (EPTM-) EPIMMUNE INC.  
 PA  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

DR WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 XX Claim 32; Page 304; 448pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 75.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 Db 3 SEQ 5  
 RESULT 59  
 ABP23175  
 ID ABP23175 standard; Peptide; 8 AA.  
 XX  
 AC ABP23175;  
 XX  
 DT 15-JUL-2002 (first entry)  
 DE HIV A11 motif pol peptide #117.  
 XX  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO200124810-A1.  
 PN  
 PD 12-APR-2001.  
 XX  
 XX 05-OCT-2000; 2000WO-US27766.  
 PF  
 XX 05-OCT-1999; 99US-0412863.  
 PR  
 XX (EPTM-) EPIMMUNE INC.  
 PA  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32; Page 343; 448pp; English.

XX

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC AB25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
|||

Db 4 SEQ 6  
|||

## RESULT 60

ABBS2109

ID ABB52109 standard; Peptide; 8 AA.

XX AC ABB52109;

XX DT 08-FEB-2002 (first entry)

XX DE Human API-73 tryptic digest peptide #2.

XX KW Human; neuroprotective; nootropic; gene therapy; vaccine;

XX KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;

XX KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;

XX KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX OS Homo sapiens.

XX PN WO200175454-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US10908.

XX PR 03-APR-2000; 2000US-194504P.

XX PR 28-NOV-2000; 2000US-253647P.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PA (PFIZ ) PFIZER INC.

XX PI Durham KL, Friedman DL, Herath HMAAC, Kimmel LH, Parekh RB;

XX PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX PI Townsend RR, White F, Williams SA;

XX DR WPI; 2001-639384/73.

XX.

PT Screening for Alzheimer's disease in a mammal, by making

PT two-dimensional array of a feature whose relative abundance correlates

PT with disease, and comparing with abundance of the feature in samples of

PT healthy persons -

PS Example; Page 28; 162pp; English.

XX

XX The invention relates to methods for the screening, diagnosis and

CC prognosis of Alzheimer's disease. The methods involve the detection

CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's

CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,

CC serum or plasma. The abundance of the AFs and APIs is then

CC normalised to an Expression Reference Protein Isoform (ERPI) in

CC order to determine whether a patient is suffering from, or has

CC a predisposition to, Alzheimer's Disease. The relative abundance of

CC the AFs and APIs correlates with the severity of Alzheimer's Disease.

CC The present sequence is a peptide produced from an API by proteolysis.

XX SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||

Db 1 EQP 3  
|||

## RESULT 61

AAO15739

ID AAO15739 standard; Peptide; 8 AA.

XX AC AAO15739;

XX DT 14-NOV-2002 (first entry)

XX DE Haemophilus influenzae BASB213 protein potential B-cell epitope 2.

XX KW BASB213; gene therapy; vaccine; otitis media; pneumonia;

XX KW Haemophilus influenzae infection; sinusitis; nosocomial infection;

XX KW invasive disease; B-cell epitope.

XX OS Haemophilus influenzae.

XX PN WO200266503-A2.

XX PD 29-AUG-2002.

XX PF 15-FEB-2002; 2002WO-EP01650.

XX PR 16-FEB-2001; 2001GB-0003866.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Thonard J;

XX DR WPI; 2002-674912/72.

XX

XX New BASB213 polypeptide and polynucleotide, useful for the preparation

PT of a medicament used in generating an immune response in an animal, and

PT for diagnosing, preventing and/or treating microbial diseases with H.

PT Influenza infection -

XX Example 13; Page 69; 87pp; English.

XX The invention comprises the amino acid and coding sequences of

CC Haemophilus influenzae BASB213 proteins. The BASB213 DNA and protein

CC sequences of the invention are useful for generating an immune response

CC in an animal. In particular, the BASB213 DNA and protein sequences are

CC useful for diagnosing, preventing and/or treating microbial diseases with

CC H. influenzae infection (e.g. otitis media, pneumonia, sinusitis,

CC nosocomial infections and invasive diseases). The present amino acid

CC sequence represents a potential B-cell epitope from a H. influenzae  
 CC BASB213 protein.  
 XX Sequence 8 AA;  
 SQ Query Match 75.0%; Score 3; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 ||||  
 Db 1 SEQ 3

RESULT 62  
 ID ABG31180 standard; Peptide: 8 AA.  
 XX AC ABG31180;  
 XX DT 05-NOV-2002 (first entry)  
 XX DE Rat delta PKC region, pseudo-delta RACK, modified peptide, #20.  
 XX KW Rat; delta protein kinase C; deltaPKC; V1 domain; vasotropic;  
 KW cerebroprotective; deltaV1-1; deltaV1-2; RACK; pseudo-delta RACK;  
 KW pseudo-delta receptor for activated C-kinase; deltaV1-5; PKC;  
 KW protein kinase C; signal transduction; cell growth; gene expression;  
 KW ion channel activity; translocation; hypoxia; stroke; ischaemic damage;  
 KW creatine kinase; antagonist; agonist; mutant; mutein.  
 XX OS Rattus norvegicus.  
 OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 6 /note= "Wild-type Asp substituted by Gln"  
 FT  
 XX WO200257413-A2.  
 XX 25-JUL-2002.  
 XX 09-NOV-2001; 2001WO-US47556.  
 XX 18-JAN-2001; 2001US-262060P.  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX Mochly-Rosen D;  
 XX WPI; 2002-599715/64.  
 XX New delta protein kinase C peptide for reducing or enhancing damage to  
 cells or tissues exposed to ischemic or hypoxic event caused by stroke,  
 or for protecting tissue from damage due to ischemia -  
 XX Claim 4; Page 21; 65pp; English.

The invention discloses peptides comprising deltaV1-1, deltaV1-2,  
 pseudo-delta receptors for activated C-kinase (RACK), deltaV1-5 or their  
 derivatives or fragments. Protein kinase C (PKC) is a key enzyme in  
 signal transduction involved in a variety of cellular functions including  
 cell growth, regulation of gene expression and ion channel activity. The  
 localisation of different PKC isozymes to different areas of the cell in  
 turn appears due to binding of the activated isozymes to the specific  
 anchoring molecules (RACKs). Peptides that mimic either the PKC-binding  
 site on RACKs or the RACK-binding site on PKC are isozyme specific  
 translocation inhibitors of PKC. The disclosed peptides are useful in  
 activating or inhibiting translocation or function of deltaPKC. The  
 deltaPKC agonists or antagonists are useful in reducing, enhancing or  
 protecting against damage to cells or tissues due to ischaemic or hypoxic  
 event caused by stroke. Acute administration of the peptides, conjugated  
 to a carrier peptide or a Tat-derived peptide, protected hearts against

CC ischaemic damage as shown by decreased release of creatine kinase. The  
 data indicate that in an intact heart, inhibition of deltaPKC conferred  
 greater than 50% protection against ischaemic damage. The peptides  
 in ABG31159-ABG31219 are the deltaV1-1, deltaV1-2, pseudo-delta RACK,  
 deltaV1-5 (or their derivatives or fragments) agonists or antagonists to  
 the rat delta protein kinase C (PKC).  
 XX Sequence 8 AA;  
 SQ Query Match 75.0%; Score 3; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
 ||||  
 Db 5 EQP 7

RESULT 63  
 ID ABG60428 standard; Peptide: 8 AA.  
 XX AC ABG60428;  
 XX DT 30-JUL-2002 (first entry)  
 XX DE Selective targeting peptide #103.  
 XX KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;  
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;  
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;  
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;  
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;  
 KW gene therapy.  
 XX OS Synthetic.  
 XX WO200220769-A1.  
 XX 14-MAR-2002.  
 XX 07-SEP-2001; 2001WO-US27692.  
 XX 08-SEP-2000; 2000US-231266P.  
 XX 17-JAN-2001; 2001US-0765101.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Arap W, Pasqualini R;  
 XX WPI; 2002-415731/44.  
 XX Targeting peptides identified by phage display, useful for targeting  
 delivery to an organ or tissue, particularly for treating a disease,  
 e.g. cancer, inflammatory or autoimmune diseases, infections or  
 cardiovascular disease -  
 XX Claim 22; Page 90; 317pp; English.

The invention relates to an isolated peptide of 100 amino acids or less  
 in size useful for targeting delivery to an organ or tissue, particularly  
 for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory  
 disease, atherosclerosis, autoimmune disease, bacterial infection, viral  
 infection, cardiovascular disease or degenerative disease. The peptide is  
 also useful for inducing apoptosis, particularly to a subject with  
 ischaemia, cancer, arthritis, diabetes, cardiovascular disease,  
 inflammation or macular degeneration. Furthermore, the peptide is useful  
 for diagnosing the diseases cited above. Targeting peptides of the  
 invention can also be used to deliver an agent to a foetus, by attaching  
 a peptide to the agent and administering the peptide to a pregnant  
 subject. Sequences ABG60326-ABG60574 represent selective targeting  
 peptides of the invention.

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 5 SEQ 7

RESULT 64

ABU38203

ID ABU38203 standard; Peptide; 8 AA.

AC ABU38203;

XX

DT 22-MAY-2003 (first entry)

XX

DE Human cytomegalovirus CTL epitope peptide SEQ ID No 261.

XX

KW Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen;  
KW human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1;  
KW IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;  
KW transplantation.

XX

OS Human cytomegalovirus.

XX

PN WO2003000720-A1.

XX

PD 03-JAN-2003.

XX

PF 26-JUN-2002; 2002WO-AU00829.

XX

PR 26-JUN-2001; 2001AU-0005931.

XX

PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX

PI Khanna R, Elkington RA, Walker SJ;

XX

DR WPI; 2003-300379/29.

XX

PT New human cytomegalovirus (HCMV) cytotoxic T-cell epitope peptide,  
PT useful for diagnosing, preventing or treating CMV infection, comprises  
PT pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11  
PT or UL18 -

XX

PS Claim 70; Page 124; 308pp; English.

XX

CC The invention relates to a novel isolated peptide comprising one or more  
CC cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen  
CC of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28,  
CC pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.  
CC The peptide comprises a sequence of about 9-20 contiguous amino acids of  
CC the antigen. The peptide epitopes are useful in diagnosing, preventing or  
CC treating cytomegalovirus infection in humans, and in monitoring immune  
CC responses in various clinical settings (e.g. transplantation or  
CC pregnancy). This sequence represents a human cytomegalovirus CTL epitope  
CC peptide of the invention.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 24; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
|||  
Db 2 EQP 4

RESULT 65

AAR26441

ID AAR26441 standard; peptide; 9 AA.

XX

AC AAR26441;

XX

DT 25-MAR-2003 (updated)

XX

DT 08-FEB-1993 (first entry)

XX

DE N-terminal auxiliary sequence.

XX

KW Negative hydrophobicity; increased renaturation yield.

XX

OS Synthetic.

XX

PN EP500108-A2.

XX

PD 26-AUG-1992.

XX

PF 20-FEB-1992; 92EP-0102864.

XX

PR 21-FEB-1991; 91DE-4105480.

XX

PA (BOEF ) BOEHRINGER MANNHEIM GMBH.

XX

PI Ambrosius D, Dony C, Rudolph R;

XX

DR WPI; 1992-286227/35.

XX

PT Increasing renaturation yield of recombinant protein from

PT prokaryotic host - by expressing it with terminal hydrophilic

PT aminoacid sequence attached, pref. detachable at specific

PT cleavage site

XX

PS Claim 11; Page 14; 18pp; German.

XX

CC The peptide is used as an auxiliary sequence which can be added to  
CC the N and/or C-terminus of recombinant proteins which exist in at  
CC least partially inactive form and are activated by solubilisation  
CC and/or renaturation techniques. The auxiliary sequence has a ratio  
CC of relative hydrophobicity:number of amino acids of -2.0 kcal/mole  
CC or smaller. Incorporation of the auxiliary sequence increases the  
CC yield during the renaturation process. This method is applied to  
CC recombinant proteins produced in prokaryotic organisms, especially  
CC E. coli. A specific application is production of recombinant  
CC granulocyte-colony stimulating factor (GM-CSF) or its derivatives.  
CC See also AAR26436-R26444.

XX

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 9 AA;

Query Match 75.0%; Score 3; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
|||  
Db 6 EQP 8

RESULT 66

AAR87291

ID AAR87291 standard; peptide; 9 AA.

XX

AC AAR87291;

XX

DT 16-MAY-1996 (first entry)

XX

DE Plasmodium falciparum HLA-B17 epitope ls42.

XX

KW Liver stage antigen; ISA-1; human leucocyte antigen; HLA; class 1;  
KW HLA-B17; epitope; malaria; vaccine; CTL induction;  
KW cytotoxic T lymphocyte.

XX

OS Plasmodium falciparum.

XX WO9526982-A2.  
 XX  
 PD 12-OCT-1995.  
 XX  
 XX 31-MAR-1995; 95WO-GB00737.  
 XX PF  
 XX PR 31-MAR-1994; 94GB-0006492.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX  
 XX Aidoo M, Allsopp CEM, Hill AVS, Lalvani A, Piebanski M;  
 XX PI Whittle HC;  
 XX  
 DR WPI; 1995-358584/46.  
 XX  
 XX Plasmodium falciparum peptide(s) - useful in vaccine compositions  
 XX PT for immunising against malaria  
 XX  
 XX Claim 1; Page 19; 23pp; English.  
 PS  
 XX Cytotoxic T lymphocytes from malaria-exposed Gambian individuals  
 CC with HLA-B17 showed significant lysis of a large pool of peptides  
 CC (AAR87287-R87299) derived from Plasmodium falciparum liver stage  
 CC antigen-1. These peptides will be useful in a malaria vaccine.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 75.0%; Score 3; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 DB 4 SEQ 6

RESULT 67  
 AAW49287  
 ID AAW49287 standard; peptide; 9 AA.  
 XX  
 AC AAW49287;  
 XX  
 DT 05-JUN-1998 (first entry)  
 XX  
 DE Human leucocyte antigen DQ4 binding peptide #178.  
 XX  
 XX Human leucocyte antigen; HLA-DQ4; combinatorial library;  
 KW autoimmune disease; chronic articular rheumatism.  
 KW  
 XX Synthetic.  
 XX  
 PN JP08151396-A.  
 XX  
 PD 11-JUN-1996.  
 XX  
 XX 28-NOV-1994; 94JP-0292657.  
 XX PF  
 XX 28-NOV-1994; 94JP-0292657.  
 XX PR  
 XX (TEIJ ) TEIJIN LTD.  
 PA  
 XX WPI; 1996-329479/33.  
 DR  
 XX HLA-binding oligopeptide and an immuno:regulator contg it - used in  
 XX PT the treatment of auto:immune disease  
 XX  
 XX Claim 4; Page 27; 61pp; Japanese.  
 PS  
 XX This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence AAV05953, by screening  
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of

CC autoimmune disease, or especially for treatment of viral diseases.  
 XX  
 SQ Sequence 9 AA;  
 XX

Query Match 75.0%; Score 3; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 DB 6 SEQ 8

RESULT 68  
 AAW07112  
 ID AAW07112 standard; peptide; 9 AA.  
 XX  
 AC AAW07112;  
 XX  
 DT 23-JAN-1997 (first entry)  
 XX  
 DE Synthetic peptide used in GalNac-transferase activity SPA.  
 XX  
 XX SPA; scintillation proximity assay; antigen; bead coating; capture;  
 KW antibody; N-acetyl-galactosamine transferase; GalNac transferase;  
 KW activity; enzyme; O-linked glycosylation.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9615258-A1.  
 PN  
 XX 23-MAY-1996.  
 PD  
 XX 08-NOV-1995; 95WO-US13483.  
 XX PF  
 XX 16-NOV-1994; 94US-0340283.  
 XX PR  
 XX (UPJO ) UPJOHN CO.  
 PA  
 XX Elhammer AP;  
 PI  
 XX WPI; 1996-268220/27.  
 DR  
 XX Scintillation proximity assay for N-acetyl:galactosaminyl activity  
 PT - esp. for large scale screening of cpds. for their effect on enzyme  
 PT activity  
 XX  
 XX Claim 14; Page 17; 29pp; English.  
 PS  
 XX AAW06985-W07180 are antigenic peptides derived from either the  
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDDK).  
 CC The peptides are useful for coating beads used in a scintillation  
 CC proximity assay for N-acetyl:galactosamine (GalNac)-transferase (GNT)  
 CC activity. The assay involves fewer steps than known assays and is  
 CC quicker, producing excellent signal-to-noise ratios. The  
 CC assay is capable of screening large numbers of cpds. for their  
 CC ability to affect GNT activity and is thus useful for identifying  
 CC inhibitors and promoters of glycosylation (in partic. O-linked  
 CC glycosylation).  
 XX  
 SQ Sequence 9 AA;  
 XX

Query Match 75.0%; Score 3; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 DB 1 EQP 3

RESULT 69  
 AAW29260

```

ID AAW29260 standard; peptide; 9 AA.
XX
AC AAW29260;
XX
DT 07-JAN-1998 (first entry)
XX
DE Soybean hydrolysate nonapeptide active oxygen inhibitor.
XX
DE soybean; Glycine max; hydrolysate; pepsin digestion; active;
XX
KW oxygen inhibitor; arthritis; rheumatism; Behcet's disease;
XX
KW cardiac infarction; heart attack.
XX
OS Glycine max.
XX
PN JP09157292-A.
XX
PD 17-JUN-1997.
XX
PF 11-DEC-1995; 95JP-0349939.
XX
PR 11-DEC-1995; 95JP-0349939.
XX
PA (SUET/) SUETSUNA Y.
XX
DR WPI; 1997-369469/34.
XX
PT New hexa:peptide and nona:peptide from soybean hydrolysate - useful
PT as active oxygen inhibitors, for treating arthritis, rheumatism,
PT cardiac infarction and Behcet's disease
XX
PS Claim 3; Page 2; 8pp; Japanese.
XX
CC AAW29259-60 were isolated from soybean (Glycine max) hydrolysate after
CC pepsin digestion. The hexa- and nonapeptide are useful in active oxygen
CC inhibitors. The oxygen inhibitors are useful for treating arthritis,
CC rheumatism, Behcet's disease and cardiac infarction.
XX
SQ Sequence 9 AA;
Query Match 75.0%; Score 3; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQP 4
Db 4 EQP 6
RESULT 70
AAV53335
ID AAV53335 standard; Protein; 9 AA.
XX
AC AAV53335;
XX
DT 18-JAN-2000 (first entry)
XX
DE Bcr-Ab1 epitope (aa 817-825) binds HLA-A2.
XX
KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
KW melanoma; malaria; parasite.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN FR2776926-A1.
XX
PD 08-OCT-1999.
XX
PF 07-APR-1998; 98FR-0004323.
XX
PR 07-APR-1998; 98FR-0004323.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
PA (INSP ) INST PASTEUR LILLE.
XX
PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
XX WPI; 1999-583113/50.
XX
XX New lipopeptide containing lipid regions and two epitopes, all
PT separated by peptide spacers that impart hydrophilicity, useful in
PT vaccines
XX
XX Disclosure; Page 17; 35pp; French.
XX
XX The invention relates to the generation of a lipopeptide comprising at
CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
CC epitope and at least one lipid residue with (i) the epitopes and lipid
CC portion and (ii) the epitopes, being separated independently by peptide
CC spacers. These spacers comprise sequences of amino acids which carry an
CC overall electrical charge in neutral media to ensure that the
CC lipopeptide is hydrophilic. The peptides AAV53301-Y53549 represents
CC examples of peptide epitopes used to generate the lipopeptides. These are
CC used in therapeutic or prophylactic compositions and vaccines to induce
CC specific immune responses against human immunodeficiency, hepatitis B or
CC papilloma viruses; p53 of melanoma or the malaria parasite.
XX
SQ Sequence 9 AA;
Query Match 75.0%; Score 3; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEQ 3
Db 3 SEQ 5
RESULT 71
AAV40157
ID AAV40157 standard; Peptide; 9 AA.
XX
AC AAV40157;
XX
DT 19-NOV-1999 (first entry)
XX
DE Amino acid sequence of a chronic myeloid leukaemia epitope.
XX
KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
KW vaccine; tumor; infection; immune response; cytokine profile;
KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
KW autoimmune disease.
XX
OS Homo sapiens.
XX
PN FR2774687-A1.
XX
PD 13-AUG-1999.
XX
PF 06-FEB-1998; 98FR-0001439.
XX
PR 06-FEB-1998; 98FR-0001439.
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP ) INST PASTEUR LILLE.
XX
PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
XX WPI; 1999-510734/43.
XX
XX New lipopeptide comprising C-terminal interferon-gamma fragment with
PT attached lipophilic groups, used as interferon mimic, e.g. for treating

```

PT cancer or virus infection  
 XX  
 PS Disclosure; Page 33; 53pp; French.  
 XX  
 CC AAY40123-Y40379 represent epitopes that are able to activate cytotoxic  
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or  
 CC B epitopes recognized by corresponding antibodies. The epitopes may be  
 CC used in the composition of the invention. The specification describes a  
 CC lipopeptide that has a peptide part derived from mammalian interferon  
 CC gamma (IFN $\gamma$ ) and one or more lipophilic parts comprising a linear or  
 CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The  
 CC lipopeptide mimics the activity of IFN $\gamma$ . Compositions comprising the  
 CC lipopeptide are used to treat or prevent any condition that responds  
 CC to IFN $\gamma$ , and as adjuvant for vaccines (particularly those directed  
 CC against tumors, viral or parasitic infections), to stimulate or  
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.  
 CC Particular applications are treatment of infections (particularly  
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and  
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers  
 CC (particularly of kidney, cutaneous T cells or ovary, chronic  
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune  
 CC diseases.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 75.0%; Score 3; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 DB 3 SEQ 5  
 RESULT 72  
 AAY26673  
 ID AAY26673 standard; peptide; 9 AA.  
 XX  
 AC AAY26673;  
 XX  
 DT 14-SEP-1999 (first entry)  
 XX  
 DE BCR-ABL-derived lipopeptide epitope (aa817-825) for mixed micelles.  
 XX  
 KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
 KW melanoma; Plasmodium falciparum; malaria.  
 XX  
 OS Synthetic.  
 OS Abelson murine leukemia virus.  
 XX  
 PN FR2771640-A1.  
 XX  
 PD 04-JUN-1999.  
 XX  
 PF 03-DEC-1997; 97FR-0015246.  
 XX  
 PR 03-DEC-1997; 97FR-0015246.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 PI Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;  
 PI Tartar A, Wieruszski JM;  
 XX  
 DR WPI; 1999-349509/30.  
 XX  
 CC Immunogenic lipopeptide micelles - comprising lipopeptides  
 PT containing cytotoxic and helper T-lymphocyte epitopes  
 PS Disclosure; Page 30; 60pp; French.

XX The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprise: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit  
 CC different from that of the first lipopeptide. This peptide represents  
 CC an example of a lipopeptide epitope used in the invention and is derived  
 CC from the BCR protein of the Abelson murine leukemia virus. The  
 CC immunogenic lipopeptide micelles are used in vaccines, especially against  
 CC HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma or  
 CC Plasmodium falciparum malaria.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 75.0%; Score 3; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEQ 3  
 DB 3 SEQ 5  
 RESULT 73  
 AAW74273  
 ID AAW74273 standard; peptide; 9 AA.  
 XX  
 AC AAW74273;  
 XX  
 DT 05-MAY-1999 (first entry)  
 XX  
 DE HJ loop peptide K105H103.  
 XX  
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;  
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;  
 KW inflammatory disorder; central nervous system disease; septic shock;  
 KW Parkinson's disease; hypertension.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 9 /note= "Myristyl-Gly"  
 FT Modified-site 9 /note= "amidated"  
 XX  
 PN WO9853051-A1.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 20-MAY-1998; 98MO-US10321.  
 XX  
 PR 21-MAY-1997; 97US-0861153.  
 XX  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX  
 PI Ben-Sasson SA;  
 XX  
 DR WPI; 1999-070143/06.  
 XX  
 PT New peptide derivatives for modulating protein tyrosine kinase  
 PT activity - comprise a sequence corresponding to the HJ loop of a  
 PT protein tyrosine kinase, used for treating cancers or immune  
 PT disorders  
 XX  
 PS Disclosure; Fig 7; 79pp; English.  
 XX  
 CC This sequence represents a peptide of the invention, and is a derivative  
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be  
 CC used for the treatment of disorders caused by overactivity or  
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic  
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and  
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,  
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression  
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel  
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's  
 CC disease, stroke and trauma), septic shock, Parkinson's disease or  
 CC hypertension. The peptides can also be used to produce antibodies which  
 CC can be used to identify cells expressing the STK and to study the  
 CC intracellular distribution of the STK. In addition, the peptides can be  
 CC used to identify and quantitate ligands which bind the HJ loop of the STK  
 CC from which the peptide was derived.

XX SQ Sequence 9 AA;

Query Match 75.0%; Score 3; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
 |||  
 Db 6 EQP 8

## RESULT 74

AAW74285

ID AAW74285 standard; peptide; 9 AA.

XX AC AAW74285;

XX DT 05-MAY-1999 (first entry)

XX DE HJ loop peptide K094H101.

XX KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

XX KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

XX KW inflammatory disorder; central nervous system disease; septic shock;

XX KW Parkinson's disease; hypertension.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "Myristyl-Gly"

XX FT Modified-site 9 /note= "amidated"

XX FT WO9853051-A1.

XX PN 26-NOV-1998.

XX PD 20-MAY-1999; 98WO-US10321.

XX PF 21-MAY-1997; 97US-0861153.

XX PR (CHL-) CHILDRENS MEDICAL CENT.

XX PA Ben-Sasson SA;

XX PI WPI; 1999-070143/06.

XX DR New peptide derivatives for modulating protein tyrosine kinase

XX PT activity - comprise a sequence corresponding to the HJ loop of a

XX PT protein tyrosine kinase, used for treating cancers or immune

XX PT disorders

XX PS Disclosure; Fig 7; 79pp; English.

XX XX

CC This sequence represents a peptide of the invention, and is a derivative

CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be

CC used for the treatment of disorders caused by overactivity or

CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic

CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and

CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,  
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression  
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel  
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's  
 CC disease, stroke and trauma), septic shock, Parkinson's disease or  
 CC hypertension. The peptides can also be used to produce antibodies which  
 CC can be used to identify cells expressing the STK and to study the  
 CC intracellular distribution of the STK. In addition, the peptides can be  
 CC used to identify and quantitate ligands which bind the HJ loop of the STK  
 CC from which the peptide was derived.

XX SQ Sequence 9 AA;

Query Match 75.0%; Score 3; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
 |||  
 Db 5 EQP 7

## RESULT 75

AAW96177

ID AAW96177 standard; peptide; 9 AA.

XX AC AAW96177;

XX DT 27-APR-1999 (first entry)

XX DE IKK-alpha polypeptide with binding activity.

XX KW I-kappa-B kinase; IKK-alpha; gene expression; modulation;

XX KW suppression; activation; tumour necrosis factor; TNF; interleukin-1;

XX KW IL-1; TNF receptor associated factor; TRAF.

XX OS Homo sapiens.

XX PN WO9901541-A1.

XX PD 14-JAN-1999.

XX PF 01-JUL-1998; 98WO-US13782.

XX PR 10-JUL-1997; 97US-0890854.

XX PR 01-JUL-1997; 97US-0887115.

XX PA (TULA-) TULARIK INC.

XX PI Cao Z, Regnier C, Rothe M;

XX XX WPI; 1999-106044/09.

XX DR Newly isolated human kinase IkkappaB Kinase (IKK- $\alpha$ ) polypeptides -

XX PT useful in screening for agents that modulate the interaction of an

XX PT IKK polypeptide to a binding target and for modulating signal

XX PT transduction involving IkkappaB in a cell

XX PS Disclosure; Page -; 32pp; English.

XX XX

CC I-kappa-B kinase (AAW96158), deletion mutants of it retaining

CC I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a

CC six residue domain of I-kappa-B containing one of Ser32 and Ser36,

CC and a candidate agent) can be used to screen for agents that

CC modulate the interaction of an IKK polypeptide to a binding target.

CC The modulation of the kinase activity of IKK-alpha forms a method

CC for modulating signal transduction involving I-kappa-B in a cell.

CC The IKK-alpha polypeptides are useful for generating oligonucleotide

CC primers and probes for use in the isolation of natural

CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as

CC translatable transcripts, hybridization probes, polymerase chain

CC reaction (PCR) probes and primers. Their diagnostic applications

CC include IKK-alpha hybridization probes for identifying wild-type and



CC mutant IKK-alpha alleles in clinical and laboratory samples.  
CC Therapeutic application includes the use of IKK- alpha nucleic acids  
CC for modulating cellular expression or intracellular  
CC concentration/availability of active IKK-alpha.  
CC Catalytically inactive IKK-alpha mutants suppress NF-kappa-B  
CC activation induced by tissue necrosis factor (TNF), interleukin-1  
CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and  
CC NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of  
CC IKK-alpha showing exemplary binding activity are described in  
CC AAW96165-W96182. These peptides all comprise one of Cys30, Glu543,  
CC Leu604, Thr679, Ser680, Pro684, Thr686 or Ser687 of the full length  
CC IKK-alpha described in AAW96157. Deletion mutants of the invention  
CC comprise at least one of these regions.  
CC N.B. The present sequence is not given in the present specification  
CC but is derived from the sequence given in AAW96157 as specified.  
XX  
SQ Sequence 9 AA;

Query Match 75.0%; Score 3; DB 20; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 1 SEQ 3

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 7.95745 Seconds  
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Title: US-09-641-801-10  
Perfect score: 4  
Sequence: 1 SEQP 4

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Minimum DB seq length: 3  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	4	15	US-10-281-652-10
2	4	100.0	14	12	US-10-234-816-40
3	4	100.0	14	15	US-10-185-050-190
4	3	75.0	5	12	US-10-168-758-3
5	3	75.0	5	15	US-10-043-487-493
6	3	75.0	6	10	US-09-873-233A-7
7	3	75.0	6	11	US-09-500-700-88
8	3	75.0	7	12	US-10-192-381-53
9	3	75.0	7	15	US-10-155-922-14
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11	3	75.0	7	15	US-10-155-922-97
12	3	75.0	7	15	US-10-155-922-99
13	3	75.0	7	15	US-10-155-922-101
14	3	75.0	8	10	US-09-758-128-24
15	3	75.0	8	10	US-09-758-128-27

16	3	75.0	8	10	US-09-826-290-124	Sequence 124, App
17	3	75.0	8	10	US-09-758-426-24	Sequence 24, Appl
18	3	75.0	8	10	US-09-758-426-27	Sequence 27, Appl
19	3	75.0	8	10	US-09-758-198-24	Sequence 24, Appl
20	3	75.0	8	10	US-09-758-198-27	Sequence 27, Appl
21	3	75.0	8	11	US-09-861-661-24	Sequence 24, Appl
22	3	75.0	8	11	US-09-861-661-27	Sequence 27, Appl
23	3	75.0	8	14	US-10-001-761-32	Sequence 32, Appl
24	3	75.0	9	10	US-09-779-308-401	Sequence 401, App
25	3	75.0	9	10	US-09-779-308-579	Sequence 579, App
26	3	75.0	9	10	US-09-779-308-698	Sequence 698, App
27	3	75.0	9	12	US-09-793-451-15	Sequence 15, Appl
28	3	75.0	9	12	US-09-793-451-144	Sequence 144, App
29	3	75.0	9	12	US-10-006-177-14	Sequence 14, Appl
30	3	75.0	9	12	US-10-062-109A-22	Sequence 22, Appl
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32	3	75.0	9	12	US-10-062-109A-272	Sequence 272, App
33	3	75.0	9	12	US-10-062-109A-281	Sequence 281, App
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38	3	75.0	9	12	US-10-005-480A-140	Sequence 140, App
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43	3	75.0	9	12	US-10-005-480A-660	Sequence 660, App
44	3	75.0	9	12	US-10-283-722-15	Sequence 15, Appl
45	3	75.0	9	12	US-10-283-722-144	Sequence 144, App
46	3	75.0	9	14	US-10-042-202-36	Sequence 36, Appl
47	3	75.0	9	15	US-10-234-432-92	Sequence 92, Appl
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50	3	75.0	10	10	US-09-779-308-161	Sequence 161, App
51	3	75.0	10	10	US-09-779-308-565	Sequence 565, App
52	3	75.0	10	11	US-09-984-245-291	Sequence 291, App
53	3	75.0	10	11	US-09-966-262-291	Sequence 291, App
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55	3	75.0	10	11	US-09-572-404B-1778	Sequence 1778, App
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59	3	75.0	10	12	US-09-793-451-306	Sequence 306, App
60	3	75.0	10	12	US-09-793-451-509	Sequence 509, App
61	3	75.0	10	12	US-09-783-451-705	Sequence 705, App
62	3	75.0	10	12	US-10-234-816-97	Sequence 97, Appl
63	3	75.0	10	12	US-10-062-109A-72	Sequence 72, Appl
64	3	75.0	10	12	US-10-062-109A-91	Sequence 91, Appl
65	3	75.0	10	12	US-10-062-109A-160	Sequence 160, App
66	3	75.0	10	12	US-10-062-109A-208	Sequence 208, App
67	3	75.0	10	12	US-10-062-109A-233	Sequence 233, App
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70	3	75.0	10	12	US-10-062-109A-334	Sequence 334, App
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72	3	75.0	10	12	US-10-005-480A-91	Sequence 91, Appl
73	3	75.0	10	12	US-10-005-480A-160	Sequence 160, App
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77	3	75.0	10	12	US-10-005-480A-319	Sequence 319, App
78	3	75.0	10	12	US-10-005-480A-334	Sequence 334, App
79	3	75.0	10	12	US-10-283-722-80	Sequence 80, Appl
80	3	75.0	10	12	US-10-283-722-84	Sequence 84, Appl
81	3	75.0	10	12	US-10-283-722-306	Sequence 306, App
82	3	75.0	10	12	US-10-283-722-509	Sequence 509, App
83	3	75.0	10	12	US-10-283-722-705	Sequence 705, App
84	3	75.0	10	15	US-10-256-865-10	Sequence 10, Appl
85	3	75.0	10	15	US-10-256-865-11	Sequence 11, Appl
86	3	75.0	10	15	US-10-143-090-291	Sequence 291, App
87	3	75.0	10	15	US-10-155-922-19	Sequence 19, Appl
88	3	75.0	10	15	US-10-155-922-35	Sequence 35, Appl

89 3 75.0 10 15 US-10-155-922-60 Sequence 60, Appl  
90 3 75.0 10 15 US-10-155-922-61 Sequence 61, Appl  
91 3 75.0 10 15 US-10-155-922-62 Sequence 62, Appl  
92 3 75.0 10 15 US-10-155-922-79 Sequence 79, Appl  
93 3 75.0 10 15 US-10-133-210-207 Sequence 207, Appl  
94 3 75.0 11 7 US-08-738-019-13 Sequence 13, Appl  
95 3 75.0 11 11 US-09-984-923A-33 Sequence 33, Appl  
96 3 75.0 11 12 US-10-239-313A-510 Sequence 510, Appl  
97 3 75.0 11 15 US-10-033-741-18 Sequence 18, Appl  
98 3 75.0 11 15 US-10-033-662-21 Sequence 21, Appl  
99 3 75.0 12 12 US-10-137-867-312 Sequence 312, Appl  
100 3 75.0 13 10 US-09-870-759-148 Sequence 148, Appl

## ALIGNMENTS

## RESULT 1

US-10-281-652-10  
; Sequence 10, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide

US-10-281-652-10

Query Match 100.0%; Score 4; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4  
Db 1 SEQ 4

## RESULT 2

US-10-234-816-40  
; Sequence 40, Application US/10234816  
; Publication No. US20030157514A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRAIN HOMOLGY DOMAIN AND PR  
; TITLE OF INVENTION: RICH DOMAIN CONTAINING ADAPTER PROTEIN, PMN29  
; FILE REFERENCE: D0117 NP  
; CURRENT APPLICATION NUMBER: US/10/234,816  
; CURRENT FILING DATE: 2002-09-04  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-234-816-40

Query Match 100.0%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4  
Db 8 SEQ 11

## RESULT 3

US-10-185-050-190  
; Sequence 190, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

US-10-185-050-190

NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE

US-10-185-050-190

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: &lt;Unknown&gt;

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 190:

US-10-185-050-190

Query Match 100.0%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4  
Db 3 SEQ 6

## RESULT 4

US-10-168-758-3  
; Sequence 3, Application US/10168758  
; Publication No. US20030207812A1  
; GENERAL INFORMATION:  
; APPLICANT: Chapdelaine, Marc J  
; APPLICANT: Katherine, Knappenberger

; APPLICANT: Steelman, Gary  
; APPLICANT: Suchard, Suzanne  
; APPLICANT: SYGOWSKI, Linda  
; TITLE OF INVENTION: CD45  
; FILE REFERENCE: 270624-1P US  
; CURRENT APPLICATION NUMBER: US/10/168,758  
; CURRENT FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-168-758-3

Query Match 75.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 1 EQP 3

RESULT 5  
US-10-043-487-493  
; Sequence 493, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIGENICS  
; APPLICANT: PIERRE, LEGRAIN  
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptides  
; FILE OF INVENTION: mammalian polypeptides  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 493  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Shigella flexneri  
US-10-043-487-493

Query Match 75.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 3 SEQ 5

RESULT 6  
US-09-873-233A-7  
; Sequence 7, Application US/09873233A  
; Patent No. US20020146434A1  
; GENERAL INFORMATION:  
; APPLICANT: UEDA, Shigeharu  
; APPLICANT: WATANABE, Michiko  
; APPLICANT: KAWANISHI, Hitomi  
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN  
; FILE REFERENCE: 0216-0451P  
; CURRENT APPLICATION NUMBER: US/09/873,233A  
; CURRENT FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 6

; TYPE: PRT  
; ORGANISM: Measles virus  
; FEATURE:  
; OTHER INFORMATION: Attenuated measles virus CAM -70 strain  
US-09-873-233A-7

Query Match 75.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 1 EQP 3

RESULT 7  
US-09-500-700-88  
; Sequence 88, Application US/09500700  
; Publication No. US20030059767A1  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: BARBAS III, Carlos F.  
; APPLICANT: GOTTESFELD, Joel M.  
; APPLICANT: WRIGHT, Peter E.  
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR  
; FILE REFERENCE: SCRIPI160-4  
; CURRENT APPLICATION NUMBER: US/09/500,700  
; CURRENT FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: US 08/863,813  
; PRIOR FILING DATE: 1997-05-27  
; PRIOR APPLICATION NUMBER: US 08/676,318  
; PRIOR FILING DATE: 1996-12-30  
; PRIOR APPLICATION NUMBER: PCT/US95/00829  
; PRIOR FILING DATE: 1995-01-18  
; PRIOR APPLICATION NUMBER: US 08/312,604  
; PRIOR FILING DATE: 1994-09-28  
; PRIOR APPLICATION NUMBER: US 08/183,119  
; PRIOR FILING DATE: 1994-01-18  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Modified sequence of finger 1 of zif268  
US-09-500-700-88

Query Match 75.0%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 1 SEQ 3

RESULT 8  
US-10-192-381-53  
; Sequence 53, Application US/10192381  
; Publication No. US20030170807A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHUI1580-4  
; CURRENT APPLICATION NUMBER: US/10/192,381

```

; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: conserved amino acid sequence
US-10-192-381-53

Query Match 75.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 3 EQP 5

RESULT 9
US-10-155-922-14
; Sequence 14, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-95

Query Match 75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 2 SEQ 4

RESULT 11
US-10-155-922-97
; Sequence 97, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903

```

```

Qy 1 SEQ 3
Db 2 SEQ 4

RESULT 10
US-10-155-922-95
; Sequence 95, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-95

Query Match 75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 2 SEQ 4

RESULT 11
US-10-155-922-97
; Sequence 97, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903

```

```

; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-97

```

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Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SEQ 3
      |||
Db      2 SEQ 4

```

```

RESULT 12
US-10-155-922-99
; Sequence 99, Application US/10155922
; Publication No. US2003008693A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-99

```

```

Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SEQ 3
      |||

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```

Db      2 SEQ 4

```

```

RESULT 13
US-10-155-922-101
; Sequence 101, Application US/10155922
; Publication No. US2003008693A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-101

```

```

Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SEQ 3
      |||
Db      2 SEQ 4

```

```

RESULT 14
US-09-758-128-24
; Sequence 24, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT

```

```
; ORGANISM: Mouse
US-09-758-128-24

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 15
US-09-758-128-27
; Sequence 27, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Simon L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-27

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 16
US-09-826-290-124
; Sequence 124, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
```

---

```
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-124

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 1 EQP 3

RESULT 17
US-09-758-426-24
; Sequence 24, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Simon L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-426-24

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 18
US-09-758-426-27
; Sequence 27, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Simon L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
```

```
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-27

Query Match          75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 19
US-09-758-198-24
; Sequence 24, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Norman L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-198-24

Query Match          75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 20
US-09-758-198-27
; Sequence 27, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Norman L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-27

Query Match          75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 21
US-09-861-661-24
; Sequence 24, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-861-661-24

Query Match          75.0%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 22
US-09-861-661-27
; Sequence 27, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-861-661-27

Query Match          75.0%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



Qy 1 SEQ 3  
|||  
Db 5 SEQ 7

RESULT 23  
US-10-007-761-32  
; Sequence 32, Application US/10007761  
; Publication No. US20020150984A1  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; TITLE OF INVENTION: Peptides for Activation and Inhibition  
; TITLE OF INVENTION: of delta-PKC  
; FILE REFERENCE: 58600-8208.US00  
; CURRENT APPLICATION NUMBER: US/10/007.761  
; CURRENT FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: US 60/262,060  
; PRIOR FILING DATE: 2001-01-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified pseudo-delta RACK peptide  
US-10-007-761-32

Query Match 75.0%; Score 3; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 5 EQP 7

RESULT 24  
US-09-779-308-401  
; Sequence 401, Application US/09779308  
; Patent No. US20020150972A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.4USU1  
; CURRENT APPLICATION NUMBER: US/09/779,308  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181,020  
; PRIOR FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 718  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 401  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-779-308-401

Query Match 75.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 4 EQP 6

RESULT 25  
US-09-779-308-579  
; Sequence 579, Application US/09779308  
; Patent No. US20020150972A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.4USU1  
; CURRENT APPLICATION NUMBER: US/09/779,308  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181,020  
; PRIOR FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 718  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 579  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-779-308-579

Query Match 75.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 4 EQP 6

RESULT 26  
US-09-779-308-698  
; Sequence 698, Application US/09779308  
; Patent No. US20020150972A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.4USU1  
; CURRENT APPLICATION NUMBER: US/09/779,308  
; CURRENT FILING DATE: 2001-02-08  
; PRIOR APPLICATION NUMBER: 60/181,020  
; PRIOR FILING DATE: 2000-02-08  
; NUMBER OF SEQ ID NOS: 718  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 698  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-779-308-698

Query Match 75.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 4 EQP 6

RESULT 27

```

US-09-793-451-15
; Sequence 15, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-15

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

RESULT 28
US-09-793-451-144
; Sequence 144, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-144

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

US-09-641-801-10
; Sequence 14, Application US/10006177
; Publication No. US20030165513A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishna, Venky
; APPLICANT: Ross, Mark
; APPLICANT: Philip, Ramila
; TITLE OF INVENTION: Cytotoxic T-Lymphocyte-Inducing Immunogens for Prevention, Tre
; TITLE OF INVENTION: Diagnosis of Cancer
; FILE REFERENCE: 26747-35
; CURRENT APPLICATION NUMBER: US/10/006,177
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US/60/251,022
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US/60/256,824
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitopic Peptide
US-10-006-177-14

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 4 EQP 6

RESULT 30
US-10-062-109A-22
; Sequence 22, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-22

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

```

```
Db          3 EQP 5
||||
RESULT 31
US-10-062-109A-140
; Sequence 140, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-140

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 EQP 4
||||
Db          6 EQP 8
||||
RESULT 32
US-10-062-109A-272
; Sequence 272, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-272

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 EQP 4
||||
Db          6 EQP 8
||||
RESULT 33
US-10-062-109A-281
; Sequence 281, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-281

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 EQP 4
||||
Db          4 EQP 6
||||
RESULT 34
US-10-062-109A-386
; Sequence 386, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-386

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      2 EQP 4
Db      1 EQP 3

RESULT 35
US-10-062-109A-498
; Sequence 498, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 498
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-498

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      1 EQP 3

RESULT 36
US-10-062-109A-660
; Sequence 660, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 660
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-660

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      1 EQP 3

RESULT 37
US-10-005-480A-22
; Sequence 22, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-22

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      3 EQP 5

RESULT 38
US-10-005-480A-140
; Sequence 140, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-140

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      2 EQP 4

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Db      |||
        6 EQP 8

RESULT 39
US-10-005-480A-272
; Sequence 272, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-272

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        5 EQP 7

RESULT 40
US-10-005-480A-281
; Sequence 281, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-281

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        4 EQP 6

RESULT 41
US-10-005-480A-386
; Sequence 386, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-386

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        1 EQP 3

RESULT 42
US-10-005-480A-498
; Sequence 498, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 498
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-498

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        1 EQP 3

RESULT 43
US-10-005-480A-660
```

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; Sequence 660, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 660
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-660

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      5 EQP 7

RESULT 44
US-10-283-722-15
; Sequence 15, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-144

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      2 EQP 4

RESULT 46
US-10-042-202-36
; Sequence 36, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton Hill, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PLEBANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WENDEROOTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street,N.W., Suite 800,
; CITY: Washington
; STATE: D.C.,
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-JAN-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0

```

```

RESULT 45
US-10-283-722-144
; Sequence 144, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-144

Query Match          75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      2 EQP 4

RESULT 46
US-10-042-202-36
; Sequence 36, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton Hill, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PLEBANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WENDEROOTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street,N.W., Suite 800,
; CITY: Washington
; STATE: D.C.,
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-JAN-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0

```

```

; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
; TELEFAX: (202)-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-042-202-36

Query Match 75.0%; Score 3; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 4 SEQ 6

RESULT 47
US-10-234-432-92
; Sequence 92, Application US/10234432
; Publication No. US20030091598A1
; GENERAL INFORMATION:
; APPLICANT: Homer, Mary J.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF BABESIA INFECTION
; FILE REFERENCE: 210121.560
; CURRENT APPLICATION NUMBER: US/10/234,432
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Babesia sp. wai
US-10-234-432-92

Query Match 75.0%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 5 EQP 7

RESULT 48
US-08-736-019-26
; Sequence 26, Application US/08736019
; Publication No. US20030207799A1
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,019
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,833
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-736-019-26

Query Match 75.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8

RESULT 49
US-09-779-308-65
; Sequence 65, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert

```

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; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-65

Query Match      75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
Db      6 EQP 8

RESULT 50
US-09-779-308-161
; Sequence 161, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-161

Query Match      75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
Db      1 EQP 3

RESULT 51
US-09-779-308-565
; Sequence 565, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin

```

```

; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-565

Query Match      75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
Db      4 EQP 6

RESULT 52
US-09-984-245-291
; Sequence 291, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: PZ004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096

```



; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,355  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,160  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,351  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,154  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/054,804  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: US 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: US 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 291  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-984-245-291

Query Match 75.0%; Score 3; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 6 EQP 8

RESULT 53

US-09-966-262-291  
; Sequence 291, Application US/09966262  
; Publication No. US20030050461A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: P2004P1  
; CURRENT APPLICATION NUMBER: US/09/966,262  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: US 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,352  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,186  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,069

; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,095  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,131  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,096  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,355  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,160  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,351  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,154  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/054,804  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: US 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: US 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 291  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-966-262-291

Query Match 75.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 6 EQP 8

RESULT 54

US-09-983-966-291  
; Sequence 291, Application US/09983966  
; Publication No. US20030060619A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: P2004P1  
; CURRENT APPLICATION NUMBER: US/09/983,966  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/050,937  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,187  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099

RESULT 56  
US-10-190-082-553  
; Sequence 553, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Heid, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,634  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO 553  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-553

Query Match 75.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
|||  
Db 1 SEQ 3

RESULT 57  
US-09-793-451-80  
; Sequence 80, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129, 2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-80

Query Match 75.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 3 EQP 5

RESULT 58

RESULT 55  
US-09-572-404B-1778  
; Sequence 1778, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1778  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in MTMR1 at 139-148 and may interact with Sequer  
US-09-572-404B-1778

Query Match 75.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
|||  
Db 6 EQP 8

Query Match 75.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred.No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
|||  
Db 3 SEQ 5

US-09-793-451-84  
; Sequence 84, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-84

Query Match 75.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
Db 6 EQP 8

RESULT 59  
US-09-793-451-306  
; Sequence 306, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 306  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-306

Query Match 75.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4

Db 6 EQP 8  
RESULT 60  
US-09-793-451-509  
; Sequence 509, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 509  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-509

Query Match 75.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
Db 6 EQP 8

RESULT 61  
US-09-793-451-705  
; Sequence 705, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 705  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-705

Query Match 75.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 4 EQP 6

## RESULT 62

US-10-234-816-97  
 ; Sequence 97, Application US/10234816  
 ; Publication No. US20030157514A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRIN HOMOMOLOGY DOMAIN AND PR  
 ; FILE OF INVENTION: RICH DOMAIN CONTAINING ADAPTER PROTEIN, PMN29  
 ; FILE REFERENCE: D0117 NP  
 ; CURRENT APPLICATION NUMBER: US/10/234,816  
 ; CURRENT FILING DATE: 2002-09-04  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 97  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-234-816-97

Query Match 75.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 8 SEQ 10

## RESULT 63

US-10-062-109A-72  
 ; Sequence 72, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; FILE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062,109A  
 ; CURRENT FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005,480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 72  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-72

Query Match 75.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 3 EQP 5

## RESULT 64

US-10-062-109A-91  
 ; Sequence 91, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; FILE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062,109A  
 ; CURRENT FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005,480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 91  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-91

Query Match 75.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 6 EQP 8

## RESULT 65

US-10-062-109A-160  
 ; Sequence 160, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agensys  
 ; APPLICANT: Challita-Eid, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; FILE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062,109A  
 ; CURRENT FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 10/005,480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 160  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-062-109A-160

Query Match 75.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
 |||  
 Db 7 EQP 9

```

Db          6 EQP 8

RESULT 66
US-10-062-109A-208
; Sequence 208, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-208

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
Db          5 EQP 7

RESULT 67
US-10-062-109A-233
; Sequence 233, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-233

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
Db          5 EQP 7

RESULT 68
US-10-062-109A-306
; Sequence 306, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-306

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
Db          6 EQP 8

RESULT 69
US-10-062-109A-319
; Sequence 319, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-319

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
Db          6 EQP 8

RESULT 69
US-10-062-109A-319
; Sequence 319, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-319

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
Db          6 EQP 8

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Db          5 EQP 7
||||
RESULT 70
US-10-062-109A-334
; Sequence 334, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-334

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          1 EQP 3

RESULT 71
US-10-005-480A-72
; Sequence 72, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-72

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          1 EQP 3

RESULT 72
US-10-005-480A-91
; Sequence 91, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-91

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          6 EQP 8

RESULT 73
US-10-005-480A-160
; Sequence 160, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-160

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          7 EQP 9
```

```

RESULT 74
US-10-005-480A-208
; Sequence 208, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-208

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 5 EQP 7

```

```

RESULT 75
US-10-005-480A-233
; Sequence 233, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-233

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8

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Search completed: November 25, 2003, 20:25:37  
 Job time :- 8.95745 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 4.3617 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	4	4	US-09-641-803-10
2	4	100.0	10	1	US-08-328-256-5
3	3	75.0	5	1	US-08-292-045-18
4	3	75.0	5	1	US-08-292-045-19
5	3	75.0	6	1	US-08-483-434A-19
6	3	75.0	6	3	US-08-476-134A-28
7	3	75.0	6	3	US-09-230-944-7
8	3	75.0	6	6	US-09-460-384-6
9	3	75.0	6	6	5190920-24
10	3	75.0	6	6	5508208-26
11	3	75.0	7	3	US-09-258-754-162
12	3	75.0	7	3	US-09-042-107-162
13	3	75.0	8	3	US-08-444-818-409
14	3	75.0	9	1	US-07-779-049-1
15	3	75.0	9	1	US-08-080-240-1
16	3	75.0	9	1	US-08-139-054-7
17	3	75.0	9	2	US-08-340-283-137
18	3	75.0	9	3	US-08-159-339A-915
19	3	75.0	9	3	US-08-159-339A-978
20	3	75.0	9	4	US-09-243-560B-3
21	3	75.0	9	4	US-09-243-560B-4
22	3	75.0	9	4	US-09-243-560B-5
23	3	75.0	9	4	US-09-243-560B-6
24	3	75.0	9	4	US-09-719-140-2
25	3	75.0	10	1	US-08-166-195A-11
26	3	75.0	10	1	US-08-166-195A-12
27	3	75.0	10	1	US-08-036-555B-26

1	US-08-469-569-26	10	3	75.0	Sequence 26, Appl
1	US-08-190-788A-61	10	3	75.0	Sequence 61, Appl
1	US-08-190-788A-62	10	3	75.0	Sequence 62, Appl
1	US-08-190-788A-64	10	3	75.0	Sequence 64, Appl
1	US-08-190-788A-238	10	3	75.0	Sequence 238, App
1	US-08-249-322A-26	10	3	75.0	Sequence 26, Appl
1	US-08-566-800A-1	10	3	75.0	Sequence 1, Appl
1	US-08-383-474B-66	10	3	75.0	Sequence 66, Appl
1	US-08-383-474B-67	10	3	75.0	Sequence 67, Appl
1	US-08-383-474B-69	10	3	75.0	Sequence 69, Appl
1	US-08-383-474B-241	10	3	75.0	Sequence 241, App
1	US-08-463-155A-6	10	3	75.0	Sequence 6, Appl
1	US-08-463-432B-6	10	3	75.0	Sequence 6, Appl
1	US-08-465-391A-61	10	3	75.0	Sequence 61, Appl
1	US-08-465-391A-62	10	3	75.0	Sequence 62, Appl
1	US-08-465-391A-64	10	3	75.0	Sequence 64, Appl
1	US-08-465-391A-238	10	3	75.0	Sequence 238, App
1	US-08-469-526A-26	10	3	75.0	Sequence 26, Appl
1	US-08-206-310A-6	10	3	75.0	Sequence 6, Appl
2	US-08-436-772-11	10	3	75.0	Sequence 11, Appl
2	US-08-436-772-12	10	3	75.0	Sequence 12, Appl
2	US-08-436-883B-11	10	3	75.0	Sequence 11, Appl
2	US-08-436-883B-12	10	3	75.0	Sequence 12, Appl
2	US-08-398-010A-6	10	3	75.0	Sequence 6, Appl
2	US-08-734-591A-26	10	3	75.0	Sequence 26, Appl
2	US-08-464-538B-61	10	3	75.0	Sequence 61, Appl
2	US-08-464-538B-62	10	3	75.0	Sequence 62, Appl
2	US-08-464-538B-64	10	3	75.0	Sequence 64, Appl
2	US-08-398-628A-6	10	3	75.0	Sequence 6, Appl
2	US-08-932-589-1	10	3	75.0	Sequence 1, Appl
2	US-08-469-660-26	10	3	75.0	Sequence 26, Appl
2	US-08-463-078E-105	10	3	75.0	Sequence 105, App
2	US-08-463-078E-106	10	3	75.0	Sequence 106, App
2	US-08-463-078E-108	10	3	75.0	Sequence 108, App
2	US-08-463-076E-290	10	3	75.0	Sequence 290, App
2	US-08-399-115A-6	10	3	75.0	Sequence 6, Appl
2	US-08-461-384B-9	10	3	75.0	Sequence 9, Appl
3	US-08-159-339A-933	10	3	75.0	Sequence 933, App
3	US-08-407-207A-6	10	3	75.0	Sequence 6, Appl
3	US-08-890-489-3	10	3	75.0	Sequence 3, Appl
3	US-08-470-335-26	10	3	75.0	Sequence 26, Appl
3	US-09-385-135-3	10	3	75.0	Sequence 3, Appl
3	US-08-735-021-26	10	3	75.0	Sequence 26, Appl
3	US-08-734-664A-26	10	3	75.0	Sequence 26, Appl
3	US-08-470-339-26	10	3	75.0	Sequence 26, Appl
4	US-08-467-602-26	10	3	75.0	Sequence 26, Appl
4	US-09-106-872A-7	10	3	75.0	Sequence 7, Appl
4	US-09-252-404A-10	10	3	75.0	Sequence 10, Appl
4	US-09-252-404A-11	10	3	75.0	Sequence 11, Appl
4	US-09-797-239A-18	10	3	75.0	Sequence 18, Appl
5	PCT-US94-05083C-26	10	3	75.0	Sequence 26, Appl
5	PCT-US95-06846A-26	10	3	75.0	Sequence 26, Appl
11	US-08-036-555B-13	11	3	75.0	Sequence 13, Appl
11	US-08-469-569-13	11	3	75.0	Sequence 13, Appl
11	US-08-249-322A-13	11	3	75.0	Sequence 13, Appl
11	US-08-469-526A-13	11	3	75.0	Sequence 13, Appl
2	US-08-734-591A-13	11	3	75.0	Sequence 13, Appl
2	US-08-469-660-13	11	3	75.0	Sequence 13, Appl
11	US-08-470-335-13	11	3	75.0	Sequence 13, Appl
11	US-08-735-021-13	11	3	75.0	Sequence 13, Appl
3	US-08-734-664A-13	11	3	75.0	Sequence 13, Appl
3	US-08-470-339-13	11	3	75.0	Sequence 13, Appl
11	US-09-347-926-4	11	3	75.0	Sequence 4, Appl
4	US-08-467-602-13	11	3	75.0	Sequence 13, Appl
11	US-10-006-937-2	11	3	75.0	Sequence 2, Appl
5	PCT-US94-05083C-13	11	3	75.0	Sequence 13, Appl
5	PCT-US95-06846A-13	11	3	75.0	Sequence 13, Appl
1	US-08-190-788A-26	12	3	75.0	Sequence 26, Appl
1	US-08-190-788A-59	12	3	75.0	Sequence 59, Appl
1	US-08-190-788A-78	12	3	75.0	Sequence 78, Appl
1	US-08-190-788A-154	12	3	75.0	Sequence 154, App
1	US-08-190-788A-157	12	3	75.0	Sequence 157, App



## ALIGNMENTS

RESULT 1  
US-09-641-803-10  
; Sequence 10, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-10

Query Match 100.0%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4  
Db 1 SEQ 4

RESULT 2  
US-08-328-256-5  
; Sequence 5, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel  
; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-328-256-5  
Query Match 100.0%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SEQ 4  
Db 5 SEQ 8  
RESULT 3  
US-08-292-045-18  
; Sequence 18, Application US/08292045  
; Patent No. 5603005  
; GENERAL INFORMATION:  
; APPLICANT: HERR, JOHN C.  
; TITLE OF INVENTION: PRIMATE INTRA-ACROSOMAL SPERM ANTIGEN  
; TITLE OF INVENTION: FOR USE IN A CONTRACEPTIVE VACCINE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,045  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,551  
; FILING DATE: 03-MAR-1989  
; APPLICATION NUMBER: US 07/481,491  
; FILING DATE: 16-FEB-1990  
; APPLICATION NUMBER: US 07/858,798  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5602005man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 494-109-0 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-292-045-18  
Query Match 75.0%; Score 3; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0; Mismatches 0;

Matches 3; Conservative 0;

QY 2 EQP 4

Db 3 EQP 5

#### RESULT 4

US-08-292-045-19  
; Sequence 19, Application US/08292045  
; Patent No. 5602005  
; GENERAL INFORMATION:  
; APPLICANT: HERR, JOHN C.  
; APPLICANT: WRIGHT, RICHARD M.  
; TITLE OF INVENTION: PRIMATE INTRA-ACROSOMAL SPERM ANTIGEN  
; TITLE OF INVENTION: FOR USE IN A CONTRACEPTIVE VACCINE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,045  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,551  
; FILING DATE: 03-MAR-1989  
; APPLICATION NUMBER: US 07/481,491  
; FILING DATE: 16-FEB-1990  
; APPLICATION NUMBER: US 07/858,798  
; FILING DATE: 27-MAR-1992

ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5602005man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 494-109-0 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-292-045-19

Query Match 75.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0; Mismatches 0; Conservative 0;

QY 2 EQP 4

Db 3 EQP 5

#### RESULT 5

US-08-483-434A-19  
; Sequence 19, Application US/08483434A  
; Patent No. 5648461  
; GENERAL INFORMATION:  
; APPLICANT: EVAL, Jacob

APPLICANT: HAMILTON, Bruce K.  
APPLICANT: TUSZYNSKI, George P.  
TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and  
TITLE OF INVENTION: Therapeutic Use Thereof  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103-2398  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,434A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/450,738  
FILING DATE: 25-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/185,614  
FILING DATE: 24-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,436  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/587,197  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/483,527  
FILING DATE: 22-FEB-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Leary Ph.D., Kathryn  
REGISTRATION NUMBER: 36,317  
REFERENCE/DOCKET NUMBER: 9598-306 (9049)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 567-2020  
TELEFAX: (215) 567-2991  
TELEX: 831-494

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-483-434A-19

Query Match 75.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0; Mismatches 0; Conservative 0;

QY 1 SEQ 3

Db 2 SEQ 4

#### RESULT 6

US-08-476-134A-28  
; Sequence 28, Application US/08476134A  
; Patent No. 6239110  
; GENERAL INFORMATION:  
; APPLICANT: EYAL, JACOB  
; APPLICANT: HAMILTON, BRUCE K.  
; APPLICANT: TUSZYNSKI, GEORGE P.  
; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPONDIN AND THERAPEUTIC USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 07206-0009

```
; CURRENT APPLICATION NUMBER: US/08/476,134A
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/587,197
; PRIOR FILING DATE: 1990-09-24
; PRIOR APPLICATION NUMBER: 07/483,527
; PRIOR FILING DATE: 1990-02-22
; PRIOR APPLICATION NUMBER: 08/450,738
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/185,614
; PRIOR FILING DATE: 1994-01-24
; PRIOR APPLICATION NUMBER: 08/024,436
; PRIOR FILING DATE: 1993-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: analog of thrombospondin
US-08-476-134A-28

Query Match          75.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||
DB      2 SEQ 4

RESULT 7
US-09-230-944-7
; Sequence 7, Application US/09230944
; Patent No. 6277360
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: WATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: Measles Virus Mutant Antigen and Gene Coding for the
; FILE REFERENCE: 0216-0407P
; CURRENT APPLICATION NUMBER: US/09/230,944
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: PCT/JP98/02481
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 9-184285 JAPAN
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Measles virus
; FEATURE:
; OTHER INFORMATION: Attenuated measles virus CAM -70 strain
US-09-230-944-7

Query Match          75.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
      |||
DB      1 EQP 3

RESULT 8
US-09-460-384-6
; Sequence 6, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
```

```
; APPLICANT: EL TAYAR, Nabil
; BLECHNER, Steven
; JAMESON, Brad
; TEPPER, Mark
; TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
; PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
; SAME
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,384
; FILING DATE: 13-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/12312
; FILING DATE: 11-JUN-1998
; APPLICATION NUMBER: US 60/049,470
; FILING DATE: 12-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: EL TAYAR=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-460-384-6

Query Match          75.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
      |||
DB      3 EQP 5

RESULT 9
5190920-24
; Patent No. 5190920
; APPLICANT: EYAL, JACOB; HAMILTON, BRUCE K.; TUSZYNASKI,
; GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:24:
; LENGTH: 6
5190920-24

Query Match          75.0%; Score 3; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SEQ 3  
|||  
Db 2 SEQ 4

RESULT 10  
US-09-258-754-162  
; Patent No. 5506208  
; APPLICANT: EYAL, JACOB; HAMILTON, BRUCE K.; TUSZYNSKI,  
; GEORGE P.  
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF  
; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY  
; NUMBER OF SEQUENCES: 45  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,181  
; FILING DATE: 22-MAR-1995  
; PRIOR APPLICATION NUMBER: 131,565  
; FILING DATE: 04-OCT-1993  
; APPLICATION NUMBER: 895,764  
; FILING DATE: 09-JUN-1992  
; APPLICATION NUMBER: 587,197  
; FILING DATE: 24-SEP-1990  
; SEQ ID NO: 26:  
; LENGTH: 6  
5506208-26

Query Match 75.0%; Score 3; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 2 SEQ 4

RESULT 11  
US-09-258-754-162  
; Sequence 162, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 162  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-162

Query Match 75.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 3 SEQ 5

RESULT 12  
US-09-042-107-162

; Sequence 162, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 162  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-162

Query Match 75.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
|||  
Db 3 SEQ 5

RESULT 13  
US-08-444-818-409  
; Sequence 409, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANEV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 409:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-444-818-409

Query Match 75.0%; Score 3; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 5 SEQ 7

## RESULT 14

US-07-779-049-1  
 ; Sequence 1, Application US/07779049  
 ; Patent No. 5310659  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARAMORI, ICHIRO  
 ; APPLICANT: FURAGAWA, MASAO  
 ; APPLICANT: ONO, HIROKI  
 ; APPLICANT: ISHITANI, YOSUKE  
 ; APPLICANT: TSUMURA, MANA  
 ; APPLICANT: IWAMI, MORITA  
 ; APPLICANT: KOJO, HITOSHI  
 ; TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; ZIP: 22202

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/779,049  
 ; FILING DATE: 19911018  
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 ; NAME: Oblon, No. 5310659man F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 18-723-0  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)521-4500  
 ; TELEFAX: (703)486-2347  
 ; TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: N-terminal  
 ; US-07-779-049-1

Query Match 75.0%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 2 SEQ 4

## RESULT 15

US-08-080-240-1  
 ; Sequence 1, Application US/08080240  
 ; Patent No. 5312750  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARAMORI, ICHIRO  
 ; APPLICANT: FURAGAWA, MASAO  
 ; APPLICANT: ONO, HIROKI

APPLICANT: ISHITANI, YOSUKE  
 APPLICANT: TSUMURA, MANA  
 APPLICANT: IWAMI, MORITA  
 APPLICANT: KOJO, HITOSHI  
 TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSEE: P.C.  
 STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 CITY: Arlington  
 STATE: Virginia  
 ZIP: 22202

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/080,240  
 ; FILING DATE: 19930622  
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 ; NAME: Oblon, No. 5312750man F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 18-803-0 DIV  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)413-3000  
 ; TELEFAX: (703)413-2220  
 ; TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: N-terminal  
 ; US-08-080-240-1

Query Match 75.0%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
 |||  
 Db 2 SEQ 4

## RESULT 16

US-08-139-054-7  
 ; Sequence 7, Application US/08139054  
 ; Patent No. 5578710  
 ; GENERAL INFORMATION:

APPLICANT: Ambrosius, Dorothea  
 APPLICANT: Dony, Carol  
 APPLICANT: Rudolph, Rainer  
 TITLE OF INVENTION: IMPROVED ACTIVATION OF RECOMBINANT  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
 STREET: 1725 K. St., N.W. Suite 1000  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20006

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/139,054  
 ; FILING DATE:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/837,779
; FILING DATE:
; APPLICATION NUMBER: DE P 41 05 480.6
; FILING DATE: 21-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: 920053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)659-2930
; TELEFAX: (202)887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-139-054-7

Query Match 75.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8

RESULT 17
US-08-340-283-137
; Sequence 137, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESSEE: (1320-32-1)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,283
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 385-7914
; TELEFAX: (616) 385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; FRAGMENT TYPE: N-terminal
; US-08-340-283-137

Query Match 75.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 1 EQP 3

RESULT 18
US-08-159-339A-915
; Sequence 915, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 915:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-915

Query Match 75.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 2 SEQ 4
```

```
RESULT 19
US-08-159-339A-978
; Sequence 978, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 978:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-978

Query Match 75.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 20
US-08-243-560B-3
; Sequence 3, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; CURRENT FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-243-560B-3

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-243-560B-3

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 1 SEQ 3

RESULT 21
US-09-243-560B-4
; Sequence 4, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; CURRENT FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-243-560B-4

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 1 SEQ 3

RESULT 22
US-09-243-560B-5
; Sequence 5, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; CURRENT FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-243-560B-5

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 SEQ 3
      |||
Db      1 SEQ 3

RESULT 23
US-09-243-560B-6
; Sequence 6, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; CURRENT FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rabbit
US-09-243-560B-6

Query Match      75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SEQ 3
      |||
Db      1 SEQ 3

RESULT 24
US-09-719-140-2
; Sequence 2, Application US/09719140
; Patent No. 6506555
; GENERAL INFORMATION:
; APPLICANT: ANDRE, PATRICE, ET AL
; TITLE OF INVENTION: NOVEL USE OF HIV PROTEASE INHIBITING COMPOUNDS
; FILE REFERENCE: P06994US00/BAS
; CURRENT APPLICATION NUMBER: US/09/719,140
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: PCT/FR99/01391
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: FR 9807373
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Lymphocytic choriomeningitis virus
US-09-719-140-2

Query Match      75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
      |||
Db      1 EQP 3

RESULT 25
US-08-166-195A-11
; Sequence 11, Application US/08166195A
; Patent No. 5480799
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.

```

---

```

; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a
; TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5480799th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,195A
; FILING DATE: 10 DEC 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470/73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-166-195A-11

Query Match      75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
      |||
Db      6 EQP 8

RESULT 26
US-08-166-195A-12
; Sequence 12, Application US/08166195A
; Patent No. 5480799
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a
; TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5480799th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,195A
; FILING DATE: 10 DEC 1993

```



Query Match	75.0%	Score 3	DB 1	Length 10
Best Local Similarity	100.0%	Pred. No. 1.5e-02		
Matches	3	Conservative 0	Mismatches 0	Indels 0
Gaps	0			
QY	2 EQP 4			
Db	3 EQP 5			
US-08-166-195A-12				
CLASSIFICATION: 435				
ATTORNEY/AGENT INFORMATION:				
NAME: Sibley, Kenneth D.				
REGISTRATION NUMBER: 31,665				
REFERENCE/DOCKET NUMBER: 5470/73				
TELEPHONE: 919-881-3140				
TELEFAX: 919-881-3175				
INFORMATION FOR SEQ ID NO: 12:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 10 amino acids				
TYPE: amino acid				
STRANDEDNESS: single				
TOPOLOGY: linear				
MOLECULE TYPE: peptide				
US-08-166-195A-12				
Query Match	75.0%	Score 3	DB 1	Length 10
Best Local Similarity	100.0%	Pred. No. 1.5e-02		
Matches	3	Conservative 0	Mismatches 0	Indels 0
Gaps	0			
QY	2 EQP 4			
Db	3 EQP 5			
US-08-036-555B-26				
Sequence 26, Application US/08036555B				
Patent No. 5530109				
GENERAL INFORMATION:				
APPLICANT: Goodearl, Andrew; Stroobant, Paul;				
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;				
APPLICANT: Chen, Maio Su; Hiles, Ian				
TITLE OF INVENTION: Glial Mitogenic Factors, Their				
TITLE OF INVENTION: Preparation and Use				
NUMBER OF SEQUENCES: 184				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Felfe & Lynch				
STREET: 805 Third Avenue				
CITY: New York City				
STATE: New York				
COUNTRY: USA				
ZIP: 10022				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage				
COMPUTER: IBM				
OPERATING SYSTEM: PC-DOS				
SOFTWARE: Wordperfect				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/036,555B				
FILING DATE: 24-MAR-1993				
CLASSIFICATION: 435				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: 07/965,173				
FILING DATE: 23-OCT-1992				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: 07/940,389				
FILING DATE: 03-SEP-1992				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: 07/907,138				
FILING DATE: 30-JUN-1992				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: 07/863,703				
FILING DATE: 03-APRIL-1992				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: U.K. 91 07566.3				
FILING DATE: 10-APRIL-1991				
ATTORNEY/AGENT INFORMATION:				
NAME: Tsai, Christine H.				
REGISTRATION NUMBER: 34,266				
REFERENCE/DOCKET NUMBER: LUD 5250.4				
TELEPHONE: (212) 838-3884				
TELEFAX: (212) 838-3884				
INFORMATION FOR SEQ ID NO: 26:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 10				

```
;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-469-569-26

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8

RESULT 29
US-08-190-788A-61
; Sequence 61, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-61

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 2 EQP 4

RESULT 30
US-08-190-788A-62
; Sequence 62, Application US/08190788A
```

```
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-62

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 4 EQP 6

RESULT 31
US-08-190-788A-64
; Sequence 64, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 02-FEB-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,567  
FILING DATE: 05-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 1019.1  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-190-788A-64

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 4 EQP 6

## RESULT 32

US-08-190-788A-238  
Sequence 238, Application US/08190788A  
Patent No. 5608035  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Stephen D.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Baldwin, David N.  
APPLICANT: Jacobs, Jeff W.  
TITLE OF INVENTION: Peptides and Compounds That Bind to the  
TITLE OF INVENTION: IL-1 Receptor  
NUMBER OF SEQUENCES: 312  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies N.V.  
STREET: 4001 Miranda Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,788A  
FILING DATE: 02-FEB-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,567  
FILING DATE: 05-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 1019.1  
TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 238:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-190-788A-238

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 3 EQP 5

## RESULT 33

US-08-249-322A-26  
Sequence 26, Application US/08249322A  
Patent No. 5716930  
GENERAL INFORMATION:  
APPLICANT: Goodearl, Andrew; Stroobant, Paul;  
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;  
APPLICANT: Chen, Mao Su; Hiles, Ian  
TITLE OF INVENTION: Gliial Mitogenic Factors, Their  
TITLE OF INVENTION: Preparation and Use  
NUMBER OF SEQUENCES: 184  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pelfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,322A  
FILING DATE: 26-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/036,555  
FILING DATE: 24-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,173  
FILING DATE: 23-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/940,389  
FILING DATE: 03-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/907,138  
FILING DATE: 30-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/863,703  
FILING DATE: 03-APRIL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.K. 91 07566.3  
FILING DATE: 10-APRIL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tsai, Christine H.  
REGISTRATION NUMBER: 34,266  
REFERENCE/DOCKET NUMBER: LUD 250.4  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-249-322A-26

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 34
US-08-566-800A-1
; Sequence 1, Application US/08566800A
; Patent No. 5736364
; GENERAL INFORMATION:
; APPLICANT: Kelley, Robert F.
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Lee, Geoffrey F.
; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/566,800A
; FILING DATE: 04-Dec-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0958B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-566-800A-1

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 35
US-08-383-474B-66
; Sequence 66, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.

```

```

; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-66

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 EQP 4
Db 2 EQP 4

RESULT 36
US-08-383-474B-67
; Sequence 67, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/383,474B  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1019.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-383-474B-67

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
Db 4 EQP 6

## RESULT 37

US-08-383-474B-69  
; Sequence 69, Application US/08383474B  
; Patent No. 5767234  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Baldwin, David N.  
; APPLICANT: Jacobs, Jeff W.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: the IL-1 Receptor  
; NUMBER OF SEQUENCES: 314  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend & Townsend & Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/383,474B  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1019.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 69:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-383-474B-69

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
Db 4 EQP 6

## RESULT 38

US-08-383-474B-241  
; Sequence 241, Application US/08383474B  
; Patent No. 5767234  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Baldwin, David N.  
; APPLICANT: Jacobs, Jeff W.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: the IL-1 Receptor  
; NUMBER OF SEQUENCES: 314  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend & Townsend & Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/383,474B  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1019.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 241:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-383-474B-241

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
Db 3 EQP 5

```
RESULT 39
US-08-463-155A-6
; Sequence 6, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-155A-6

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8
|||

RESULT 40
US-08-463-432B-6
; Sequence 6, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
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; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-432B-6

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8
|||

RESULT 41
US-08-465-391A-61
; Sequence 61, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331v1el, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 61:
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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-391A-61

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 2 EQP 4

RESULT 42  
US-08-465-391A-62  
; Sequence 62, Application US/08465391A  
; Patent No. 5786331  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Phillippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 405  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,391A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5786331viel, Vern  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-391A-62

Query Match 75.0%; Score 3; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 2 EQP 4

RESULT 43  
US-08-465-391A-64  
; Sequence 64, Application US/08465391A  
; Patent No. 5786331  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Phillippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Pottorf, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 405  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,391A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5786331viel, Vern  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-391A-64

Query Match 75.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db 4 EQP 6

RESULT 44

US-08-465-391A-238  
 ; Sequence 238, Application US/08465391A  
 ; Patent No. 5786331  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barrett, Ronald W.  
 ; APPLICANT: Yanofsky, Stephen D.  
 ; APPLICANT: Baldwin, David  
 ; APPLICANT: Jacobs, Jeff W.  
 ; APPLICANT: Bovy, Philippe R.  
 ; APPLICANT: Leahy, Ellen M.  
 ; APPLICANT: Pottorf, Richard S.  
 ; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
 ; TITLE OF INVENTION: IL-1 Receptor  
 ; NUMBER OF SEQUENCES: 405  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/465,391A  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/373,474  
 ; FILING DATE: 01-FEB-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/190,788  
 ; FILING DATE: 02-FEB-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5786331v1el, Vern  
 ; REGISTRATION NUMBER: 32,483  
 ; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 238:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-465-391A-238

Query Match 75.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No.1.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4  
 Db 3 EQP 5

RESULT 45  
 US-08-469-526A-26  
 ; Sequence 26, Application US/08469526A  
 ; Patent No. 5792849  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodearl, Andrew  
 ; APPLICANT: Stroobant, Paul  
 ; APPLICANT: Minghetti, Luisa  
 ; APPLICANT: Waterfield, Michael  
 ; APPLICANT: Marchionni, Mark

; APPLICANT: Chen, Maio Su  
 ; APPLICANT: Hiles, Ian  
 ; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
 ; TITLE OF INVENTION: PREPARATION AND USE  
 ; NUMBER OF SEQUENCES: 187  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Clark & Elbing LLP  
 ; STREET: 176 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/469,526A  
 ; FILING DATE: 06 June 1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/036,555  
 ; FILING DATE: 24-MAR-1993  
 ; APPLICATION NUMBER: 07/965,173  
 ; FILING DATE: 23-OCT-1992  
 ; APPLICATION NUMBER: 07/940,389  
 ; FILING DATE: 03-SEP-1992  
 ; APPLICATION NUMBER: 07/907,138  
 ; FILING DATE: 03-JUN-1992  
 ; APPLICATION NUMBER: 07/863,703  
 ; FILING DATE: 03-APRIL-1992  
 ; APPLICATION NUMBER: U.K. 91 07566.3  
 ; FILING DATE: 10-APR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bieker-Brady, Kristina  
 ; REGISTRATION NUMBER: 39,109  
 ; REFERENCE/DOCKET NUMBER: 04585/00200A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-428-0200  
 ; TELEFAX: 617-428-7045  
 ; INFORMATION FOR SEQ ID NO: 26:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-469-526A-26

Query Match 75.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No.1.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3  
 Db 6 SEQ 8

RESULT 46  
 US-08-206-310A-6  
 ; Sequence 6, Application US/08206310A  
 ; Patent No. 5795954  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lazarus, Robert A.  
 ; APPLICANT: Dennis, Mark S.  
 ; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ DOMAIN  
 ; TITLE OF INVENTION: PROTEINS  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California



```
;
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/206,310A
; APPLICATION NUMBER: 32,637
; FILING DATE: 04-Mar-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Daryl B.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: 882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1249
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-206-310A-6
;
; Query Match 75.0%; Score 3; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 SEQ 3
Db 6 SEQ 8
;
; RESULT 47
; US-08-436-772-11
; Sequence 11, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,772
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-436-772-11
;
; Query Match 75.0%; Score 3; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 EQP 4
Db 3 EQP 5
;
; RESULT 49
; US-08-436-883B-11
; Sequence 11, Application US/08436883B
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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-436-772-11
;
; Query Match 75.0%; Score 3; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 EQP 4
Db 6 EQP 8
;
; RESULT 48
; US-08-436-772-12
; Sequence 12, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,772
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-436-772-12
;
; Query Match 75.0%; Score 3; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 2 EQP 4
Db 3 EQP 5
;
; RESULT 49
; US-08-436-883B-11
; Sequence 11, Application US/08436883B
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; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-883B-11

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8

RESULT 50
US-08-436-883B-12
; Sequence 12, Application US/08436883B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-883B-12

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 3 EQP 5

RESULT 51
US-08-398-010A-6
; Sequence 6, Application US/08398010A
; Patent No. 5834244
; GENERAL INFORMATION:
; APPLICANT: Robert A. Lazarus and Mark S. Dennis
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
; TITLE OF INVENTION: DOMAIN PROTEINS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,010A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: P0882P1-3
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-010A-6
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Query Match 75.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 6 SEQ 8

RESULT 52  
US-08-734-591A-26  
; Sequence 26, Application US/08734591A  
; Patent No. 5854220  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Hiles, Ian  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 187  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: WordPerfect (Version 7.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,591A  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/470,335  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 03-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 428-0200  
; TELEFAX: (617) 428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: amino acid

Query Match 75.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-734-591A-26

Query Match 75.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 6 SEQ 8

RESULT 53  
US-08-464-538B-61  
; Sequence 61, Application US/08464538B  
; Patent No. 5861476  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Yanofsky, Stephen D.  
; APPLICANT: Baldwin, David  
; APPLICANT: Jacobs, Jeff W.  
; APPLICANT: Bovy, Philippe R.  
; APPLICANT: Leahy, Ellen M.  
; APPLICANT: Portorof, Richard S.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to the  
; TITLE OF INVENTION: IL-1 Receptor  
; NUMBER OF SEQUENCES: 402  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,538B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,474  
; FILING DATE: 01-FEB-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/190,788  
; FILING DATE: 02-FEB-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 16528A-001810  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-464-538B-61

Query Match 75.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	2 EQP 4	3	4 EQP 6
RESULT 54	US-08-464-538B-62	US-08-464-538B-238	US-08-464-538B-64
Sequence 62, Application US/08464538B	Sequence 62, Application US/08464538B	Sequence 238, Application US/08464538B	Sequence 64, Application US/08464538B
Patent No. 5861476	Patent No. 5861476	Patent No. 5861476	Patent No. 5861476
GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.	APPLICANT: Barrett, Ronald W.	APPLICANT: Barrett, Ronald W.	APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.	APPLICANT: Yanofsky, Stephen D.	APPLICANT: Yanofsky, Stephen D.	APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David	APPLICANT: Baldwin, David	APPLICANT: Baldwin, David	APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.	APPLICANT: Jacobs, Jeff W.	APPLICANT: Jacobs, Jeff W.	APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.	APPLICANT: Bovy, Philippe R.	APPLICANT: Bovy, Philippe R.	APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.	APPLICANT: Leahy, Ellen M.	APPLICANT: Leahy, Ellen M.	APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorff, Richard S.	APPLICANT: Pottorff, Richard S.	APPLICANT: Pottorff, Richard S.	APPLICANT: Pottorff, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the	TITLE OF INVENTION: Peptides and Compounds That Bind to the	TITLE OF INVENTION: Peptides and Compounds That Bind to the	TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor	TITLE OF INVENTION: IL-1 Receptor	TITLE OF INVENTION: IL-1 Receptor	TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402	NUMBER OF SEQUENCES: 402	NUMBER OF SEQUENCES: 402	NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP	ADDRESSEE: Townsend and Townsend and Crew LLP	ADDRESSEE: Townsend and Townsend and Crew LLP	ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor	STREET: Two Embarcadero Center, 8th Floor	STREET: Two Embarcadero Center, 8th Floor	STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco	CITY: San Francisco	CITY: San Francisco	CITY: San Francisco
STATE: California	STATE: California	STATE: California	STATE: California
COUNTRY: USA	COUNTRY: USA	COUNTRY: USA	COUNTRY: USA
ZIP: 94111	ZIP: 94111	ZIP: 94111	ZIP: 94111
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B	APPLICATION NUMBER: US/08/464,538B	APPLICATION NUMBER: US 08/190,788	APPLICATION NUMBER: US 08/373,474
FILING DATE: 05-JUN-1995	FILING DATE: 05-JUN-1995	FILING DATE: 02-FEB-1994	FILING DATE: 01-FEB-1995
CLASSIFICATION: 514	CLASSIFICATION: 514	CLASSIFICATION: 514	CLASSIFICATION: 514
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474	APPLICATION NUMBER: US 08/373,474	APPLICATION NUMBER: US 08/190,788	APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995	FILING DATE: 01-FEB-1995	FILING DATE: 02-FEB-1994	FILING DATE: 01-FEB-1995
CLASSIFICATION: 514	CLASSIFICATION: 514	CLASSIFICATION: 514	CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.	NAME: Smith, William M.	NAME: Smith, William M.	NAME: Smith, William M.
REGISTRATION NUMBER: 30,223	REGISTRATION NUMBER: 30,223	REGISTRATION NUMBER: 16528A-001810	REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810	REFERENCE/DOCKET NUMBER: 16528A-001810	REFERENCE/DOCKET NUMBER: 16528A-001810	REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400	TELEPHONE: 415-326-2400	TELEPHONE: 415-326-2400	TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422	TELEFAX: 415-326-2422	TELEFAX: 415-326-2422	TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 62:	INFORMATION FOR SEQ ID NO: 62:	INFORMATION FOR SEQ ID NO: 64:	INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids	LENGTH: 10 amino acids	LENGTH: 10 amino acids	LENGTH: 10 amino acids
TYPE: amino acid	TYPE: amino acid	TYPE: amino acid	TYPE: amino acid
STRANDEDNESS: single	STRANDEDNESS: single	STRANDEDNESS: single	STRANDEDNESS: single
TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear
MOLECULE TYPE: peptide	MOLECULE TYPE: peptide	MOLECULE TYPE: peptide	MOLECULE TYPE: peptide
US-08-464-538B-62	US-08-464-538B-62	US-08-464-538B-64	US-08-464-538B-64
Query Match	Query Match	Query Match	Query Match
Best Local Similarity 100.0%;	Best Local Similarity 100.0%;	Best Local Similarity 100.0%;	Best Local Similarity 100.0%;
Score 3; DB 2; Length 10;	Score 3; DB 2; Length 10;	Score 3; DB 2; Length 10;	Score 3; DB 2; Length 10;
Mismatches 0; Conservative 0; Indels 0;	Mismatches 0; Conservative 0; Indels 0;	Mismatches 0; Conservative 0; Indels 0;	Mismatches 0; Conservative 0; Indels 0;
Matches 3; Gaps 0;	Matches 3; Gaps 0;	Matches 3; Gaps 0;	Matches 3; Gaps 0;
Patent No. 5861476	Patent No. 5861476	Patent No. 5861476	Patent No. 5861476
GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.	APPLICANT: Barrett, Ronald W.	APPLICANT: Barrett, Ronald W.	APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.	APPLICANT: Yanofsky, Stephen D.	APPLICANT: Yanofsky, Stephen D.	APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David	APPLICANT: Baldwin, David	APPLICANT: Baldwin, David	APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.	APPLICANT: Jacobs, Jeff W.	APPLICANT: Jacobs, Jeff W.	APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.	APPLICANT: Bovy, Philippe R.	APPLICANT: Bovy, Philippe R.	APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.	APPLICANT: Leahy, Ellen M.	APPLICANT: Leahy, Ellen M.	APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorff, Richard S.	APPLICANT: Pottorff, Richard S.	APPLICANT: Pottorff, Richard S.	APPLICANT: Pottorff, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the	TITLE OF INVENTION: Peptides and Compounds That Bind to the	TITLE OF INVENTION: Peptides and Compounds That Bind to the	TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor	TITLE OF INVENTION: IL-1 Receptor	TITLE OF INVENTION: IL-1 Receptor	T

NUMBER OF SEQUENCES: 402  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,538B  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/373,474  
FILING DATE: 01-FEB-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 16528A-001810  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 238:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-464-538B-238

Query Match 75.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
DB 3 EQP 5

RESULT 57  
US-08-398-628A-6  
Sequence 6, Application US/08398628A  
Patent No. 5863893  
GENERAL INFORMATION:  
APPLICANT: Robert A. Lazarus and Mark S. Dennis  
TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ  
TITLE OF INVENTION: DOMAIN PROTEINS  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/398,628A

FILING DATE: 03-Mar-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/206310  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0882P1-1  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-398-628A-6

Query Match 75.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
DB 6 SEQ 8

RESULT 58  
US-08-932-589-1  
Sequence 1, Application US/08932589  
Patent No. 5874407  
GENERAL INFORMATION:  
APPLICANT: Kelley, Robert P.  
APPLICANT: Lazarus, Robert A.  
TITLE OF INVENTION: No. 5874407el Factor VIIa Inhibitors  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/932,589  
FILING DATE: 17-Sep-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/566800  
FILING DATE: 12/04/95  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0958BD1  
TELEPHONE: 650/225-8228  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-932-589-1

Query Match

75.0%; Score 3; DB 2; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

Qy 1 SEQ 3
   |||
Db 6 SEQ 8

RESULT 59
US-08-469-660-26
; Sequence 26, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-469-660-26

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
   |||
Db 6 SEQ 8

RESULT 60
US-08-463-076E-105
; Sequence 105, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514

```

```

; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-105

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
   |||
Db 2 EQP 4

RESULT 61
US-08-463-076E-106
; Sequence 106, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514

```

```
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-106

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 4 EQP 6

RESULT 62
US-08-463-076E-108
; Sequence 108, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-076E-290

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 3 EQP 5

RESULT 64
US-08-399-115A-6
; Sequence 6, Application US/08399115A
; Patent No. 5880256
; GENERAL INFORMATION:
; APPLICANT: Robert A. Lazarus and Mark S. Dennis
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
; TITLE OF INVENTION: DOMAIN PROTEINS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,115A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0882P1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-399-115A-6

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
   |||
Db 6 SEQ 8

RESULT 65
US-08-461-384B-9
; Sequence 9, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
```

```
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-384B-9

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
   |||
Db 8 SEQ 10

RESULT 66
US-08-159-339A-933
; Sequence 933, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 933:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-933

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



QY 1 SEQ 3  
Db |||  
2 SEQ 4

## RESULT 67

US-08-407-207A-6  
; Sequence 6, Application US/08407207A  
; Patent No. 6063621  
; GENERAL INFORMATION:  
; APPLICANT: Deeley, Roger G.  
; APPLICANT: Cole, Susan P.C.  
; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PARTIQ RESEARCH & DEVELOPMENT INNOVATIONS  
; STREET: Queen's University at Kingston  
; CITY: Kingston  
; STATE: Ontario  
; COUNTRY: CANADA  
; ZIP: K7L 3N6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/407,207A  
; FILING DATE: 20-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/966,923  
; FILING DATE: 27-OCT-1992  
; APPLICATION NUMBER: 08/029,340  
; FILING DATE: 8-MAR-1993  
; APPLICATION NUMBER: 08/141,893  
; FILING DATE: 26-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steeg, Carol Miernicki  
; REGISTRATION NUMBER: 39,539  
; REFERENCE/DOCKET NUMBER: Q1512  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613) 545-2342  
; TELEFAX: (613) 545-6853  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-407-207A-6

Query Match 75.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No.1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db |||  
8 SEQ 10

## RESULT 68

US-08-890-489-3  
; Sequence 3, Application US/08890489A  
; Patent No. 6090917  
; GENERAL INFORMATION:  
; APPLICANT: UNILEVER UNITED STATES, INC.  
; TITLE OF INVENTION: FROZEN FOOD PRODUCT  
; FILE REFERENCE: FROZEN FOOD PRODUCT 2  
; CURRENT APPLICATION NUMBER: US/08/890,489A  
; CURRENT FILING DATE: 1997-07-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: MIXED GRASS  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: Xaa represents any amino acid found in plant  
; OTHER INFORMATION: protein  
US-08-890-489-3

Query Match 75.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No.1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4  
Db |||  
2 EQP 4

## RESULT 69

US-08-470-335-26  
; Sequence 26, Application US/08470335F  
; Patent No. 6147190  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBANT, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; FILE REFERENCE: PREPARATION AND USE  
; FILE REFERENCE: 04585/00200B  
; CURRENT APPLICATION NUMBER: US/08/470,335F  
; CURRENT FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036,555  
; EARLIER FILING DATE: 1993-03-24  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-08-470-335-26

Query Match 75.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No.1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db |||  
6 SEQ 8

## RESULT 70

US-09-385-135-3  
; Sequence 3, Application US/09385135  
; Patent No. 6162789  
; GENERAL INFORMATION:  
; APPLICANT: UNILEVER UNITED STATES, INC.  
; TITLE OF INVENTION: FROZEN FOOD PRODUCT  
; FILE REFERENCE: FROZEN FOOD PRODUCT 3  
; CURRENT APPLICATION NUMBER: US/09/385,135  
; CURRENT FILING DATE: 1999-08-30  
; EARLIER APPLICATION NUMBER: 08/890,489  
; EARLIER FILING DATE: 1997-07-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT

```

; ORGANISM: MIXED GRASS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)1..(8)
; OTHER INFORMATION: Xaa represents any amino acid found in plant
; OTHER INFORMATION: protein
US-09-385-135-3

```

```

Query Match          75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 2 EQP 4
Db 2 EQP 4

```

## RESULT 71

```

US-08-735-021-26
; Sequence 26, Application US/08735021B
; Patent No. 6194377
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/00200L
; CURRENT APPLICATION NUMBER: US/08/735,021B
; CURRENT FILING DATE: 1996-10-22
; EARLIER APPLICATION NUMBER: 08/472,065
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/965,173
; EARLIER FILING DATE: 1992-10-23
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-735-021-26

```

```

Query Match          75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SEQ 3
Db 6 SEQ 8

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## RESULT 72

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US-08-734-664A-26
; Sequence 26, Application US/08734664A
; Patent No. 6204241
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark

```

```

; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/08/734,664A
; APPLICATION NUMBER: US/08/734,664A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322
; FILING DATE: 26-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-734-664A-26

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Query Match          75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SEQ 3
Db 6 SEQ 8

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## RESULT 73

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US-08-470-339-26
; Sequence 26, Application US/08470339C
; Patent No. 6212286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW

```

APPLICANT: STROOBANT, PAUL  
APPLICANT: MINGHETTI, LUISA  
APPLICANT: WATERFIELD, MICHAEL  
APPLICANT: MARCHIONNI, MARK  
APPLICANT: CHEN, MARIO S.  
APPLICANT: HILES, IAN  
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
FILE REFERENCE: 04585/002008  
CURRENT APPLICATION NUMBER: US/08/470,339C  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/036,555  
EARLIER FILING DATE: 1993-03-24  
EARLIER APPLICATION NUMBER: 07/940,389  
EARLIER FILING DATE: 1992-09-03  
EARLIER APPLICATION NUMBER: 07/907,138  
EARLIER FILING DATE: 1992-06-30  
EARLIER APPLICATION NUMBER: 07/863,703  
EARLIER FILING DATE: 1992-04-03  
EARLIER APPLICATION NUMBER: 91 07566.3 GB  
EARLIER FILING DATE: 1999-04-10  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Bos taurus  
US-08-470-339-26

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 6 SEQ 8

RESULT 74  
US-08-467-602-26  
Sequence 26, Application US/08467602C  
Patent No. 644642  
GENERAL INFORMATION:  
APPLICANT: Sklar, Robert  
APPLICANT: Marchionni, Mark  
APPLICANT: Gwynne, David I.  
TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND  
FILE REFERENCE: 04585/028003  
CURRENT APPLICATION NUMBER: US/08/467,602C  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/209,204  
EARLIER FILING DATE: 1994-03-08  
EARLIER APPLICATION NUMBER: 08/059,022  
EARLIER FILING DATE: 1993-05-06  
NUMBER OF SEQ ID NOS: 420  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Bos taurus  
US-08-467-602-26

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 6 SEQ 8

RESULT 75

US-09-106-872A-7  
Sequence 7, Application US/09106872A  
Patent No. 6486311  
GENERAL INFORMATION:  
APPLICANT: Burks Jr., A. Wesley  
APPLICANT: Stanley, J. Steven  
APPLICANT: Cockrell, Gael  
APPLICANT: King, Nina E.  
APPLICANT: Sampson, Hugh A.  
APPLICANT: Helm, Ricki M.  
APPLICANT: Rannon, Gary A.  
TITLE OF INVENTION: Peanut Allergens and Methods  
FILE REFERENCE: HS 103 CIP  
CURRENT APPLICATION NUMBER: US/09/106,872A  
CURRENT FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: PCT/US96/15222  
PRIOR FILING DATE: 1996-09-23  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Soy  
US-09-106-872A-7

Query Match 75.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3  
Db 8 SEQ 10

Search completed: November 25, 2003, 20:16:07  
Job time : 6.3617 secs